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> O <
O | O IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "seq99var" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "kaml07.key":
seq99 (AA) ID seq99 AA preliminary pattern
1 followed by
2 cf
2 w or a
2 q or l
2 any character
2 x or k or a
2 any character
2 m or l
2 x or k
2 kvr

Selected files:
File : hu.pep

-- Output Parameters --

Format Options:
Nucleic acid code matching Exact Indirect file
Find non-matching hits only No Sequence or key file
Report key used Yes List of hits
Note position of hit Yes Hit display
Display full annotations Yes Name and annotations
Sequence context 50

-- Run Parameters --

Run mode Batch
Time to start comparison now
Notify at end of run No

-----
1 match found in sequence:
tthul ; TOIG of: tthul check: 8418 from: 1 to: 711
(from "hu.pep")
TOIG of: tthul check: 8418 from: 1 to: 711

PI:TFHUL - lactotransferrin precursor [validated] - human
N/Alternate names: lactoferrin
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000
C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169;
A31000; S74119; A03261; A38029
R/Cho. Y.
Submitted to the EMBL Data Library, March 1994
A/Reference number: G06820
A/Accession: G01394
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-711 <CHO>
A/Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237
R/Rey. M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.
Nucleic Acids Res. 18, 5288, 1990
A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.
A/Reference number: S11228; MUID:90384839; PMID:2402455
A/Accession: S11228
A/Molecule type: mRNA
A/Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>
A/Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
Mol. Endocrinol. 6, 1969-1981, 1992
A/Title: Differential molecular mechanism of the estrogen action that regulates
lactoferrin gene in human and mouse.
A/Reference number: A45401; MUID:93125571; PMID:1480183
A/Accession: A45401
A/Molecule type: DNA
A/Residues: 1-15 <TEN>
A/Cross-references: GB:SS2659; NID:G263311; PIDN:AAB24877.1; PID:G263312
A/Experimental source: placenta
A/Note: sequence extracted from NCBI backbone (NCBIP:122202)
R/Powell, M.J.; Ogden, J.E.
Nucleic Acids Res. 18, 4013, 1990
A/Title: Nucleotide sequence of human lactoferrin cDNA.
A/Reference number: S10324; MUID:90326549; PMID:2374734
A/Accession: S10324
A/Molecule type: mRNA
A/Residues: 3-711 <FOV>
A/Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412
R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Biochem. J. 276, 349-355, 1991
A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A/Reference number: S15853; MUID:91264786; PMID:2049066
A/Accession: S15853
A/Status: nucleic acid sequence not shown; not compared with conceptual
translation
A/Molecule type: mRNA
A/Residues: 20-31 <ST1>
A/Accession: S20841
A/Molecule type: protein
A/Residues: 20-28, 'X', 30-31 <ST2>
R/Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A/Title: Isolation of lactoferrin cDNA from a human myeloid library and
expression of mRNA during normal and leukemic myelopoiesis.
A/Reference number: S07160; MUID:88001031; PMID:3477300
A/Accession: S07160
A/Molecule type: mRNA
A/Residues: 436-487, 'A', 489-711 <RAD>
A/Cross-references: EMBL:M18642; NID:G186815; PIDN:AAA86665.1; PID:G386855
R/Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A/Title: Polymorphism and altered methylation of the lactoferrin gene in normal
leukocytes, leukemic cells, and breast cancer.
A/Reference number: A61169; MUID:91235214; PMID:1674448
A/Accession: A61169
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 3-701, 'SWKPVN' <PAN>
A/Experimental source: normal breast tissue
R/Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.;
Spij, G.; Montreuil, J.; Jolles, P.
Eur. J. Biochem. 145, 659-666, 1984
A/Title: Human lactotransferrin: amino acid sequence and structural comparisons
with other transferrins.
A/Reference number: A31000; MUID:85076667; PMID:6510420
A/Accession: A31000
A/Molecule type: protein
A/Residues:
20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-409, '
N', 411, 'SVLMDSEGGFLAR', 412-531, 'E', 533-694, 'R', 696-711 <MET>
A/Note: this is the final paper in a series
R/Houen, G.; Hoegdall, E.V.; Barkholt, V.; Nørskov, L.
Eur. J. Biochem. 241, 303-308, 1996
A/Title: Lactoferrin: similarity to diamine oxidase and purification by
aminoethyl affinity chromatography.
A/Reference number: S74119; MUID:97054624; PMID:8898921
A/Accession: S74119
A/Molecule type: protein
A/Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOV>
A/Experimental source: neutrophil granulocytes
C/Genetics:
A/Gene: GDB:LTf

```

A;Cross-references: GDB:119368; OMIM:150210
A;Map position: 3q21-3q23
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein; iron binding; milk
F;1-19/Domain: signal sequence #status predicted <Sig>
F;20-71/Product: lactotransferrin #status experimental <MAT>
F;21-356/Domain: transferrin repeat homology <TRH1>
F;360-699/Domain: transferrin repeat homology <TRH2>
F;29-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds:
#status experimental
F;157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,428-706,447-669,479-554,513-527,524-537,647-652/Disulfide
bonds: #status predicted

TFHUL Length: 711 January 24, 2003 09:39 Type: P Check: 8418 ..
Found using 'seq99' (kam107.key)

1 MKLVFLVLLFGALGLCLAGRRRSVONCAVSQPEATKCFQWQRMKRVGPPVSCIKRD
39 50
61 SPIQIOIAENRADAVTLDDGGFIYEAGLAPYKLRPVAAE

1 match found in sequence:
trfhuman; Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin
(from "hu.pep")
TOIG of: trf_human check: 8418 from: 1 to: 711

ID TREL_HUMAN STANDARD; PRT; 711 AA.
AC P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H1Z3; Q96KZ4;
AC Q96KZ5;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin A;
Lactoferrin B; Lactoferrin C]
OS LTP OR LF.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=9038483; PubMed=2402455;
RA Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";
RL Nucleic Acids Res. 18:5288-5288(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cho Y.Y.;
RL Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
RN [3]
RP SEQUENCE FROM N.A.
RA Conneely O.M.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Liang Q., Jimenez-Flores R., Richardson T.;
RT "Molecular cloning and sequence analysis of human lactoferrin";
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Wei X., Han J., Rado T.A.;
RT "Human neutrophil lactoferrin coding and 5' flanking region DNA
sequences.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.

RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary Gland;
RA Cheng H., Chen X., Huan L.;
RT "cDNA cloning and sequence analysis of human lactoferrin.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE=Mammary Gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ogden J.E.;
RT "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
LeGrand D., Spik G., Montreuil J., Jolles P.;
RT "Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1984).
RN [10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
Jolles P.;
RT "The present state of the human lactotransferrin sequence. Study and
alignment of the cyanogen bromide fragments and characterization of
N- and C-terminal domains";
RL Biochim. Biophys. Acta 670:243-254(1981).
RN [11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
lactotransferrin";
RL FEBS Lett. 142:107-110(1982).
RN [12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
RN [13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
Sagripanti J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human diferric lactoferrin refined at 2.2-A
resolution.";
RL Acta Crystallogr. D 51:629-646(1995).

[16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
BA Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
binding properties and crystal structure of the histidine-
253-->methionine mutant.";
RL Biochemistry 36:341-346(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347; Jameson G.B., Baker E.N.;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in Aspergillus
awamori.";
RN Acta Crystallogr. D 55:403-407(1999).
[18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
and analysis of ligand-induced conformational change.";
RN Acta Crystallogr. D 54:1319-1335(1998).
[19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1169293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of opioid antagonist peptides derived
from human lactoferrin.";
RN Agric. Biol. Chem. 54:1803-1810(1990).
[20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873063;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
RA Qumsiyah M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
RA Sugar J., Kumarananickavel G., Munier F., Schorderet D.F.,
RA El Matti L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
RA Hejtmancik J.P., Teng C.T.;
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RN Mol. Vision 4:31-32(1998).
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
CC -!- FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST
ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements/>
CC or send an email to license@ebi.ac.uk).

CC EMBL; X53961; CRA37914.1; -
CC EMBL; U07643; AAB60324.1; -
CC EMBL; M93150; AAA36159.1; -
CC EMBL; M83202; AAA59511.1; -
CC EMBL; M83205; AAA58656.1; -
CC EMBL; M8642; AAA86665.1; -
CC EMBL; AF332168; AAG48753.1; -
CC EMBL; BC015822; AAH15822.1; -
CC EMBL; BC015823; AAH15823.1; -
CC EMBL; M73700; AAA59479.1; -
CC EMBL; X52941; CRA37116.1; -
CC EMBL; U95626; AAB57795.1; -
PIR; S11228; TFHUL.
PDB; 1LCF; 31-AUG-94.
PDB; 1LCF; 31-OCT-93.
PDB; 1LFG; 31-JUL-94.
PDB; 1LPH; 31-OCT-93.
PDB; 1LFI; 31-OCT-93.
PDB; 1LGB; 31-AUG-94.
PDB; 1LGC; 31-AUG-94.
PDB; 1BKA; 08-NOV-96.
PDB; 1DSN; 08-MAR-96.
PDB; 1HSE; 12-MAR-97.
PDB; 1VFD; 21-APR-97.
PDB; 1VFE; 01-APR-97.
PDB; 1BOL; 18-NOV-98.
PDB; 1CB6; 12-MAR-99.
GlycoSuiteDB; P02788; -
Genew; HGNC:6720; LTF.
MIM; 150210; -
MIM; 245480; -
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal; Polymorphism; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 711 LACTOTRANSFERRIN.
FT PEPTIDE 339 344 LACTOFERROXIN A.
FT PEPTIDE 544 548 LACTOFERROXIN B.
FT PEPTIDE 681 687 LACTOFERROXIN C.
FT REPEAT 20 364 1.
FT REPEAT 365 711 2.
FT DISULFID 29 65
FT DISULFID 39 56
FT DISULFID 135 218
FT DISULFID 177 193
FT DISULFID 190 201
FT DISULFID 251 265
FT DISULFID 368 400
FT DISULFID 378 391
FT DISULFID 425 706
FT DISULFID 447 669
FT DISULFID 479 554
FT DISULFID 503 697
FT DISULFID 513 527
FT DISULFID 524 537
FT DISULFID 595 609
FT DISULFID 647 652
FT METAL 80
FT METAL 112 112
FT METAL 212 212
FT METAL 273 273
FT METAL 415 415
FT METAL 455 455
FT METAL 548 548
FT METAL 617 617
FT BINDING 141 141 ANION (POTENTIAL).
FT BINDING 485 485 ANION (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC.).
FT CARBOHYD 498 498 N-LINKED (GLCNAC.).
FT VARIANT 30 30 A -> T.
FT VARIANT 48 48 /FTID=VAR_013504.
FT VARIANT 149 149 K -> R (IN DBSNP:1126478).
FT VARIANT 423 423 I -> T (IN DBSNP:1126479).
FT VARIANT 423 423 /FTIG=VAR_013506.
FT VARIANT 580 580 G -> C (IN DBSNP:1042055).
FT VARIANT 580 580 /FTID=VAR_013507.
FT VARIANT 580 580 E -> D (IN DBSNP:2073495).
FT /FTIG=VAR_013508.

```

FT CONFLICT 14 14
PT CONFLICT 21 21
PT CONFLICT 24 24
PT CONFLICT 131 131
PT CONFLICT 141 141
PT CONFLICT 170 170
PT CONFLICT 410 410
PT CONFLICT 416 416
PT CONFLICT 432 432
PT CONFLICT 457 457
PT CONFLICT 488 488
PT CONFLICT 532 532
PT CONFLICT 538 538
PT CONFLICT 695 695
PT STRAND 28 29
PT HELIX 33 48
PT TURN 49 50
PT STRAND 56 57
PT HELIX 62 70
PT TURN 71 72
PT STRAND 76 79
PT HELIX 81 88
PT TURN 90 92
PT STRAND 94 104
PT TURN 105 106
PT STRAND 107 109
PT STRAND 111 119
PT TURN 120 121
PT TURN 126 127
PT TURN 130 131
PT STRAND 133 136
PT TURN 139 140
PT TURN 142 145
PT HELIX 146 155
PT TURN 156 157
PT TURN 161 162
PT HELIX 165 172
PT STRAND 175 177
PT TURN 179 180
PT TURN 183 185
PT HELIX 187 190
PT TURN 191 192
PT TURN 198 201
PT TURN 205 206
PT TURN 208 209
PT HELIX 211 220
PT TURN 221 222
PT STRAND 226 230
PT TURN 231 232
PT HELIX 233 237
PT TURN 241 243
PT HELIX 244 246
PT STRAND 247 251
PT TURN 252 254
PT STRAND 255 258
PT TURN 259 260
PT HELIX 262 264
PT STRAND 268 271
PT STRAND 274 278
PT HELIX 284 298
PT TURN 300 301
PT TURN 308 309
PT TURN 313 314
PT TURN 322 323
PT STRAND 326 329
PT TURN 332 333
PT HELIX 336 340
PT HELIX 342 352
PT STRAND 355 363
PT STRAND 365 370
PT HELIX 372 383
PT TURN 384 387
PT STRAND 389 394

L -> P (IN REF. 4; AAAS8656).
R -> S (IN REF. 7).
MISSING (IN REF. 5).
G -> C (IN REF. 7; AAH15823).
MISSING (IN REF. 9).
DA -> NASVLMDSGGGFLAR (IN REF. 9 AND 11).
G -> E (IN REF. 4; AAAS9511).
A -> G (IN REF. 4; AAAS8656).
A -> T (IN REF. 7).
G -> A (IN REF. 12).
Q -> E (IN REF. 9).
V -> E (IN REF. 7; AAH15822).
K -> R (IN REF. 9 AND 11).

397 405
406 407
411 414
416 424
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428 434
445 446
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455 462
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466 467
470 472
474 475
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483 484
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490 500
511 513
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536 537
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544 545
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562 566
567 567
568 572
573 573
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588 590
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596 597
600 602
603 608
612 614
618 621
623 640
642 643
645 650
653 654
657 658
665 666
669 672
674 675
679 683
685 695
696 697
701 710
SQ SEQUENCE 711 AA; 78338 MW; 1D703BA623685F45 CRC64;

TRELL HUMAN Length: 711 January 24, 2003 09:39 Type: P Check: 8418 ..
Found using 'seq99' (kam107.key)

1 MKLVFLVLLFLGALGLCLAGRRRRSVQWCAVSQPEATKCFQWQNRKVRGPPVSCIKRD
39 50
61 SPIQCIQAIENRADAVTLDOGFYEAGLAPYKLRPVAAE
...

-- Search Statistics --
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of sequences searched: 2
```

Number of sequence hits: 2
Number of separate matches: 2
Number of sequence hits saved: 0

XX Inhibitor against viral infection and proliferation - contains
 PT peptide having sequence from lactoferrin
 XX Claim 1; Page 2; 10pp; Japanese.
 XX The sequence is one of six peptides disclosed as having inhibitory
 CC effect against viral infection. The peptides are derived from
 CC lactoferrin. Their activity is demonstrated against cytomegalovirus.
 XX Sequence 16 AA;
 SQ Query Match 100.0%; Score 51; DB 16; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPPVSCIKR 9
 DB 8 GPPVSCIKR 16
 RESULT 2
 AAY68866
 ID AAY68866 standard; Peptide; 22 AA.
 XX AC AAY68866;
 XX DT 16-MAY-2000 (first entry)
 XX DE Amino acid sequence of human lactoferrin derived from PRL100.
 XX KW Human; lactoferrin; mass production; antibacterial.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 2 /note= "encoded by GC"
 FT Misc-difference 19 /note= "encoded by GC"
 XX WO200004132-A1.
 XX PD 27-JAN-2000.
 XX PF 14-JUL-1999; 99WO-KR00373.
 XX PR 15-JUL-1998; 98KR-0029351.
 XX PR 13-JUL-1999; 98KR-0029042.
 XX (SAMY-) SAMYANG GENEX CORP.
 XX FI Sung CK, Joo IS, Woo MS, Kim SK, Lee JH, Lee KS, Kim YH;
 XX PI Hong SS, Lee H;
 XX WPI; 2000-182411/16.
 XX DR N-PSDB; AAZ60706.
 XX Lactoferrin polypeptides used as e.g. bactericides or growth promoters,
 PT are mass produced from genetically engineered micro-organisms -
 XX Example 2; Page 8; 24pp; English.
 XX The present sequence is encoded by a fragment of the lactoferrin gene
 CC derived from plasmid PRL100. The nucleotide sequence acts as a template
 CC for PCR. The peptide fragment contains the disulphide cysteine bond.
 CC The amplified fragment was cloned, and used in the method of the
 CC invention. The specification describes a method for the mass production
 CC and culture of lactoferrin polypeptides from micro-organisms. The
 CC method uses plasmid vectors to transform yeast cells that are resistant
 CC to lactoferrin polypeptides. As the micro-organism is resistant to the
 CC antibacterial peptide produced, the number of contaminating organisms
 CC is reduced whilst maintaining high polypeptide production rates. The

CC micro-organism is useful in the mass production of lactoferrin
 CC polypeptides. The micro-organism can also be used to produce other
 CC antibacterial peptides that are difficult to mass produce due to their
 CC ability to slow down the growth of, or even kill, host cells.
 XX SQ Sequence 22 AA;
 Query Match 100.0%; Score 51; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPPVSCIKR 9
 DB 14 GPPVSCIKR 22
 RESULT 3
 AAY78004
 ID AAY78004 standard; Peptide; 23 AA.
 XX AC AAY78004;
 XX DT 25-APR-2000 (first entry)
 XX DE Human lactoferrin derived peptide SEQ ID NO:4.
 XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX FN WO200001730-A1.
 XX PD 13-JAN-2000.
 XX PF 06-JUL-1999; 99WO-SE01230.
 XX PR 06-JUL-1998; 98SE-0002441.
 XX PR 17-JUL-1998; 98SE-0002562.
 XX PR 29-DEC-1998; 98SE-0004614.
 XX PA (ASCI-) A+ SCI INVEST AB.
 XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 5; Page 57-58; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX SQ Sequence 23 AA;

Qy 1 GPPVSCIKR 9
|||
Db 15 GPPVSCIKR 23

Key	Location/Qualifiers
2..12	
Peptide	/note= "lactoferrisin antibacterial peptide"
XX	

PN JP07274970-A.
 XX 24-OCT-1995.
 XX 01-APR-1994; 94JP-0085244.
 XX 01-APR-1994; 94JP-0085244.
 XX (MORG) MORINAGA MILK IND CO LTD.
 XX WPI; 1995-399338/51.
 XX Recombinant vector contg. lactoferrisin gene - used to prepare an
 PT antibacterial peptide
 XX Claim 6; Page 11; 18pp; Japanese.
 XX A recombinant vector in which a DNA sequence encoding at least the
 CC generic lactoferrisin antibacterial peptide AAR88216 (specific
 CC examples of which are given in AAR84083-85) is inserted, pref.
 CC downstream of the vector's regulatory sequence, is claimed. Pref.
 CC examples of amino acid sequences contg. the above peptide are
 CC given in AAR88217/18. The regulatory sequence is the tac promoter
 CC from shuttle vector pGEX2, the GAL1 promoter from vector pKOM2 or
 CC Rous Sarcoma Virus long terminal repeat from vector pRSVNot.
 XX
 XX Sequence 25 AA;
 SQ
 Query Match 100.0%; Score 51; DB 16; Length 25;
 Best Local Similarity 100.0%; Pred. NO. 0.051;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPPVSCIKR 9
 DB 15 GPPVSCIKR 23
 RESULT 7
 ID AAW24267 standard; peptide; 25 AA.
 AC AAW24267;
 XX
 XX 15-OCT-1997 (first entry)
 DE Antifungal peptide #3, derived from lactoferrin.
 XX Lactoferrin; hydrolysis; antifungal agent; hydrolysate; food;
 KW azole-type anti-fungal compound; dermatophytosis; dermatomycosis.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Disulfide-bond 3..20
 FT
 XX JP09165342-A.
 XX 24-JUN-1997.
 XX 14-DEC-1995; 95JP-0347405.
 XX 14-DEC-1995; 95JP-0347405.
 XX (MORG) MORINAGA MILK IND CO LTD.
 XX WPI; 1997-381279/35.
 XX Antifungal agents containing azole(s) and lactoferrin hydrolysate -
 PT for treatment of dermatophytosis and dermatomycosis
 XX Claim 4; Page 8; 10pp; Japanese.
 XX The sequences given in AAW24265-72 are peptides which are derived from
 lactoferrin by hydrolysis. These peptides may be used in the antifungal
 agents of the invention which also contain as the active component an
 azole-type anti-fungal compound. The antifungal agents are used for
 treatment of dermatophytosis and dermatomycosis. The antifungal agents
 of this invention show the same as or higher effect at one quarter to
 one sixteenth the dose of known antifungal compounds, so the dose of
 these compounds having adverse reactions can be reduced. Lactoferrin
 hydrolysates have no toxicity since they have been used as a part
 of food.
 XX Sequence 25 AA;
 SQ
 Query Match 100.0%; Score 51; DB 16; Length 25;
 Best Local Similarity 100.0%; Pred. NO. 0.051;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPPVSCIKR 9
 DB 15 GPPVSCIKR 23
 RESULT 8
 ID AAW24268 standard; peptide; 25 AA.
 AC AAW24268;
 XX
 XX 15-OCT-1997 (first entry)
 DE Antifungal peptide #4, derived from lactoferrin.
 XX Lactoferrin; hydrolysis; antifungal agent; hydrolysate; food;
 KW azole-type anti-fungal compound; dermatophytosis; dermatomycosis.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Disulfide-bond 3..20
 FT
 XX JP09165342-A.
 XX 24-JUN-1997.
 XX 14-DEC-1995; 95JP-0347405.
 XX 14-DEC-1995; 95JP-0347405.
 XX (MORG) MORINAGA MILK IND CO LTD.
 XX WPI; 1997-381279/35.
 XX Antifungal agents containing azole(s) and lactoferrin hydrolysate -
 PT for treatment of dermatophytosis and dermatomycosis
 XX Claim 4; Page 9; 10pp; Japanese.
 XX The sequences given in AAW24265-72 are peptides which are derived from
 lactoferrin by hydrolysis. These peptides may be used in the antifungal
 agents of the invention which also contain as the active component an
 azole-type anti-fungal compound. The antifungal agents are used for
 treatment of dermatophytosis and dermatomycosis. The antifungal agents
 of this invention show the same as or higher effect at one quarter to
 one sixteenth the dose of known antifungal compounds, so the dose of
 these compounds having adverse reactions can be reduced. Lactoferrin
 hydrolysates have no toxicity since they have been used as a part
 of food.
 XX Sequence 25 AA;
 SQ
 Query Match 100.0%; Score 51; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. NO. 0.051;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPPVSCIKR 9
 DB 15 GPPVSCIKR 23

Qy 1 GPPVSCIQR 9
Db 15 GPPVSCIQR 23

RESULT 9

AAy07252
ID AAY07252 standard; peptide; 25 AA.

XX AC AAY07252;
XX XX

DT 06-JUL-1999 (first entry)
XX XX

DE Lactoferrin peptide #2.
XX XX

XX Lactoferrin; hydrolysate; quinolone; bactericidal; antibacterial; drug.
XX XX

OS Unidentified.
XX XX

FT Key Location/Qualifiers
FT Disulfide-bond 3..20 /note= "optional"
FT XX

PN JP11092375-A.
XX XX

XX 06-APR-1999.
XX XX

XX 25-SEP-1997; 97JP-0278113.
XX XX

XX 25-SEP-1997; 97JP-0278113.
XX XX

XX (MORG) MORINAGA MILK IND CO LTD.
XX XX

XX WPI; 1999-283486/24.
XX XX

PT New anti-bactericide - for enhancing bactericidal ability of new
XX XX

PT quinolone anti-bactericide
XX XX

PS Claim 4; Page 7; 10pp; Japanese.
XX XX

CC This sequence represents a peptide derived from a lactoferrin hydrolysate
CC which is used with a novel quinolone bactericidal compound to generate an
CC antibacterial composition. Addition of the lactoferrin hydrolysate, or
CC peptides from it, can reduce the dosage of quinolone drugs required in
CC the composition.
XX XX

SQ Sequence 25 AA;
XX XX

Query Match 100.0%; Score 51; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9
Db 15 GPPVSCIQR 23

RESULT 10

AAy83109
ID AAY83109 standard; peptide; 25 AA.

XX AC AAY83109;
XX XX

DT 24-JUL-2000 (first entry)
XX XX

DE Synthetic lactoferrin fragment.
XX XX

XX Lactoferrin; antimicrobial; cytostatic; infection; tumour;
XX sterilisation; wound healing; spermicide; human.
XX XX

OS Synthetic.
XX XX

OS Homo sapiens.
XX XX

PN WO200012541-A2.
XX XX

PD 09-MAR-2000.
XX XX

PF 31-AUG-1999; 99WO-GB02850.
XX XX

PR 28-AUG-1998; 98GB-0018938.
XX XX

PA (ALPH-) ALPHARMA AS.
(GARD/) GARDNER R.
XX XX

PI Svendsen JS, Rekdal O, Sveinbjornsson B, Vorland L;
XX XX

DR WPI; 2000-270793/23.
XX XX

PT Cytotoxic peptides useful as medicament for treating tumors and
bacterial infections, comprises one or more non-genetic bulky and
lipophilic amino acids
XX XX

PS Example 1; Figure 1; 114pp; English.
XX XX

CC Cytotoxic 7-25 mer lactoferrin peptides which comprise three or more
cationic residues and have one or more non-genetic bulky and
lipophilic amino acids have cytostatic and antimicrobial activity.
CC The peptides are useful as medicament for treating bacterial
infections and tumours. They are also useful for sterilising
agents for materials susceptible to microbial contamination. They may
also be used as promoters of wound healing and spermicides. The small
size of the peptides gives them an increased half life and allows
efficient biodelivery. The peptides can be administered without need
for an injection, such as by inhalation or by absorption across the
blood capillaries of the nasal passages. This synthetic lactoferrin
peptide corresponds to amino acids 18-42 of human lactoferrin.
XX XX

SQ Sequence 25 AA;
XX XX

Query Match 100.0%; Score 51; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9
Db 15 GPPVSCIQR 23

RESULT 11

AAy85010
ID AAY85010 standard; peptide; 25 AA.

XX AC AAY85010;
XX XX

DT 20-JUN-2000 (first entry)
XX XX

DE Human lactoferricin peptide LFH(18-42) amino acid sequence.
XX XX

XX Lactoferrin; lactoferricin; antibacterial; bacterial infection;
XX bacterial growth; solid tumour; treatment; human.
XX XX

OS Homo sapiens.
XX XX

PN WO200012542-A2.
XX XX

PD 09-MAR-2000.
XX XX

PF 31-AUG-1999; 99WO-GB02851.
XX XX

PR 28-AUG-1998; 98GB-0018938.
XX XX

PA (ALPH-) ALPHARMA AS.
(GARD/) GARDNER R.
XX XX

PI Svendsen JS, Rekdal O, Sveinbjornsson B, Vorland L;
XX XX

CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 25 AA;

Query Match 100.0%; Score 51; DB 21; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.051; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 GPPVSCIKR 9
 DB 17 GPPVSCIKR 25

RESULT 14
 AAR87907
 ID AAR87907 standard; peptide; 28 AA.

XX AC AAR87907;

DT 01-MAR-1996 (first entry)

XX DE Human lactoferrin (25-52).

XX KW antiviral; lactoferrin;

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Disulfide-bond 13..22

XX FT /note= "optionally this bond may be reduced"

XX PN JP07069915-A.

XX PD 14-MAR-1995.

XX PF 02-SEP-1993; 93JP-0240284.

XX PR 02-SEP-1993; 93JP-0240284.

XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.

XX DR WPI; 1995-144726/19.

XX PT Inhibitor against viral infection and proliferation - contains
 PT peptide having sequence from lactoferrin

XX PS Claim 3; Page 2; 10pp; Japanese.

XX CC The sequence is one of six peptides disclosed as having inhibitory
 CC effect against viral infection. The peptides are derived from
 CC lactoferrin. Their activity is demonstrated against cytomegalovirus.

XX SQ Sequence 28 AA;

Query Match 100.0%; Score 51; DB 16; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
 DB 17 GPPVSCIKR 25

DB 8 GPPVSCIKR 16

RESULT 15

AAV57320
 ID AAV57320 standard; peptide; 29 AA.

XX AC AAV57320;

DT 13-JUN-2000 (first entry)

XX DE Human lactoferrin partial peptide sequence.

XX KW Lactoferrin; anti-microbial; adhesive; coating material; clothing;
 KW waste water treatment; leather; fiber; human.

XX OS Homo sapiens.

XX PN JP2000045182-A.

XX PD 15-FEB-2000.

XX PF 23-JUL-1998; 98JP-0207751.

XX PR 23-JUL-1998; 98JP-0207751.

XX PA (PEPU-) PEPUCHIDO SCI YG.

XX PA (FUJI-) FUJII KAIHATSU KENKYUSHO YG.

XX PA (MARU-) MARUJU KK.

XX DR WPI; 2000-306598/27.

XX PT Antimicrobial fiber for bandage, gauze, sheet and fiber goods comprises
 PT anti-microbial component fixed to fiber by water soluble resin -

XX PS Disclosure; Page 4; 10pp; Japanese.

XX CC The invention provides water soluble resin-based fixing agent which
 CC dissociates the anionic polymer component in water, fixes cationic anti-
 CC microbial component into a fiber to form anti-microbial fiber. Cow or
 CC human lactoferrin peptides may be used as the anti-microbial component
 CC in the anti-microbial fiber of the invention. The agent is useful as
 CC adhesive, coating material, waste water treatment and in fixing
 CC antimicrobial component to a fiber to form antimicrobial fiber useful as
 CC a bandage, gauze, sheet, clothing others or leathers, and fiber goods.
 CC The antimicrobial activity is measured against E. coli, S. aureus,
 CC methicillin-resistant S. aureus and P. aeruginosa. The antimicrobial
 CC fiber formed has excellent antimicrobial activity and wash durability.
 CC The leather used has excellent antimicrobial processing agent. Fixing of
 CC lactoferrin to the fiber is reliable. The present sequence represents a
 CC human lactoferrin partial peptide fragment.

XX SQ Sequence 29 AA;

Query Match 100.0%; Score 51; DB 21; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.059; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 GPPVSCIKR 9

DB 21 GPPVSCIKR 29

Search completed: February 21, 2003, 07:56:46
 Job time : 22.0698 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:50:40 ; Search time 6.69767 Seconds
(without alignments)
39.537 Million cell updates/sec

Title: US-09-743-107B-101
Perfect score: 51
Sequence: 1 GPPVSCIKR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCUTS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	51	100.0	22	4	US-09-508-734-4
2	51	100.0	25	1	US-07-755-161A-10
3	51	100.0	25	1	US-07-891-174-10
4	51	100.0	25	1	US-08-204-487-7
5	51	100.0	29	4	US-09-508-734-8
6	51	100.0	36	1	US-07-755-161A-8
7	51	100.0	36	1	US-07-891-174-8
8	51	100.0	36	1	US-08-356-771-30
9	51	100.0	36	1	US-08-381-984-29
10	51	100.0	47	2	US-08-464-182A-6
11	51	100.0	47	2	US-08-406-271-6
12	51	100.0	50	2	US-08-693-274A-7
13	51	100.0	54	2	US-08-464-182A-2
14	51	100.0	54	2	US-08-406-271-2
15	51	100.0	694	3	US-08-724-586-2
16	51	100.0	694	4	US-09-421-632-2
17	51	100.0	694	4	US-09-332-190-2
18	51	100.0	705	2	US-08-655-640-2
19	51	100.0	708	2	US-08-655-640-4
20	51	100.0	709	1	US-08-154-019-2
21	51	100.0	709	1	US-08-461-333-2
22	51	100.0	709	3	US-08-464-167-2
23	51	100.0	709	3	US-09-158-313-2
24	51	100.0	709	4	US-08-476-798-2
25	51	100.0	711	1	US-08-145-681-2
26	51	100.0	711	1	US-08-250-308-2
27	51	100.0	711	1	US-08-154-019-4

28	51	100.0	711	1	US-08-461-333-4	Sequence 4, Appli
29	51	100.0	711	1	US-08-453-703-2	Sequence 2, Appli
30	51	100.0	711	1	US-08-456-106-2	Sequence 2, Appli
31	51	100.0	711	3	US-08-464-167-4	Sequence 4, Appli
32	51	100.0	711	3	US-08-158-313-4	Sequence 4, Appli
33	51	100.0	711	3	US-08-456-108-2	Sequence 2, Appli
34	51	100.0	711	4	US-08-476-798-4	Sequence 4, Appli
35	51	100.0	711	4	US-09-265-577-2	Sequence 2, Appli
36	51	100.0	711	5	PCT-US93-03614-3	Sequence 2, Appli
37	49	96.1	52	4	US-09-017-043A-3	Sequence 3, Appli
38	49	96.1	53	2	US-08-464-182A-5	Sequence 5, Appli
39	49	96.1	53	2	US-08-406-271-5	Sequence 5, Appli
40	45	88.2	24	4	US-09-508-734-6	Sequence 6, Appli
41	44	86.3	48	2	US-08-693-274A-10	Sequence 10, Appli
42	44	86.3	50	4	US-09-017-043A-5	Sequence 5, Appli
43	44	86.3	52	2	US-08-464-182A-17	Sequence 17, Appli
44	44	86.3	52	2	US-08-406-271-17	Sequence 17, Appli
45	41	80.4	20	1	US-07-755-161A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 4
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4

Query Match 100.0%; Score 51; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
DB 14 GPPVSCIKR 22

RESULT 2
US-07-755-161A-10
; Sequence 10, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb

COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
LOCATION: 21
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

Query Match 100.0%; Score 51; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPPVSCIKR 9
DB 16 GPPVSCIKR 24
RESULT 3
US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:

NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
LOCATION: 21
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

US-07-891-174-10

Query Match 100.0%; Score 51; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9
Db 16 GPPVSCIQR 24

RESULT 4

US-08-204-487-7
Sequence 7, Application US/08204487
Patent No. 5565425

GENERAL INFORMATION:

APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MITSUCHI, WATARU
APPLICANT: TANAKA, SHIGEKI
APPLICANT: DOSAKO, SHUN-ICHI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: UCHIDA, TOSHIKI

TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &

ADDRESSEE: THIBEAULT

STREET: 53 STATE STREET

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/204,487

FILING DATE: 02-MAR-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: CAMPBELL, PAULA A.

REGISTRATION NUMBER: 32,503

REFERENCE/DOCKET NUMBER: FUN-019

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..25
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
OTHER INFORMATION: (18-48)"
US-08-204-487-7

Query Match 100.0%; Score 51; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9
Db 15 GPPVSCIQR 23

RESULT 5

US-09-508-734-8
Sequence 8, Application US/09508734
Patent No. 6423509

GENERAL INFORMATION:

APPLICANT: Samyang Genex Corporation

TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and

FILE REFERENCE: PA/SYG/00139

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: PCT/KR99/00373

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: KR1998-29351

PRIOR FILING DATE: 1998-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71

SEQ ID NO 8

LENGTH: 29

TYPE: PRT

ORGANISM: Homo sapiens

US-09-508-734-8

Query Match 100.0%; Score 51; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9
Db 20 GPPVSCIQR 28

RESULT 6

US-07-755-161A-8
Sequence 8, Application US/07755161A
Patent No. 5304633

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: Antimicrobial Peptides and an

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Weideroth, Lind & Ponack

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 9
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 9 connected by disulfide bond with
thiol group of Cys residue at location 26"
FEATURE:
NAME/KEY: modified site
LOCATION: 26
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 26 connected by disulfide bond with
thiol group of Cys residue at location 9"
FEATURE:
NAME/KEY: modified site
LOCATION: 35
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 35 connected by disulfide bond with
thiol group of Cys residue at location 10 of SEQ ID NO. 9"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:

ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-8
Query Match 100.0%; Score 51; DB 1; Length 36;
Best Local Similarity 100.0%; Pred No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 GPPVSCIKR 9
Db 21 GPPVSCIKR 29
RESULT 7
US-07-891-174-8
Sequence 8, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C. U.S.A.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:

ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 9
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 9 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 26"
FEATURE:
NAME/KEY: modified site
LOCATION: 26
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 26 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 9"
FEATURE:
NAME/KEY: modified site
LOCATION: 35
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 35 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 10 of SEQ ID NO. 9"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-8

Query Match 100.0%; Score 51; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
DB 21 GPPVSCIKR 29

RESULT 8
US-08-256-771-30
Sequence 30, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues at positions 9 and
OTHER INFORMATION: 26 are linked by disulfide bond, and Cys residue at position 10 of SEQ ID NO.
OTHER INFORMATION: by disulfide bond to Cys residue at position 10 of SEQ ID NO.
US-08-256-771-30

Query Match 100.0%; Score 51; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
DB 21 GPPVSCIKR 29

RESULT 9
US-08-381-984-29
Sequence 29, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850

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; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at positions 9
; OTHER INFORMATION: and 26 are linked by disulfide linkage"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at position 35
; OTHER INFORMATION: is linked by disulfide linkage with the cysteine residue at P
; OTHER INFORMATION: SEQ ID NO. 5804555 32"
; US-08-381-984-29

Query Match 100.0%; Score 51; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
Db 21 GPPVSCIKR 29

RESULT 10
US-08-464-182A-6
; Sequence 6, Application US/08464182A
; Patent No. 5849885
; GENERAL INFORMATION:
; APPLICANT: Nuijens, Jan H.
; APPLICANT: Van Veen, Harry H.
; TITLE OF INVENTION: Isolation of Lactoferrin from Milk
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,182A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,271
; FILING DATE: 09-MAR-1995
; CLASSIFICATION: 530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,182A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,271
; FILING DATE: 09-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,321
; FILING DATE: 16-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.

```

```

; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016994-004920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 326-2400
; TELEFAX: (650) 326-2422
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..47
; OTHER INFORMATION: /note= "Lactoferricin H"
; US-08-464-182A-6

Query Match 100.0%; Score 51; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
Db 32 GPPVSCIKR 40

RESULT 11
US-08-406-271-6
; Sequence 6, Application US/08406271
; Patent No. 591913
; GENERAL INFORMATION:
; APPLICANT: Nuyens, Jan H.
; APPLICANT: Van Veen, Harry H.
; TITLE OF INVENTION: Isolation of Lactoferrin from Milk
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: One Market Plaza, Steuart Street Tower, 20th
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,271
; FILING DATE: 09-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,321
; FILING DATE: 16-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016994-004910
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..47

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OTHER INFORMATION: /note= "Lactoferricin H"
US-08-406-271-6

Query Match 100.0%; Score 51; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.021; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9
Db 32 GPPVSCIQR 40

RESULT 12

US-08-693-274A-7
; Sequence 7, Application US/08693274A
; Patent No. 5861491
; GENERAL INFORMATION:
; APPLICANT: Nuijens, Jan H.
; APPLICANT: Van Veen, Harry H.
; TITLE OF INVENTION: Isolation of Lactoferrin from Milk
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,274A
; FILING DATE: 16-OCT-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/464,182
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,271
; FILING DATE: 09-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00583
; FILING DATE: 16-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,321
; FILING DATE: 16-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016994-0049300S
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..50
; OTHER INFORMATION: /note= "HLP cDNA GPE N-terminus"
US-08-693-274A-7

Query Match 100.0%; Score 51; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.023; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9
Db 32 GPPVSCIQR 40

RESULT 13

US-08-464-182A-2
; Sequence 2, Application US/08464182A
; Patent No. 5849885
; GENERAL INFORMATION:
; APPLICANT: Nuijens, Jan H.
; APPLICANT: Van Veen, Harry H.
; TITLE OF INVENTION: Isolation of Lactoferrin from Milk
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,182A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,271
; FILING DATE: 09-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,321
; FILING DATE: 16-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016994-0049200S
; TELEPHONE: (650) 326-2400
; TELEFAX: (650) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..54
; OTHER INFORMATION: /note= "HLP cDNA of GPE"
US-08-464-182A-2

Query Match 100.0%; Score 51; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.024; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9
Db 32 GPPVSCIQR 40

RESULT 14

US-08-406-271-2
; Sequence 2, Application US/08406271
; Patent No. 5919913
; GENERAL INFORMATION:
; APPLICANT: Nuyens, Jan H.
; APPLICANT: Van Veen, Harry H.

;; TITLE OF INVENTION: Isolation of Lactoferrin from Milk
;; NUMBER OF SEQUENCES: 28
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
;; STREET: One Market Plaza, Steuart Street Tower, 20th
;; CITY: San Francisco
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94105
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/406,271
;; FILING DATE: 09-MAR-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/198,321
;; FILING DATE: 16-FEB-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 016994-004910
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 54 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..54
;; OTHER INFORMATION: /note= "HLF cdna of GPE"
US-08-406-271-2

Query Match 100.0%; Score 51; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.024; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIQR 9
|||
Db 32 GPPVSCIQR 40

RESULT 15
US-08-724-586-2
;; Sequence 2, Application US/08724586
;; Patent No. 6066469
;; GENERAL INFORMATION:
;; APPLICANT: Kruzel, Marian L.
;; APPLICANT: Kurecki, Tomasz
;; APPLICANT: Gollnick, Paul D.
;; APPLICANT: Doyle, Darrell J.
;; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
;; LACTOFERRIN
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Jacobson, Price, Holman & Stern
;; STREET: 400 Seventh St. N.W.
;; CITY: Washington D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20004
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/724,586
;; FILING DATE: 30-SEPT-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/238,445
;; FILING DATE: 05-MAY-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Player, William E.
;; REGISTRATION NUMBER: 31,409
;; REFERENCE/DOCKET NUMBER: 10505/P58185C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 638-6666
;; TELEFAX: (202) 393-5350
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 694 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-724-586-2

Query Match 100.0%; Score 51; DB 3; Length 694;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIQR 9
|||
Db 34 GPPVSCIQR 42

Search completed: February 21, 2003, 08:04:28
Job time : 6.69767 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 08:08:15 ; Search time 5.16279 Seconds
(without alignments)
54.162 Million cell updates/sec

Title: US-09-743-107B-101

Perfect score: 51

Sequence: 1 GPPVSCIKR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US03_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	25	9	US-09-798-869-20
2	51	100.0	694	9	US-10-023-096-2
3	44	86.3	25	9	US-09-798-869-22
4	39	76.5	191	9	US-09-989-442-145
5	39	76.5	1924	9	US-09-866-557A-2
6	36	70.6	64	10	US-09-917-340-87
7	36	70.6	64	10	US-09-917-340-88
8	36	70.6	164	9	US-09-854-133-203
9	36	70.6	164	10	US-09-738-973-203
10	35	68.6	162	10	US-09-977-034-24
11	35	68.6	240	10	US-09-925-297-810
12	34	66.7	156	10	US-09-764-870-402
13	33	64.7	33	10	US-09-864-761-45683
14	33	64.7	64	10	US-09-917-340-85
15	33	64.7	75	10	US-09-764-878-165
16	33	64.7	179	9	US-09-924-340-36
17	33	64.7	179	9	US-09-992-600A-36
18	33	64.7	197	9	US-09-905-558C-2
19	33	64.7	231	10	US-09-925-302-474

20	64.7	234	9	US-09-941-831-23	Sequence 23, Appl
21	64.7	234	10	US-09-764-877-1775	Sequence 1775, Ap
22	64.7	26926	9	US-09-759-508B-2	Sequence 2, Appli
23	62.7	143	10	US-09-864-761-37379	Sequence 37379, A
24	61	51	10	US-09-864-761-44156	Sequence 44156, A
25	60.8	65	10	US-09-864-761-35016	Sequence 35016, A
26	60.8	90	10	US-09-925-300-1777	Sequence 1777, Ap
27	60.8	121	9	US-09-974-879-143	Sequence 143, App
28	60.8	138	9	US-09-738-626-3842	Sequence 3842, Ap
29	60.8	144	10	US-09-864-761-37049	Sequence 37049, A
30	60.8	240	10	US-09-864-761-47947	Sequence 47947, A
31	60.8	278	10	US-09-925-301-1245	Sequence 1245, Ap
32	60.8	381	9	US-09-808-602-6	Sequence 6, Appli
33	60.8	381	9	US-09-977-418-22	Sequence 22, Appl
34	60.8	2724	9	US-09-808-602-13	Sequence 13, Appl
35	60.8	2733	9	US-09-808-602-8	Sequence 8, Appli
36	60.8	2764	9	US-09-808-602-80	Sequence 80, Appl
37	60.8	2765	9	US-09-808-602-84	Sequence 84, Appl
38	60.8	2802	9	US-09-808-602-81	Sequence 81, Appl
39	60.8	4861	10	US-09-919-497-70	Sequence 70, Appl
40	58.8	35	10	US-09-864-761-44144	Sequence 44144, A
41	58.8	42	10	US-09-917-340-64	Sequence 64, Appl
42	58.8	50	10	US-09-764-869-985	Sequence 985, App
43	58.8	51	10	US-09-864-761-44562	Sequence 44562, A
44	58.8	53	10	US-09-864-761-48454	Sequence 48454, A
45	58.8	108	9	US-09-789-145-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (VSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798.869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match 100.0%; Score 51; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV 1 GPPVSCIKR 9
DB 15 GPPVSCIKR 23

RESULT 2
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.

APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
Lactoferrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P58185C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-023-096-2

Query Match 100.0%; Score 51; DB 9; Length 694;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIKR 9
Db 34 GPPVSCIKR 42

RESULT 3
US-09-798-869-22
Sequence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 25
TYPE: PRT
ORGANISM: MURINE
US-09-798-869-22

Query Match 86.3%; Score 44; DB 9; Length 25;
Best Local Similarity 66.7%; Pred. No. 0.12;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIKR 9
Db 15 GPPVSCVKK 23

RESULT 4
US-09-389-442-145
Sequence 145, Application US/09989442
Publication No. US20030013649A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PZ08
CURRENT APPLICATION NUMBER: US/09/989,442
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/225,757
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/226,868
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/216,647
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/225,267
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/216,880
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/225,270
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/251,869
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/235,834
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/234,274
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/234,223
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/228,924
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/224,518
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236,369
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/224,519
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,964
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/241,809
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/249,299
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/236,327
PRIOR FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: 60/241,785
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/244,617
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/225,268
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236,368
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/251,856
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/251,868
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/229,344
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/234,997
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: 60/229,343
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,345
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,287
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,513
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/231,413
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/229,509
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/236,367
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/237,039
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,038
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/236,370
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/236,802
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,037
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,040
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/240,960
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/239,935
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/239,937
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/241,787
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,474
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,532
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,216
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,210
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/226,681
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,759
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,213
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/227,182
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,214
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/235,836
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/230,438
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/215,135

PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/225,266
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/249,218
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,208
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,213
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,212
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PRIOR APPLICATION NUMBER: 60/249,244
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PRIOR APPLICATION NUMBER: 60/249,211
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PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,264
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,214
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,297
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/232,400
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/231,242
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/232,081
PRIOR FILING DATE: 2000-09-08
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PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,414
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,244
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/233,064
PRIOR FILING DATE: 2000-09-14
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PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,397
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,399
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,401
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/241,808
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,826
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,786
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,475
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/233,065
PRIOR FILING DATE: 2000-09-14

Query Match 76.5%; Score 39; DB 9; Length 191;
Best Local Similarity 85.7%; Pred. No. 7.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCI 7
|||||

Db 180 GPPVSCL 186

RESULT 5
 US-09-866-557A-2
 ; Sequence 2, Application US/09866557A
 ; Patent No. US20020162126A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hammond, S.
 ; APPLICANT: Hammon, G.
 ; APPLICANT: Beach, D.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RNA INTERFERENCE
 ; FILE REFERENCE: GNCRA-P02-007
 ; CURRENT APPLICATION NUMBER: US/09/866,557A
 ; PRIOR FILING DATE: 2002-03-26
 ; PRIOR APPLICATION NUMBER: 60/189,739
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/243,097
 ; PRIOR FILING DATE: 2000-10-24
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 1924
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-866-557A-2

Query Match 76.5%; Score 39; DB 9; Length 1924;
 Best Local Similarity 62.5%; Pred. No. 74;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 8
 |||:|:|:
 Db 683 GPPWSCVR 690

RESULT 6
 US-09-917-340-87
 ; Sequence 87, Application US/09917340
 ; Patent No. US20020090369A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Murphy, Christopher J.
 ; APPLICANT: McNulty, Jonathan F.
 ; APPLICANT: Reid, Ted W.
 ; TITLE OF INVENTION: Transplant Media
 ; FILE REFERENCE: TPLANT-06468
 ; CURRENT APPLICATION NUMBER: US/09/917,340
 ; CURRENT FILING DATE: 2001-07-29
 ; PRIOR APPLICATION NUMBER: 60/221,632
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: 60/249,602
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/290,932
 ; PRIOR FILING DATE: 2001-05-15
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 87
 ; LENGTH: 64
 ; TYPE: PRT
 ; ORGANISM: Capra hircus
 US-09-917-340-87

Query Match 70.6%; Score 36; DB 10; Length 64;
 Best Local Similarity 55.6%; Pred. No. 8;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
 |||:|:|:
 Db 55 GPPVKCCRK 63

RESULT 7
 US-09-917-340-88
 ; Sequence 88, Application US/09917340

; Patent No. US20020090369A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Murphy, Christopher J.
 ; APPLICANT: McNulty, Jonathan F.
 ; APPLICANT: Reid, Ted W.
 ; TITLE OF INVENTION: Transplant Media
 ; FILE REFERENCE: TPLANT-06468
 ; CURRENT APPLICATION NUMBER: US/09/917,340
 ; CURRENT FILING DATE: 2001-07-29
 ; PRIOR APPLICATION NUMBER: 60/221,632
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: 60/249,602
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/290,932
 ; PRIOR FILING DATE: 2001-05-15
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 88
 ; LENGTH: 64
 ; TYPE: PRT
 ; ORGANISM: Capra hircus
 US-09-917-340-88

Query Match 70.6%; Score 36; DB 10; Length 64;
 Best Local Similarity 55.6%; Pred. No. 8;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
 |||:|:|:
 Db 55 GPPVKCCRK 63

RESULT 8
 US-09-854-133-203
 ; Sequence 203, Application US/09854133
 ; Publication No. US20020183499A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Mohamath, Raedon
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Secrist, Heather
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; FILE REFERENCE: 210121.475C10
 ; CURRENT APPLICATION NUMBER: US/09/854,133
 ; CURRENT FILING DATE: 2001-05-11
 ; NUMBER OF SEQ ID NOS: 735
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 203
 ; LENGTH: 164
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-854-133-203

Query Match 70.6%; Score 36; DB 9; Length 164;
 Best Local Similarity 55.6%; Pred. No. 21;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
 |||:|:|:
 Db 53 GPPVACVKK 61

RESULT 9
 US-09-738-973-203
 ; Sequence 203, Application US/09738973
 ; Patent No. US20020110563A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Fling, Steven P.

; APPLICANT: Mohamath, Raodoh
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Secret, Heather
 ; APPLICANT: Indrias, Carol Yoseph
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Elliot, Mark
 ; APPLICANT: Mannion, Jane
 ; APPLICANT: Kalos, Michael D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.475C9
 ; CURRENT APPLICATION NUMBER: US/09/738,973
 ; CURRENT FILING DATE: 2000-12-14
 ; NUMBER OF SEQ ID NOS: 587
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 203
 ; LENGTH: 164
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-738-973-203

Query Match 70.6%; Score 36; DB 10; Length 164;
 Best Local Similarity 55.6%; Pred. No. 21;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
 |||||
 Db 53 GPSVACVKK 61

RESULT 10
 US-09-977-034-24
 ; Sequence 24, Application US/09977034
 ; Patent No. US20020081664A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lo, Kin-Ming
 ; APPLICANT: Sun, Yaping
 ; APPLICANT: Gallies, Stephen D.
 ; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as
 ; TITLE OF INVENTION: FC Fusion Proteins
 ; FILE REFERENCE: LEX-009
 ; CURRENT APPLICATION NUMBER: US/09/977,034
 ; CURRENT FILING DATE: 2001-10-11
 ; PRIOR APPLICATION NUMBER: US/09/575,503
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: US 60/134,895
 ; PRIOR FILING DATE: 1999-05-19
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 24
 ; LENGTH: 162
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; OTHER INFORMATION: Mouse IFN alpha-4 protein
 ; US-09-977-034-24

Query Match 68.6%; Score 35; DB 10; Length 162;
 Best Local Similarity 71.4%; Pred. No. 31;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPSVCLK 8
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 Db 25 PPSVCLK 31

RESULT 11
 US-09-925-297-810
 ; Sequence 810, Application US/09925297
 ; Patent No. US20020081659A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA105
 ; CURRENT APPLICATION NUMBER: US/09/925,297
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05989
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 928
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 810
 ; LENGTH: 240
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (9)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (77)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (195)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; US-09-925-297-810

Query Match 68.6%; Score 35; DB 10; Length 240;
 Best Local Similarity 66.7%; Pred. No. 45;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
 |||||
 Db 83 GPPVLCPRR 91

RESULT 12
 US-09-764-870-402
 ; Sequence 402, Application US/09764870
 ; Patent No. US20020042386A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P1214
 ; CURRENT APPLICATION NUMBER: US/09/764,870
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 646
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 402
 ; LENGTH: 156
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-764-870-402

Query Match 66.7%; Score 34; DB 10; Length 156;
 Best Local Similarity 83.3%; Pred. No. 44;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSC 6
 |||||
 Db 10 GPPVAC 15

RESULT 13
 US-09-864-761-45683
 ; Sequence 45683, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

```

; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45683
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC015772.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93
; OTHER INFORMATION: EST HUMAN HIT: AW003063.1, EVALUATE 3.00e-10
; OTHER INFORMATION: SWISSPROT HIT: P10286, EVALUATE 8.60e-02
US-09-864-761-45683

Query Match 64.7%; Score 33; DB 10; Length 33;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSC 6
| | | | |
DB 24 GPPVQC 29

RESULT 14
US-09-917-340-85
; Sequence 85, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; APPLICANT: Reid, Ted W.

; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TELANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-917-340-85

Query Match 64.7%; Score 33; DB 10; Length 64;
Best Local Similarity 82.5%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSCIK 8
| | | | |
DB 26 GDPVCLK 33

RESULT 15
US-09-764-878-165
; Sequence 165, Application US/09764878
; Patent No. US20020090615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121
; CURRENT APPLICATION NUMBER: US/09/764,878
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 165
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-878-165

Query Match 64.7%; Score 33; DB 10; Length 79;
Best Local Similarity 62.5%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPVSCIKR 9
| | | | |
DB 32 PPVSCCKK 39

Search completed: February 21, 2003, 08:11:59
Job time : 6.16279 secs
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; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45683
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC015772.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93
; OTHER INFORMATION: EST HUMAN HIT: AW003063.1, EVALUATE 3.00e-10
; OTHER INFORMATION: SWISSPROT HIT: P10286, EVALUATE 8.60e-02
US-09-864-761-45683

Query Match 64.7%; Score 33; DB 10; Length 33;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSC 6
| | | | |
DB 24 GPPVQC 29

RESULT 14
US-09-917-340-85
; Sequence 85, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; APPLICANT: Reid, Ted W.
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:48:01 ; Search time 7.95349 Seconds
(without alignments)
108.784 Million cell updates/sec

Title: US-09-743-107b-101

Perfect score: 51

Sequence: 1 GPPVSCIKR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: pirl.*

2: pirl.*

3: pirl.*

4: pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	711	1 TFHUL	lactotransferrin p
2	44	86.3	707	1 A28438	lactoferrin precu
3	41	80.4	704	2 I47328	carbonic anhydrase
4	37	72.5	636	1 S01384	transferrin - pig
5	36	70.6	155	1 KRCHS	keratin, scale - c
6	36	70.6	170	2 AB2715	conserved hypotet
7	36	70.6	189	2 F97496	hypothetical prote
8	36	70.6	698	1 TFHUP	transferrin precu
9	35	70.6	723	2 T32136	hypothetical prote
10	35	68.6	186	1 IVMSA4	interferon alpha-1
11	35	68.6	262	2 A71575	4-hydroxybenzoate
12	35	68.6	310	2 T31799	hypothetical prote
13	35	68.6	316	1 A38743	lactoferrin - human
14	35	68.6	450	2 D86356	hypothetical prote
15	35	68.6	479	2 F86356	T16E15.2 protein -
16	35	68.6	481	2 F86356	hypothetical prote
17	35	68.6	487	2 C86356	UDP-glucose glucos
18	35	68.6	489	2 H86356	probable UDP-gluc
19	35	68.6	1402	2 I46707	translation initia
20	34	66.7	121	2 AE3598	transposase BME10
21	34	66.7	470	2 A87508	hypothetical prote
22	34	66.7	1752	2 A45407	collagen alpha 3(I
23	34	66.7	3898	1 GNWYTB	genome polyprotein
24	33	64.7	64	2 A47438	airway epithelial
25	33	64.7	185	2 D82418	Mutfr/nudix family
26	33	64.7	185	2 T51003	hypothetical prote
27	33	64.7	187	2 A71328	probable survival
28	33	64.7	219	1 A37243	hemopoietic cell s
29	33	64.7	291	2 A81696	stationary-phase s

30 33 64.7 293 2 A71543
31 33 64.7 314 2 A00482
32 33 64.7 344 2 C72395
33 33 64.7 353 2 D89799
34 33 64.7 401 2 T05025
35 33 64.7 432 2 F70575
36 33 64.7 435 2 T48638
37 33 64.7 467 2 A81148
38 33 64.7 530 2 D70476
39 33 64.7 542 2 H86239
40 33 64.7 586 2 T39457
41 33 64.7 887 1 ICHCL
42 33 64.7 1154 2 T18525
43 33 64.7 1520 1 TVFFA
44 33 64.7 1530 1 S01393
45 33 64.7 26926 1 I38344

probable acid phos
sugar-binding tran
transcription regu
conserved hypotet
heat shock transcr
probable PurA - My
polygalacturonase-
DNA photolysase hom
DNA helicase - Aqu
protein P20B24.8 [
hypothetical prote
E-cadherin precurs
diacylglycerol kin
protein-tyrosine k
DNA-directed RNA p
titin, cardiac mus

ALIGNMENTS

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text change 08-Dec-2000

C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74

R:Cho, Y.

submitted to the EMBL Data Library, March 1994

A:Reference number: G06820

A:Accession: G01394

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-711 <CHO>

A:Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237

R:Rev. M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A:Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A:Reference number: S11228; MUID:90384839; PMID:2402455

A:Accession: S11228

A:Molecule type: mRNA

A:Residues: 1-148, 'T', 150-422, 'C', 424-711 <REV>

A:Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R:Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A:Title: Differential molecular mechanism of the estrogen action that regulates lactofer

A:Reference number: A45401; MUID:93125571; PMID:1480183

A:Molecule type: DNA

A:Residues: 1-15 <TEN>

A:Cross-references: GB:S52659; NID:G263311; PIDN:AAB24877.1; PID:G263312

A:Experimental source: placenta

A>Note: sequence extracted from NCBI backbone (NCBIP:122202)

R:Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A:Title: Nucleotide sequence of human lactoferrin cDNA.

A:Reference number: S10324; MUID:90326549; PMID:2374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <POW>

A:Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A:Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A:Reference number: S15853; MUID:91264786; PMID:2049066

A:Accession: S15853

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 20-31 <ST1>

A:Accession: S20841

A:Molecule type: protein

A:Residues: 20-26, 'X', 30-31 <ST2>

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
 Blood 70, 989-993, 1987
 A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
 A;Reference number: S07160; MUID:88001031; PMID:3477300
 A;Accession: S07160
 A;Molecule type: mRNA
 A;Residues: 436-487, 'A', 489-711 <RAD>
 A;Cross-references: EMBL:M18642; NID:g186815; PIDN:AAA86665.1; PID:g386855
 R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
 Cancer Res. 51, 3037-3043, 1991
 A;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
 A;Reference number: A61169; MUID:91235214; PMID:1674448
 A;Accession: A61169
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 3-701, 'SWKPVN' <PAN>
 A;Experimental source: normal breast tissue
 R;Vet-Boutique, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.; Eur. J. Biochem. 145, 659-666, 1984
 A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with other
 A;Reference number: A31000; MUID:85076667; PMID:6510420
 A;Accession: A31000
 A;Molecule type: protein
 A;Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-400
 A;Note: this is the final paper in a series
 R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norrskov, L.
 Eur. J. Biochem. 241, 303-308, 1996
 A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity chromatography
 A;Reference number: S74119; MUID:97054624; PMID:8898921
 A;Accession: S74119
 A;Molecule type: protein
 A;Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>
 A;Experimental source: neutrophil granulocytes
 C;Genetics:
 A;Gene: GDB:LTF
 A;Cross-references: GDB:119368; OMIM:150210
 A;Map position: 3q21-3q23
 C;Superfamily: transferrin; transferrin repeat homology
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-711/Product: lactotransferrin #status experimental <MAT>
 F;21-356/Domain: transferrin repeat homology <TRH1>
 F;360-699/Domain: transferrin repeat homology <TRH2>
 F;29-65, 39-56, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status experimental
 F;157, 498/Binding site: carbohydrate (asn) (covalent) #status experimental
 F;368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #status experimental

Query Match 100.0%; Score 51; DB 1; Length 711;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
 Db 51 GPPVSCIKR 59

RESULT 2
 A28438
 N;Alternate names: lactotransferrin
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A28438; A1205
 R;Pentecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secretory cells
 A;Reference number: A92596; MUID:87280033; PMID:3611056
 A;Accession: A28438
 A;Molecule type: mRNA
 A;Residues: 3-707 <PEN>
 A;Cross-references: EMBL:J03298
 R;Lin, Y.; Teng, C.T.
 J. Biol. Chem. 266, 21880-21885, 1991

A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
 A;Reference number: A41205; MUID:92042099; PMID:1939212
 A;Accession: A41205
 A;Molecule type: DNA
 A;Residues: 1-15 <LTJ>
 A;Cross-references: GB:M74778
 C;Superfamily: transferrin; transferrin repeat homology
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-707/Product: lactotransferrin #status predicted <MAT>
 F;358-695/Domain: transferrin repeat homology <TRH2>
 F;494/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 86.3%; Score 44; DB 1; Length 707;
 Best Local Similarity 66.7%; Pred. No. 3.1;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
 Db 49 GPPVSCIKR 57

RESULT 3
 I47228
 carbonic anhydrase II inhibitor (transferrin homolog) precursor - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999
 C;Accession: I47228
 R;Roush, E.D.; Fierke, C.A.
 Biochemistry 31, 12536-12542, 1992
 A;Title: Purification and characterization of a carbonic anhydrase II inhibitor from porcine
 A;Reference number: I47228; MUID:93099129; PMID:1463741
 A;Accession: I47228
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-704 <ROU>
 A;Cross-references: EMBL:U36916; NID:g1016329; PIDN:AAB58956.1; PID:g1016330
 C;Genetics:
 A;Gene: PICA
 C;Superfamily: transferrin; transferrin repeat homology
 F;20-350/Domain: transferrin repeat homology <TRH1>

Query Match 80.4%; Score 41; DB 2; Length 704;
 Best Local Similarity 77.8%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
 Db 53 GPPVSCIKR 61

RESULT 4
 S01384
 transferrin - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 11-May-2000
 C;Accession: S01384; A60520; A61573
 R;Baldwin, G.S.; Weinstein, J.
 Nucleic Acids Res. 16, 8720, 1988
 A;Title: Nucleotide sequence of porcine liver transferrin.
 A;Reference number: S01384; MUID:88335629; PMID:3419934
 A;Accession: S01384
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-696 <BAL>
 A;Cross-references: EMBL:X12386; NID:g2126; PIDN:CAA30943.1; PID:g833800
 A;Note: 308-Arg was also found
 R;Baldwin, G.S.; Bacic, T.; Chandler, R.; Grego, B.; Pedersen, J.; Simpson, R.J.; Tch, I
 Comp. Biochem. Physiol. B 95, 261-268, 1990
 A;Title: Isolation of transferrin from porcine gastric mucosa: comparison with porcine
 A;Reference number: A60520; MUID:90227903; PMID:2328566
 A;Accession: A60520

A/Molecule type: protein
A/Residues: 1-8,'X',10-11,'X',13-15 <BA2>
A/Experimental source: gastric mucosa
A/Note: the authors suggest transferrin from gastric mucosa may act in dietary iron uptake
R/Chung, W.C.M.; Chan, S.L.; Shimizu, S.
Int. J. Biochem. 23, 609-616, 1991
A/Title: Purification of transferrins and lactoferrin using DEAE Affi-Gel Blue.
A/Reference number: A61573; MUID:91293379; PMID:2065820
A/Accession: A61573
A/Molecule type: protein
A/Residues: 1-8,'X',10-18,'XE' <CHU>
C/Superfamily: transferrin; transferrin repeat homology
C/Keywords: duplication; glycoprotein; iron transport; plasma
F/1-696/Product: transferrin status predicted <MAT>
F/1-335/Domain: transferrin repeat homology <TRH1>

Query Match 72.5%; Score 37; DB 1; Length 696;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSCIQR 9
|||
Db 33 GPLVSCVKQ 41
|||
|||

RESULT 5
KRCHS
N/Alternate names: chicken keratin, scale - chicken
C/Species: Gallus gallus (chicken)
C/Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 22-Jun-1999
C/Accession: A02851; B60136; I50168
R/Gregg, K.; Wilton, S.D.; Parry, D.A.D.; Rogers, G.E.
EMBO J. 3, 175-178, 1984
A/Title: A comparison of genomic coding sequences for feather and scale keratins: structure
A/Reference number: A90988; MUID:84158528; PMID:6200321
A/Accession: A02851
A/Molecule type: DNA
A/Residues: 1-155 <GRE>
A/Cross-references: GB:X00315; NID:963548; PIDN:CAA25084.1; PID:G63549
R/Wilton, S.D.; Crocker, L.A.; Rogers, G.E.
Biochim. Biophys. Acta 824, 201-208, 1985
A/Title: Isolation and characterization of keratin mRNA from the scale epidermis of the
A/Reference number: A60136; MUID:85122780; PMID:2578818
A/Accession: B60136
A/Molecule type: mRNA
A/Residues: 90-155 <WIL>
A/Cross-references: GB:M25642; NID:G212231; PIDN:AAA48931.1; PID:G212232
A/Note: this mRNA was designated clone CSK12. See entry A60136 for clone CSK9
R/Sawyer, R.H.; Shames, R.B.
Curr. Top. Dev. Biol. 22, 235-253, 1987
A/Title: Expression of beta-keratin genes during development of avian skin appendages.
A/Reference number: I50168; MUID:88003561; PMID:2443313
A/Accession: I50168
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 137-155 <SAW>
A/Cross-references: GB:M28422; NID:G211271; PIDN:AAA48631.1; PID:G211272
C/Superfamily: feather keratin
C/Keywords: duplication; epidermis; fibrous protein; horn; integument; tandem repeat
F/70-128/Region: 13-residue repeats (G-G-S-S-L-G-Y-G-G-L-Y-G-Y)

Query Match 70.6%; Score 36; DB 1; Length 155;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPVSCIQR 9
|||
Db 8 PPTSCIQR 15
|||
|||

RESULT 6
AB2715

conserved hypothetical protein Atul123 [imported] - Agrobacterium tumefaciens (strain C5)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C/Accession: AB2715
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell;
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; PMID:11743193
A/Accession: AB2715
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-170 <KUR>
A/Cross-references: GB:AE008688; PIDN:AA42136.1; PID:gl77739521; GSPDB:GN00186
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: Atul123
A/Map position: circular chromosome

Query Match 70.6%; Score 36; DB 2; Length 170;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPVSCIQR 9
|||
Db 94 PPVECVKQ 101
|||
|||

RESULT 7
F97496
Hypothetical protein AGR_C_2080 [imported] - Agrobacterium tumefaciens (strain C58, Cere;
C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C/Accession: F97496
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A/Reference number: A97359; PMID:11743194
A/Accession: F97496
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-189 <KUR>
A/Cross-references: GB:AE007869; PIDN:AAK86927.1; PID:gl5156157; GSPDB:GN00169
C/Genetics:
A/Gene: AGR_C_2080
A/Map position: circular chromosome

Query Match 70.6%; Score 36; DB 2; Length 189;
Best Local Similarity 62.5%; Pred. No. 28;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPVSCIQR 9
|||
Db 113 PPVECVKQ 120
|||
|||

RESULT 8
TPHUP
transferrin precursor [validated] - human
N/Alternate names: siderophilin
C/Species: Homo sapiens (man)
C/Date: 15-Oct-1982 #sequence_revision 30-Sep-1993 #text_change 08-Dec-2000
C/Accession: A20981; A92417; A94044; A29090; A32739; I51959; I63133; I54011; I68160; A03;
R/Yang, F.; Lum, J.B.; McGill, J.R.; Moore, C.M.; Naylor, S.L.; van Bragt, P.H.; Baldwin,
Proc. Natl. Acad. Sci. U.S.A. 81, 2752-2756, 1984
A/Title: Human transferrin: cDNA characterization and chromosomal localization.
A/Reference number: A20981; MUID:84194084; PMID:6585826
A/Contents: variant C
A/Accession: A20981

A;Molecule type: mRNA
A;Residues: 1-698 <YAN>
A;Cross-references: EMBL:M12530; NID:G339452; PIDN:AAA61140.1; PID:G339453
A;Note: the authors translated the codon CAA for residue 203 as Glu
R;Macgillivray, R.T.A.; Mendez, E.; Shevale, J.G.; Sinha, S.K.; Lineback-Zins, J.; Brew, J. Mol. Cell. Biol. 258, 3543-3553, 1983
A;Title: The primary structure of human serum transferrin. The structures of seven cyano
A;Reference number: A92417; MUID:83160878; PMID:6833213
A;Accession: A92417
A;Molecule type: protein
A;Residues: 20-263, 'E', 265-328, 'N', 330-379, 'SD', 382-435, 'D', 437-557, 'T', 559-560, 'P', 562-
A;Note: the sequence shown is the predominant electrophoretic genetic variant (C or T/C)
R;Patk, I.; Schaeffer, E.; Sidoli, A.; Baralle, F.E.; Cohen, G.N.; Zakin, M.M. Proc. Natl. Acad. Sci. U.S.A. 82, 3149-3153, 1985
A;Title: Organization of the human transferrin gene: direct evidence that it originated
A;Reference number: A94044; MUID:85216459; PMID:3859812
A;Accession: A94044
A;Molecule type: DNA
A;Residues: 73-263, 'E', 265-328, 'N', 330-562 <PAR>
A;Cross-references: EMBL:M11361
R;Adrian, G.S.; Korinek, B.W.; Bowman, B.H.; Yang, F. Gene 49, 167-175, 1986
A;Title: The human transferrin gene: 5' region contains conserved sequences which match
A;Reference number: A29090; MUID:87192006; PMID:3106157
A;Accession: A29090
A;Molecule type: DNA
A;Residues: 1-72, 291-300 <ADR>
A;Cross-references: EMBL:M15673
R;Ruan, G.; Frain, M.; Park, I.; Beaumont, C.; Maessen, G.; Trepatt, J.S.; Zakin, M.M.; Ka Biochem. Biophys. Res. Commun. 119, 273-281, 1984
A;Title: Molecular cloning and sequence analysis of cDNA for human transferrin.
A;Reference number: A32739; MUID:84153910; PMID:6322780
A;Accession: A32739
A;Molecule type: mRNA
A;Residues: 422-690, 'G', 692-698 <UZA>
A;Cross-references: EMBL:M12525; NID:G339468; PIDN:AAA61142.1; PID:G339469
R;Macgillivray, R.T.A.; Mendez, E.; Sinha, S.K.; Sutton, M.R.; Lineback-Zins, J.; Brew, Proc. Natl. Acad. Sci. U.S.A. 79, 2504-2508, 1982
A;Title: The complete amino acid sequence of human serum transferrin.
A;Reference number: A93911; MUID:82222166; PMID:6953407
A;Contents: annotation; disulfide bonds
R;Herzharger, C.L.; Larson, J.L.; Arnold, B.; Rosteck, P.R. Ann. N. Y. Acad. Sci. 646, 140-154, 1991
A;Title: A cloned gene for human transferrin.
A;Reference number: I51959; MUID:92231399; PMID:1809186
A;Accession: I51959
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-698 <RES>
A;Cross-references: GB:S95936; NID:G248647; PIDN:AA822049.1; PID:G248648
R;Duguid, J.R.; Bohmont, C.W.; Liu, N.G.; Tourtelotte, W.W. Proc. Natl. Acad. Sci. U.S.A. 86, 7260-7264, 1989
A;Title: Changes in brain gene expression shared by scrapie and Alzheimer disease.
A;Reference number: I48174; MUID:89386721; PMID:2780570
A;Accession: I63133
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 636-696 <RE2>
A;Cross-references: GB:M26641; NID:G339988; PIDN:AAA61233.1; PID:G339989
R;Schaeffer, E.; Lucero, M.A.; Jeltsch, J.M.; Py, M.C.; Levin, M.J.; Chambon, P.; Cohen, Gene 56, 109-116, 1987
A;Title: Complete structure of the human transferrin gene. Comparison with analogous chi
A;Reference number: I54011; MUID:88056305; PMID:3678832
A;Accession: I54011
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-72 <RE3>
A;Cross-references: GB:M17611; NID:G339480; PIDN:AAA61147.1; PID:G339485
A;Accession: I68160
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 564-698 <RE4>

A;Cross-references: GB:M17614; NID:G339483; PIDN:AAA61148.1; PID:G339486
C;Comment: Each of the two repetitive domains binds a ferric ion and a bicarbonate anion
C;Genetics:
A;Gene: GDB:TF
A;Cross-references: GDB:120432; OMIM:190000
A;Map position: 3q21-3q21
A;Introns: 15/1; 72/3; 119/1; 169/1; 212/2; 231/1; 290/3; 350/1; 401/3; 433/1; 444/1; 45
C;Function:
A;Description: binds iron for delivery into cells
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-698/Product: transferrin #status experimental <MAT>
F;20-350/Domain: transferrin repeat homology <TRH1>
F;356-686/Domain: transferrin repeat homology <TRH2>
F;28-67, 38-58, 137-213, 156-350, 177-193, 180-196, 246-260, 358-615, 364-396, 374-387, 42
F;432, 630/Binding site: carbohydrate (Asn) #status experimental
Query Match 70.6%; Score 36; DB 1; Length 698;
Best Local Similarity 55.6%; Pred. No. 91;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 GPPVSCIKR 9
DB 53 GPSVACVK 61
RESULT 9
T32136
hypothetical protein R07C3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 03-Nov-2000
C;Accession: T32136
R;Lamar, B.; Kramer, J.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid R07C3.
A;Reference number: Z21125
A;Accession: T32136
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-723 <LAM>
A;Cross-references: EMBL:AF016686; PIDN:AA866234.1; GSPDB:GN00020; CSDP:R07C3.4
A;Experimental source: strain Bristol N2; clone R07C3
C;Genetics:
A;Gene: CSDP:R07C3.4
A;Map position: 2
A;Introns: 25/3; 83/3; 149/3; 198/1; 326/2; 420/2; 622/3; 654/1
C;Superfamily: human long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homology
F;133-691/Domain: acetate-CoA ligase homology <ACL>
Query Match 70.6%; Score 36; DB 2; Length 723;
Best Local Similarity 83.3%; Pred. No. 94;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPPVSC 6
DB 497 GPPISC 502
RESULT 10
IVMSA4
interferon alpha-I-4 precursor - mouse
N;Alternate names: MuIFN-alpha-I-4; type I interferon
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 22-Jun-1999
C;Accession: B23087
R;Kelly, K.A.; Pitha, P.M.
Nucleic Acids Res. 13, 805-823, 1985
A;Title: Characterization of a mouse interferon gene locus. I. Isolation of a cluster of
A;Reference number: A93600; MUID:85215516; PMID:2987811
A;Accession: B23087
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-186 <REL>

A:Cross-references: GB:X01973; GB:M15456; GB:M23830; GB:X01967; NID:G51544; PIDN:CAA260d
 C:Genetics:
 A:Map position: 4
 C:Superfamily: interferon alpha
 C:Keywords: antiviral; glycoprotein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:1-186/Product: interferon alpha-I-4 #status predicted <MAT>
 F:25-123,53-158/Bisulfide bonds: #status predicted
 F:102/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 68.6%; Score 35; DB 1; Length 186;
 Best Local Similarity 71.4%; Pred. No. 41;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPVSCIK 8
 |||:|:
 Db 49 PPLSCLK 55

RESULT 11
 A71675
 4-hydroxybenzoate octaprenyltransferase (ubiA) RP686 - Rickettsia prowazekii
 C:Species: Rickettsia prowazekii
 C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
 C:Accession: A71675
 R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U.
 Nature 396, 133-140, 1998
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
 A:Reference number: A71675; MUID:99039499; PMID:9823893
 A:Accession: A71675
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-282 <AND>
 A:Cross-references: GB:AJ235272; GB:AJ235269; NID:G3861033; PIDN:CAA15123.1; PID:G386122
 A:Experimental source: strain Madrid E
 C:Genetics:
 A:Gene: ubiA; RP686
 C:Superfamily: 4-hydroxybenzoate octaprenyltransferase

Query Match 68.6%; Score 35; DB 2; Length 282;
 Best Local Similarity 85.7%; Pred. No. 61;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PVSCIKR 9
 |||:|:
 Db 260 PVNCIKR 266

RESULT 12
 T31799
 hypothetical protein F29G9.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T31799
 R:Langston, Y.
 submitted to the EMBL Data Library, July 1997
 A:Description: The sequence of C. elegans cosmid F29G9.
 A:Reference number: Z21088
 A:Accession: T31799
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-310 <LAN>
 A:Cross-references: EMBL:AF016440; PIDN:AA65905.1; GSPDB:GN00023; CESP:F29G9.4
 A:Experimental source: strain Bristol N2; clone F29G9
 C:Genetics:
 A:Gene: CESP:F29G9.4
 A:Map position: 5
 A:Introns: 36/3; 203/3; 271/1

Query Match 68.6%; Score 35; DB 2; Length 310;
 Best Local Similarity 71.4%; Pred. No. 66;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPVSCIK 8
 |||:|:
 Db 145 PPISCIQ 151

RESULT 13
 A38743
 lorixin - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Sep-1991 #sequence_revision 23-Aug-1996 #text_change 20-Oct-2000
 C:Accession: A38743; A43410
 R:Hohl, D.; Mehrel, T.; Lichti, U.; Turner, M.L.; Roop, D.R.; Steinert, P.M.
 J. Biol. Chem. 266, 5626-5636, 1991
 A:Title: Characterization of human lorixin. Structure and function of a new class of ep:
 A:Reference number: A38743; MUID:91177926; PMID:2007607
 A:Accession: A38743
 A:Molecule type: mRNA
 A:Residues: 1-316 <HOH>
 A:Cross-references: GB:M61120; NID:G187184; PIDN:AAA36180.1; PID:G187185
 A:Note: translation of Met-1 is not shown
 R:Yoneda, K.; Hohl, D.; McBride, O.W.; Wang, M.; Cehre, K.U.; Idler, W.W.; Steinert, P.M.
 J. Biol. Chem. 267, 18060-18066, 1992
 A:Title: The human lorixin gene.
 A:Reference number: A43410; MUID:92388173; PMID:1355480
 A:Accession: A43410
 A:Molecule type: DNA
 A:Residues: 2-151, C, 153-232, C, 234-316 <YON>
 A:Cross-references: GB:M94077; NID:G187186; PIDN:AAA36181.1; PID:G187187
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:112880, NCBIP:112882)
 C:Comment: During the terminal differentiation of epidermal (stratum corneum) cell, this
 n insoluble, cross-linked envelope (the cornified cell envelope) under the plasma membrar
 C:Genetics:
 A:Gene: GDB:LOR
 A:Cross-references: GDB:132049; OMIM:152445
 A:Map position: 1q21-1q21
 A:Introns: #status absent
 A:Note: polymorphisms include variants of different lengths
 C:Superfamily: lorixin
 C:Keywords: cornified cell envelope; disulfide bond; duplication; epidermis; tandem repe:
 F:89/Cross-link: isopeptide (lys) (interchain to Gln-154) (partial) #status experimental
 F:89/Cross-link: isopeptide (lys) (interchain to Gln-220) (partial) #status experimental
 F:154/Cross-link: isopeptide (Gln) (interchain to Lys-89) #status experimental
 F:216/Cross-link: isopeptide (Gln) (interchain to Lys-316) #status experimental
 F:220/Cross-link: isopeptide (Gln) (interchain to Lys-89) #status experimental
 F:316/Cross-link: isopeptide (lys) (interchain to Gln-216) (partial) #status experimental

Query Match 68.6%; Score 35; DB 1; Length 316;
 Best Local Similarity 71.4%; Pred. No. 67;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPVSCIK 8
 |||:|:
 Db 12 PPVDCVK 18

RESULT 14
 D86356
 hypothetical protein T16E15.4 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
 C:Accession: D86356
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.
 C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D86356
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-450 <STO>
A:Cross-references: GB:AE005172; NID:99392678; PIDN:AAF87258.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: flavonol O3-glucosyltransferase

Query Match 68.6%; Score 35; DB 2; Length 450;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFVSCI 7
Db 118 PFVSCI 123

RESULT 15
F86356
Ti6E15.2 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
C:Accession: F86356
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F86356
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <STO>
A:Cross-references: GB:AE005172; NID:99392678; PIDN:AAF87255.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: flavonol O3-glucosyltransferase

Query Match 68.6%; Score 35; DB 2; Length 479;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFVSCI 7
Db 118 PFVSCI 123

Search completed: February 21, 2003, 08:02:53
Job time : 9.95349 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:28:06 ; Search time 3.90698 Seconds
(without alignments)
95.544 Million cell updates/sec

Title: US-09-743-107B-101
Perfect score: 51
Sequence: 1 GPPVSCIKR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	711	1 TRPL_HUMAN	P02788 homo sapien
2	44	86.3	707	1 TRPL_MOUSE	P08071 mus musculus
3	41	80.4	704	1 ICA_PIG	Q29545 sus scrofa
4	38	74.5	1189	1 ITRA_HUMAN	Q9UKX5 homo sapien
5	37	72.5	695	1 TRPL_HORSE	O77811 equus caball
6	37	72.5	696	1 TRFE_PIG	P09571 sus scrofa
7	36	70.6	64	1 BD01_CAPHI	O97946 capra hircu
8	36	70.6	64	1 BD01_SHERP	O19038 ovis aries
9	36	70.6	154	1 KRSC_CHICK	P04459 gallus gall
10	36	70.6	698	1 TRPE_HUMAN	P02787 homo sapien
11	36	70.6	704	1 TRPE_BOVIN	Q29443 bos taurus
12	36	70.6	708	1 TRPL_CAMDR	Q9TUM0 camelus dro
13	35	68.6	186	1 INA4_MOUSE	P07351 mus musculus
14	35	68.6	316	1 LORI_HUMAN	P23490 homo sapien
15	35	68.6	367	1 VE2_HPV54	Q81021 human papil
16	35	68.6	1402	1 IF4G_RABIT	P41110 cryptolagus
17	34	66.7	64	1 BD02_SHEEP	O19039 ovis aries
18	34	66.7	431	1 VE2_HV23	P50769 human papil
19	34	66.7	3898	1 POLG_HCVB	P21530 hog cholera
20	33	64.7	64	1 BD02_HUMAN	O15263 homo sapien
21	33	64.7	64	1 TAP_BOVIN	P25068 bos taurus
22	33	64.7	187	1 SURE_TREPA	O81434 treponema p
23	33	64.7	203	1 SHX_HUMAN	Q9NGF3 homo sapien
24	33	64.7	219	1 CD53_HUMAN	P19397 homo sapien
25	33	64.7	283	1 SURE_CHLMU	Q9PKH4 chlamydia m
26	33	64.7	283	1 SURE_CHLTR	O84220 chlamydia t
27	33	64.7	314	1 SEHL_HUMAN	Q9H418 homo sapien
28	33	64.7	401	1 VE2_HPV1A	P03118 human papil
29	33	64.7	432	1 PURA_MYCTU	O08381 mycobacteri
30	33	64.7	539	1 U175_MOUSE	Q825F4 mus musculus
31	33	64.7	875	1 XLNR_ASPNG	O42804 aspergillus
32	33	64.7	887	1 CAD1_CHICK	P08641 gallus gall
33	33	64.7	1103	1 DP0D_MESAU	P97283 mesocricetu

RESULT 1
TRPL_HUMAN
ID TRPL_HUMAN STANDARD; PRT; 711 AA.
AC P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H1Z3; Q96KZ4;
AC Q96KZ5;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactoferrin precursor (lactoferrin) [Contains: Lactoferrin A;
DE Lactoferrin B; Lactoferrin C].
GN LFP OR LF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90384839; PubMed=2402455;
RA Ray M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";
RL Nucleic Acids Res. 18:5288-5288(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cho Y.Y.;
RL Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
RN [3]
RP SEQUENCE FROM N.A.
RA Conneely O.N.;
RT Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Liang Q., Jimenez-Flores R., Richardson T.;
RT "Molecular cloning and sequence analysis of human lactoferrin.";
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Wei X., Han J., Rado T.A.;
RT "Human neutrophil lactoferrin coding and 5' flanking region DNA
sequences.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cheng H., Chen X., Huan L.;
RT "cDNA cloning and sequence analysis of human lactoferrin.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [8]

34 33 64.7 1154 1 KOGD_MESAU
35 33 64.7 1520 1 ABL_DROME
36 33 64.7 1530 1 RPCI_TRIEB
37 32 62.7 128 1 YQ82_CABEL
38 32 62.7 362 1 INX1_DROME
39 32 62.7 390 1 VE2_CREVK
40 32 62.7 395 1 INX3_DROME
41 32 62.7 464 1 NR0T_HUMAN
42 32 62.7 602 1 SP08_YEAST
43 32 62.7 697 1 TRFE_MOUSE
44 32 62.7 698 1 TRFE_RAT
45 32 62.7 728 1 PKPI_MOUSE

ALIGNMENTS

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ogden J.E.;
RT "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
RX LeGrand G., Spik G., Montreuil J., Jolles P.;
RT "Human lactoferrin: amino acid sequence and structural
RT comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1984).
RN [10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RX Jolles P.;
RT "The present state of the human lactotransferrin sequence. Study and
RT alignment of the cyanogen bromide fragments and characterization of
RT N- and C-terminal domains.";
RL Biochim. Biophys. Acta 670:243-254(1981).
RN [11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
RX Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
RT lactotransferrin.";
RL FEBS Lett. 142:107-110(1982).
RN [12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=8801031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
RN [13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie M.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nnan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Guo L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sagripanti J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human diferric lactoferrin refined at 2.2-A
RT resolution.";
RL Acta Crystallogr. D 51:629-646(1995).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
RA Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RT 253--methionine mutant.";
RL Biochemistry 36:341-346(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in *Aspergillus*
RT *awamori*.";
RL Acta Crystallogr. D 55:403-407(1999).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
RT and analysis of ligand-induced conformational change.";
RL Acta Crystallogr. D 54:1319-1335(1998).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Ito K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of opioid antagonist peptides derived
RT from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810(1990).
RN [20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., O'Brien G., Han L., Ahmed M.N.,
RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
RA Sugar J., Kumaranickavel G., Munier F., Schorderet D.F.,
RA El Matrici L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
RA Hejmancik J.F., Teng C.T.;
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RL Mol. Vision 4:31-32(1998).
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -!- FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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CC
CC EMBL; X53961; CAA37914.1; -
CC EMBL; U07643; AAB60324.1; -
CC EMBL; M93150; AAA36159.1; -
CC EMBL; M83202; AAA59511.1; -
CC EMBL; M83205; AAA58656.1; -
CC EMBL; M18642; AAA86665.1; -
CC EMBL; AF332168; AAG48753.1; -
CC EMBL; BC015822; AAH15822.1; -
CC EMBL; BC015823; AAH15823.1; -
CC EMBL; M73700; AAA59479.1; -
CC EMBL; X52941; CAA37116.1; -
CC EMBL; U95626; AAB57795.1; -
CC PIR; S11228; TFHUL.
CC PDB; 1ILCF; 31-AUG-94.
CC PDB; 1ILCT; 31-OCT-93.
CC PDB; 1LFG; 31-JUL-94.
CC PDB; 1LFH; 31-OCT-93.
CC PDB; 1LFI; 31-OCT-93.
CC PDB; 1LGB; 31-AUG-94.
CC PDB; 1LGC; 31-AUG-94.
CC PDB; 1BXA; 08-NOV-96.
CC PDB; 1DSN; 08-MAR-96.
CC PDB; 1HSE; 12-MAR-97.
CC PDB; 1VFD; 21-APR-97.


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Query Match 100.0%; Score 51; DB 1; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIQR 9
DB 51 GPPVSCIQR 59

RESULT 2
TRFL_MOUSE STANDARD; PRT; 707 AA.
AC P08071; P70690; Q61799; Q922P2;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN LTF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=87280033; PubMed=3611056;
RA Pentecost B.T.; Teng C.T.;
RT "Lactotransferrin is the major estrogen inducible protein of mouse
RT uterine secretions."
RL J. Biol. Chem. 262:10134-10139(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Morishita K.;
RT Submitted (NOV-1996) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBSJ databases.
RN [4]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=92042099; PubMed=1939212;
RA Liu Y.; Teng C.T.;
RT "Characterization of estrogen-responsive mouse lactoferrin promoter."
RL J. Biol. Chem. 266:21880-21885(1991)
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -!- SUBUNIT: MONOMER.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC -----
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CC -----
DR EMBL; J03298; AAA40525.1; -
DR EMBL; D88510; BAA1363.1; -
DR EMBL; BC006904; AAA06904.1; -
DR EMBL; M74778; AAA39427.1; -
DR PIR; A28438; A28438.
DR HSP; P02788; ICB6.
DR MGD; MGI:96837; Itf.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PRO0422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.

DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal.
FT CHAIN 1 19 BY SIMILARITY.
FT REPEAT 20 707 LACTOTRANSFERRIN.
FT REPEAT 20 357 1.
FT REPEAT 358 707 2.
FT DISULFID 27 63 BY SIMILARITY.
FT DISULFID 37 54 BY SIMILARITY.
FT DISULFID 133 216 BY SIMILARITY.
FT DISULFID 175 191 BY SIMILARITY.
FT DISULFID 188 199 BY SIMILARITY.
FT DISULFID 249 263 BY SIMILARITY.
FT DISULFID 366 398 BY SIMILARITY.
FT DISULFID 376 389 BY SIMILARITY.
FT DISULFID 423 702 BY SIMILARITY.
FT DISULFID 443 665 BY SIMILARITY.
FT DISULFID 475 550 BY SIMILARITY.
FT DISULFID 499 693 BY SIMILARITY.
FT DISULFID 509 523 BY SIMILARITY.
FT DISULFID 520 533 BY SIMILARITY.
FT DISULFID 591 605 BY SIMILARITY.
FT DISULFID 643 648 BY SIMILARITY.
FT METAL 78 78 IRON 1 (BY SIMILARITY).
FT METAL 110 110 IRON 1 (BY SIMILARITY).
FT METAL 210 210 IRON 1 (BY SIMILARITY).
FT METAL 271 271 IRON 1 (BY SIMILARITY).
FT METAL 413 413 IRON 2 (BY SIMILARITY).
FT METAL 451 451 IRON 2 (BY SIMILARITY).
FT METAL 544 544 IRON 2 (BY SIMILARITY).
FT METAL 613 613 IRON 2 (BY SIMILARITY).
FT BINDING 139 139 ANION (POTENTIAL).
FT BINDING 481 481 ANION (POTENTIAL).
FT CARBOHYD 118 118 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 494 494 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 1 2 MR -> IQG (IN REF. 1).
FT CONFLICT 25 25 R -> Q (IN REF. 2).
FT CONFLICT 82 82 S -> L (IN REF. 2).
FT CONFLICT 359 359 M -> T (IN REF. 2).
FT CONFLICT 382 382 A -> D (IN REF. 1).
FT CONFLICT 449 449 E -> G (IN REF. 2).
FT CONFLICT 629 629 L -> V (IN REF. 1).
SQ SEQUENCE 707 AA; 77865 MW; F26AE0340A4C19A8 CRC64;

Query Match 86.3%; Score 44; DB 1; Length 707;
Best Local Similarity 66.7%; Pred. No. 0.72;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIQR 9
DB 49 GPPVSCIQR 57

RESULT 3
ICA_PIG STANDARD; PRT; 704 AA.
ID ICA_PIG
AC Q29545;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Inhibitor of carbonic anhydrase precursor.
GN ICA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97254619; PubMed=9100029;
RA Wuebbens M.W.; Roush E.D.; Decastro C.M.; Fierke C.A.;
RT "Cloning, sequencing, and recombinant expression of the porcine
```

RT inhibitor of carbonic anhydrase; a novel member of the transferrin family".

RL Biochemistry 36:4327-4336(1997).

RN [2]

RP CHARACTERIZATION. PubMed=1463741;

RX MEDLINE=93099129; PubMed=1463741;

RA Roush E.D., Fierke C.A.;

RT "Purification and characterization of a carbonic anhydrase II inhibitor from porcine plasma".

RL Biochemistry 31:12536-12542(1992).

CC -1- FUNCTION: SPECIFICALLY BINDS AND INHIBITS CARBONIC ANHYDRASE II

CC -1- WITH NANOMOLAR AFFINITY.

CC -1- SUBUNIT: MONOMER.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: PLASMA.

CC -1- PTM: N-GLYCOSYLATED.

CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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CC -----

CC EMBL: U36916; AAB58956.1; -

CC HSPSP; P19134; ITFD.

CC InterPro: IPR001156; Transferrin.

CC Pfam: PF00405; transferrin; 2.

CC PRINTS: PR00422; TRANSFERRIN.

CC SMART: SMC0094; TR_FER; 2.

CC PROSITE: PS00205; TRANSFERRIN_1; 2.

CC PROSITE: PS00206; TRANSFERRIN_2; 1.

CC PROSITE: PS00207; TRANSFERRIN_3; 2.

CC KW Glycoprotein; Signal.

CC FT SIGNAL 1 19 POTENTIAL.

CC FT CHAIN 20 704 INHIBITOR OF CARBONIC ANHYDRASE.

CC FT CARBOHYD 491 491 N-LINKED (GLCNAC...) (POTENTIAL).

CC SQ SEQUENCE 704 AA; 77634 MW; 16BB0E65193E336 CRC64;

Query Match 80.4%; Score 41; DB 1; Length 704;

Best Local Similarity 77.8%; Pred. No. 2.7;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPPVSCIKS 9

Db 53 GPHVSCVKR 61

RESULT 4

ID ITAH HUMAN STANDARD; PRT; 1189 AA.

AC Q9UKX5; Q9UKQ1;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Integrin alpha-11 precursor.

GN ITG11.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RI [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal heart, and Osteoblast;

RX MEDLINE=99417678; PubMed=10486209;

RA Lehnert K., Ni J., Leung E., Gough S.M., Weaver A., Yao W.P., Liu D., Wang S.-X., Morris C.M., Kriessansen G.W.;

RT "Cloning, sequence analysis, and chromosomal localization of the novel human integrin alpha11 subunit (ITG11).";

RL Genomics 60:179-187(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal muscle, and Uterus;

RX MEDLINE=9395147; PubMed=10464311;

RA Velling T., Kusche-Gullberg M., Seijersen T., Gullberg D.;

RT "cDNA Cloning and Chromosomal Localization of Human alpha(11) Integrin. A collagen-binding, 1 domain-containing, beta(1)-associated integrin alpha-chain present in muscle tissues.";

RL J. Biol. Chem. 274:25735-25742(1999).

RN [3]

RP SEQUENCE OF 954-1188 FROM N.A.

RC TISSUE=Fibroblast;

RA Andreu N., Estivill X., Escarceller M., Sunoy L.;

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: INTEGRIN ALPHA-11/BETA-1 IS A RECEPTOR FOR COLLAGEN.

CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-11 ASSOCIATES WITH BETA-1.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- TISSUE SPECIFICITY: ACCORDING REF.2 HIGHEST LEVELS IN UTERUS AND HEART. INTERMEDIATE LEVELS IN SKELETAL MUSCLE AND INTERMEDIATE TO LOW LEVELS IN PANCREAS, KIDNEY AND PLACENTA. ACCORDING REF.1 ALSO FOUND IN BRAIN, COLON, LUNG, SMALL INTESTINE, STOMACH, TESTIS, SALIVARY GLANDS, THYROID GLANDS AND PROSTATE. VERY LOW LEVELS IN PERIPHERAL BLOOD LYMPHOCYTES, FETAL BRAIN AND FETAL LIVER.

CC -1- DEVELOPMENTAL STAGE: STRONGLY UP-REGULATED IN DIFFERENTIATING FETAL MUSCLE CELLS (IN VITRO).

CC -1- DOMAIN: THE INTEGRIN 1-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH 1-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.

CC -1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.

CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.

CC -1- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.

CC -----

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CC -----

CC EMBL: AF109681; AAF01258.1; -

CC EMBL: AF137378; AAD51919.2; -

CC EMBL: AL359064; CAB94392.1; -

CC HSPSP; P17301; IAOX.

CC Genew; HGNC:6136; ITG11.

CC MIM: 604789; -

CC InterPro: IPR000413; Integrin_alpha.

CC InterPro: IPR002035; VWF_A.

CC Pfam: PF00092; vwa; 1.

CC Pfam: PF01839; FG-GAP; 5.

CC PRINTS: PR01185; INTEGRINA.

CC PRINTS: PR00453; VWFADOMAIN.

CC SMART: SMO0191; Int_alpha; 5.

CC SMART: SMO0327; VWF_1

CC PROSITE: PS00242; INTEGRIN_ALPHA; FALSE_NEG.

CC PROSITE: PS50234; VWFA; 1.

CC Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane; Signal; Repeat; Calcium; Magnesium; Polymorphism.

CC SIGNAL 1 22 POTENTIAL.

CC CHAIN 23 1189 INTEGRIN ALPHA-11.

CC DOMAIN 23 1142 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 1143 1165 POTENTIAL.

CC DOMAIN 1166 1189 CYTOPLASMIC (POTENTIAL).

CC REPEAT 38 94 FG-GAP 1.

CC REPEAT 102 163 FG-GAP 2.

CC DOMAIN 167 345 VWFA.

CC REPEAT 359 420 FG-GAP 3.

CC REPEAT 422 475 FG-GAP 4.

CC REPEAT 477 537 FG-GAP 5.

CC REPEAT 539 598 FG-GAP 6.

CC REPEAT 601 653 FG-GAP 7.

CC DOMAIN 1154 1162 POLY-LEU.

CC DOMAIN 1174 1177 POLY-ARG.

CC CA_BIND 488 496 POTENTIAL.


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RESULT 6
TRFE_PIG
ID TRFE_PIG STANDARD; PRT; 696 AA.
AC P09571;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serotransferrin (Transferrin) (Siderophilin) (Beta-1-metal binding
globulin).
GN TF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88335629; PubMed=3419934;
RA Baldwin G.S., Weinstock J.;
RT "Nucleotide sequence of porcine liver transferrin.";
CC -1- Nucleic Acids Res. 16:8720-8720(1988).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE. IT IS RESPONSIBLE FOR THE
CC TRANSPORT OF IRON FROM SITES OF ABSORPTION AND HEME DEGRADATION
CC TO THOSE OF STORAGE AND UTILIZATION. SERUM TRANSFERRIN MAY ALSO
CC HAVE A FURTHER ROLE IN STIMULATING CELL PROLIFERATION.
CC -1- SUBUNIT: MONOMER.
CC -1- TISSUE SPECIFICITY: Expressed in liver; secreted in plasma.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC
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CC
CC EMBL; X12386; CAA30943.1; -.
CC PIR; S01384; S01384.
CC HSP; P19134; ITFD.
CC InterPro; IPR001156; Transferrin.
CC Pfam; PF00405; transferrin; 2.
CC PRINTS; PR00422; TRANSFERRIN.
CC SMART; SM00094; TR_FER; 2.
CC PROSITE; PS00205; TRANSFERRIN 1; 2.
CC PROSITE; PS00206; TRANSFERRIN 2; 2.
CC PROSITE; PS00207; TRANSFERRIN 3; 2.
CC TRANSPORT; iron transport; Glycoprotein; Metal-binding; Repeat.
CC REPEAT 1 340
CC REPEAT 2 696
CC BY SIMILARITY.
FT DISULFID 9 47
FT FT 38 BY SIMILARITY.
FT DISULFID 117 198
FT FT 173 BY SIMILARITY.
FT DISULFID 157 173
FT FT 181 BY SIMILARITY.
FT DISULFID 160 181
FT FT 183 BY SIMILARITY.
FT DISULFID 170 183
FT FT 183 BY SIMILARITY.
FT DISULFID 231 245
FT FT 245 BY SIMILARITY.
FT DISULFID 343 605
FT FT 605 BY SIMILARITY.
FT DISULFID 349 381
FT FT 381 BY SIMILARITY.
FT DISULFID 359 372
FT FT 372 BY SIMILARITY.
FT DISULFID 406 682
FT FT 682 BY SIMILARITY.
FT DISULFID 423 646
FT FT 646 BY SIMILARITY.
FT DISULFID 456 532
FT FT 532 BY SIMILARITY.
FT DISULFID 480 673
FT FT 673 BY SIMILARITY.
FT DISULFID 490 504
FT FT 504 BY SIMILARITY.
FT DISULFID 501 515
FT FT 515 BY SIMILARITY.
FT DISULFID 572 586
FT FT 586 BY SIMILARITY.

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FT DISULFID 624 629 BY SIMILARITY.
FT METAL 62 IRON 1 (BY SIMILARITY).
FT METAL 94 IRON 1 (BY SIMILARITY).
FT METAL 192 IRON 1 (BY SIMILARITY).
FT METAL 253 IRON 1 (BY SIMILARITY).
FT METAL 396 IRON 2 (BY SIMILARITY).
FT METAL 431 IRON 2 (BY SIMILARITY).
FT METAL 526 IRON 2 (BY SIMILARITY).
FT METAL 594 IRON 2 (BY SIMILARITY).
FT BINDING 123 ANION (POTENTIAL).
FT BINDING 462 ANION (POTENTIAL).
FT CARBOHYD 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 497 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 308 K -> R.
SQ SEQUENCE 696 AA; 76967 MW; 787C59F42D844B26 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 696;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
Db 33 GPLVSCVKK 41

RESULT 7
BD01_CAPHI STANDARD; PRT; 64 AA.
AC O97945; 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Beta-defensin 1 precursor (BD-1).
GN DEFB1.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tongue;
RA Zhao C., Nguyen T., Lehrer R.I.;
RT "Molecular cloning and tissue expression of goat b-defensin-1.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: HAS BACTERICIDAL ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC
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CC
CC EMBL; Y17679; CAA76811.1; -.
CC HSP; P46170; IBNB.
CC InterPro; IPR001855; Defensin beta.
CC InterPro; IPR001271; Defensin mammal.
CC Pfam; PF00711; Defensin beta; 1.
CC SMART; SM00048; DEFSN; 1.
CC Antibiotic; Signal.
FT SIGNAL 1 20
FT PROPEP 21 26
FT CHAIN 27 64
FT DISULFID 31 60
FT DISULFID 38 53
FT DISULFID 43 61
FT SEQUENCE 64 AA; 7258 MW; 492B824C8F57B042 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 64;

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Best Local Similarity 55.6%; Pred. No. 2.2;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
Db 55 GPPVKCKRK 63

RESULT 8
BD01 SHEEP
ID BD01 SHEEP STANDARD; PRT; 64 AA.
AC O19038;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-defensin 1 precursor (BD-1) (sBD1).
GN DEFBI.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98138497; PubMed=9478010;
RA Huttner K.M., Bredinski-Calguri D.J., Mahoney M.M., Diamond G.;
RT "Antimicrobial peptide expression is developmentally regulated in the
RT ovine gastrointestinal tract.";
RL J. Nutr. 128:2978-2998(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Trachea;
RX MEDLINE=98121317; PubMed=9461419;
RA Huttner K.M., Lambeth M.R., Burk H.R., Broad T.E.;
RT "Localization and genomic organization of sheep antimicrobial peptides
RT genes.";
RL Gene 206:85-91(1998).
CC -1- FUNCTION: HAS BACTERICIDAL ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC
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CC
CC EMBL; U75250; AAB61995.1; -.
CC HSP; P46170; IBB.
CC InterPro; IPR001855; Defensin_beta.
CC Pfam; PF00711; Defensin_beta; 1.
CC SMART; SM00048; DEFEN; 1.
CC Anticlot; Signal.
FT SIGNAL 1 22 BY SIMILARITY
FT CHAIN 23 64 BETA-DEFENSIN 1.
FT DISULFID 31 60 BY SIMILARITY.
FT DISULFID 38 53 BY SIMILARITY.
FT DISULFID 43 61 BY SIMILARITY.
SQ SEQUENCE 64 AA; 7244 MW; 3529A9B76ABD023A CRC64;

Query Match 70.6%; Score 36; DB 1; Length 64;
Best Local Similarity 55.6%; Pred. No. 2.2;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
Db 55 GPPVKCKRK 63

RESULT 9

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KRSC CHICK
ID KRSC CHICK STANDARD; PRT; 154 AA.
AC P04459;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Scale keratin (S-ker) (sKer).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84158528; PubMed=6200321;
RA Gregg K., Wilton S.D., Parry D.A.D., Rogers G.E.;
RT "A comparison of genomic coding sequences for feather and scale
RT keratins: structural and evolutionary implications.";
RL EMBO J. 3:175-178(1984).
CC -1- SUBUNIT: THE AVIAN KERATINS (F-KER, S-KER, C-KER AND B-KER) ARE A
CC COMPLEX MIXTURE OF VERY SIMILAR POLYPEPTIDES.
CC -1- SIMILARITY: BELONGS TO THE AVIAN KERATIN FAMILY.
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CC
CC EMBL; X00315; CAA25084.1; ALT_SEQ.
CC PIR; A02851; KRCHS.
CC InterPro; IPR003461; Keratin.
CC Pfam; PF02422; Keratin; 1.
CC Keratin; Multigene family; Repeat.
FT INIT MET 0 0 BY SIMILARITY.
FT REPEAT 59 75
FT REPEAT 76 88
FT REPEAT 89 101
FT REPEAT 102 114
FT REPEAT 115 127
SQ SEQUENCE 154 AA; 15710 MW; 65B337485EC00466 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 154;
Best Local Similarity 75.0%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRVSCIKR 9
Db 7 PPTSCISR 14

RESULT 10
TRFE HUMAN
ID TRFE HUMAN STANDARD; PRT; 698 AA.
AC P02787; OSUHV0; O9NOB8; O43890;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
DE binding globulin) (PRO1400).
GN TF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.; AND VARIANTS TF*B2; TF*CHI AND TF*DL.
RX MEDLINE=84194084; PubMed=6585826;
RA Yang F., Lum J.B., McGill J.R., Moore C.M., Naylor S.L.,
RA van Bragt P.H., Baldwin W.D., Bowman B.H.;
RT "Human transferrin: cDNA characterization and chromosomal

```

RT localization.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:2752-2756(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8056305; PubMed=3678832;
 RA Schaeffer E., Lucero M.A., Jeltsch J.-M., Py M.-C., Levin M.J.,
 RA Chambon P., Cohen G.N., Zakin M.M.;
 RT "Complete structure of the human transferrin gene. Comparison with
 RT analogous chicken gene and human pseudogene.";
 RL Gene 56:109-116(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92231399; PubMed=1809186;
 RA Hershenberger C.L., Larson J.L., Arnold B., Rostock P.R. Jr.,
 RA Williams P., Dehoff B., Dunn P., O'Neal K.L., Riemen M.W.,
 RA Tice P.A.;
 RT "A cloned gene for human transferrin.";
 RL Ann. N.Y. Acad. Sci. 646:140-154(1991).
 RN [4]
 RP SEQUENCE FROM N.A. AND VARIANT ATRANSFERRINEMIA PRO-477.
 RX MEDLINE=20563920; PubMed=1110675;
 RA Beutler E., Gelbart T., Lee P.L., Trevino R., Fernandez M.A.,
 RA Fairbanks V.F.;
 RT "Molecular characterization of a case of atransferrinemia.";
 RL Blood 96:4071-4074(2000).
 RN [5]
 RP SEQUENCE OF 99-698 FROM N.A.
 RC TISSUE=Fetal liver;
 RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
 RA He F.;
 RT "Functional prediction of the coding sequences of 33 new genes deduced
 RT by analysis of cDNA clones from human fetal liver.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 422-698 FROM N.A.
 RX MEDLINE=84153910; PubMed=6322780;
 RA Uzan G., Frain M., Kahn A.;
 RA Zakin M.M., Park I., Desmond C., Maessen G., Trepat J.S.,
 RT "Molecular cloning and sequence analysis of cDNA for human
 RT transferrin.";
 RL Biochem. Biophys. Res. Commun. 119:273-281(1984).
 RN [7]
 RP SEQUENCE OF 20-698.
 RX MEDLINE=83166878; PubMed=6833213;
 RA McGilivray R.T.A., Mendez E., Shewale J.G., Sinha S.K.,
 RA Lineback-Zins J., Brew K.;
 RT "The primary structure of human serum transferrin. The structures of
 RT seven cyanogen bromide fragments and the assembly of the complete
 RT structure.";
 RL J. Biol. Chem. 258:3543-3553(1983).
 RN [8]
 RP SEQUENCE OF 73-698 FROM N.A.
 RX MEDLINE=85216459; PubMed=3858812;
 RA Park I., Schaeffer E., Sidoli A., Baralle F.E., Cohen G.N.,
 RA Zakin M.M.;
 RT "Organization of the human transferrin gene: direct evidence that it
 RT originated by gene duplication.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3149-3153(1985).
 RN [9]
 RP SEQUENCE OF 1-14 FROM N.A.
 RX MEDLINE=87066744; PubMed=3786138;
 RA Lucero M.A., Schaeffer E., Cohen G.N., Zakin M.M.;
 RT "The 5' region of the human transferrin gene: structure and potential
 RT regulatory sites.";
 RL Nucleic Acids Res. 14:8692-8692(1986).
 RN [10]
 RP SEQUENCE OF 1-72 AND 291-300 FROM N.A.
 RX MEDLINE=87192006; PubMed=3106157;
 RA Adrian G.S., Korinek B.W., Bowman B.H., Yang F.;
 RT "The human transferrin gene: 5' region contains conserved sequences
 RT which match the control elements regulated by heavy metals,
 RT glucocorticoids and acute phase reaction.";
 RL Gene 49:167-175(1986).
 RN [11]
 RP SEQUENCE OF 45-72 FROM N.A.
 RX PubMed=10931525;
 RA de Arriba Zarpa G.A., Saleh M.-C., Fernandez P.M., Guillou F.,
 RA Espinosa de los Monteros A., de Vellis J., Zakin M.M., Baron B.;
 RT "Alternative splicing prevents transferrin secretion during
 RT differentiation of a human oligodendrocyte cell line.";
 RL J. Neurosci. Res. 61:388-395(2000).
 RN [12]
 RP SEQUENCE OF 564-624 FROM N.A., AND VARIANT TF*C2.
 RC TISSUE=Brain;
 RX MEDLINE=97418135; PubMed=9272172;
 RA Namekata K., Oyama F., Imagawa M., Ihara Y.;
 RT "Human transferrin (Tf): a single mutation at codon 570 determines Tf
 RT Cl or Tf C2 variant.";
 RL Hum. Genet. 100:457-458(1997).
 RN [13]
 RP SEQUENCE OF 564-624 FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=96007936; PubMed=7498159;
 RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
 RA Erebova E.S., Egorov T.A., Musalyanov A.K.;
 RT "The major protein expression profile and two-dimensional protein
 RT database of human heart.";
 RL Electrophoresis 16:1160-1169(1995).
 RN [16]
 RP DISULFIDE BONDS.
 RX MEDLINE=8222165; PubMed=6953407;
 RA McGilivray R.T.A., Mendez E., Sinha S.K., Sutton M.R.,
 RA Lineback-Zins J., Brew K.;
 RT "The complete amino acid sequence of human serum transferrin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2504-2508(1982).
 RN [17]
 RP MUTAGENESIS.
 RX MEDLINE=92031536; PubMed=1932003;
 RA Woodworth R.C., Mason A.B., Funk W.D., McGilivray R.T.A.;
 RT "Expression and initial characterization of five site-directed
 RT mutants of the N-terminal half-molecule of human transferrin.";
 RL Biochemistry 30:10824-10829(1991).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 22-350.
 RX MEDLINE=98272565; PubMed=9609885;
 RA McGilivray R.T.A., Moore S.A., Chen J., Anderson B.F., Baker H.,
 RA Luo Y., Bewley M.C., Smith C.A., Murphy M.E.P., Wang Y., Mason A.B.,
 RA Woodworth R.C., Brayer G.D., Baker E.N.;
 RT "Two high-resolution crystal structures of the recombinant N-lobe of
 RT human transferrin reveal a structural change implicated in iron
 RT release.";
 RL Biochemistry 37:7919-7928(1998).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-350.
 RX MEDLINE=98434369; PubMed=9760232;
 RA Jeffery P.D., Bewley M.C., McGilivray R.T.A., Mason A.B.,
 RA Woodworth R.C., Baker E.N.;
 RT "Ligand-induced conformational change in transferrins: crystal
 RT structure of the open form of the N-terminal half-molecule of human
 RT transferrin.";
 RL Biochemistry 37:13978-13986(1998).
 RN [20]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 23-352.
 RX MEDLINE=99155227; PubMed=10029548;

RA Bewley M.C., Tam B.M., Grewal J., He S., Shewry S., Murphy M.E.P.,
 RA Mason A.B., Woodworth R.C., Baker E.N., Macmillan R.A.,
 RT "X-ray crystallography and mass spectroscopy reveal that the N-lobe
 RT of human transferrin expressed in *Pichia pastoris* is folded correctly
 RL but is glycosylated on serine-32.";
 RL Biochemistry 38:2535-2541(1999).
 RN [21]
 RN VARIANT SER-142.
 RP MEDLINE=98019079; PubMed=9358047;
 RA Evans P., Kemp J.;
 RT "Exon/intron structure of the human transferrin receptor gene.";
 RL Gene 199:133-131(1997).
 RN [22]
 RP VARIANT GLU-646.
 RX PubMed=9803271;
 RA Pang H., Koda Y., Soejima M., Kimura H.;
 RT "Identification of a mutation (A1879G) of transferrin from cDNA
 RT prepared from peripheral blood cells.";
 RL Ann. Hum. Genet. 62:271-274(1998).
 RN [23]
 RP VARIANTS SER-277; SER-589 AND GLU-671, AND CHARACTERIZATION OF
 RP VARIANT SER-277.
 RX MEDLINE=21560268; PubMed=11703331;
 RA Lee P.L., Halloran C., Trevino R., Felitti V., Beutler E.;
 RT "Human transferrin G277S mutation: a risk factor for iron deficiency
 RT anaemia.";
 RL Br. J. Haematol. 115:329-333(2001).
 RN [24]
 RP VARIANTS SER-277 AND SER-589.
 RX MEDLINE=21558434; PubMed=11702220;
 RA Douabin-Gicquel V., Soriano N., Ferran H., Wojcik F., Palierne E.,
 RA Tamam S., Jovelin T., Mokie A.T., Le Gall J.-Y., David V., Mosser J.;
 RT "Identification of 96 single nucleotide polymorphisms in eight genes
 RT involved in iron metabolism: efficiency of bioinformatic extraction
 RT compared with a systematic sequencing approach.";
 RL Hum. Genet. 109:393-401(2001).

Query Match 70.6%; Score 36; DB 1; Length 698;
 Best Local Similarity 55.6%; Pred. No. 24;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
 |||:
 Db 53 GPSVACVKK 61

RESULT 11
 ID TRFE BOVIN STANDARD; PRT; 704 AA.
 AC Q29443;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
 DE binding globulin).
 GN TP.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI TaxID=9913;
 RN [1]_TaxID=9913;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96132861; PubMed=8557646;
 RA Retzer M.D., Kabani A., Button L.L., Yu R.H., Schryvers A.B.;
 RT "Production and characterization of chimeric transferrins for the
 RT determination of the binding domains for bacterial transferrin
 RT receptors.";
 RL J. Biol. Chem. 271:1166-1173(1996).
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE. IT IS RESPONSIBLE FOR THE

CC TRANSPORT OF IRON FROM SITES OF ABSORPTION AND HEME DEGRADATION
 CC TO THOSE OF STORAGE AND UTILIZATION. SERUM TRANSFERRIN MAY ALSO
 CC HAVE A FURTHER ROLE IN STIMULATING CELL PROLIFERATION.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: Expressed in liver; secreted in plasma.
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U02564; AAA96735.1; -.
 DR HSP; P19134; ITFD.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 1.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 1.
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal.
 FT CHAIN 1 19 BY SIMILARITY.
 FT SEROTRANSFERRIN.
 FT REPEAT 20 704
 FT REPEAT 20 359 1.
 FT REPEAT 360 704 2.
 FT DISULFID 28 66 BY SIMILARITY.
 FT DISULFID 38 57 BY SIMILARITY.
 FT DISULFID 136 192 BY SIMILARITY.
 FT DISULFID 176 192 BY SIMILARITY.
 FT DISULFID 179 200 BY SIMILARITY.
 FT DISULFID 189 202 BY SIMILARITY.
 FT DISULFID 250 264 BY SIMILARITY.
 FT DISULFID 362 622 BY SIMILARITY.
 FT DISULFID 367 399 BY SIMILARITY.
 FT DISULFID 377 390 BY SIMILARITY.
 FT DISULFID 424 699 BY SIMILARITY.
 FT DISULFID 441 663 BY SIMILARITY.
 FT DISULFID 473 549 BY SIMILARITY.
 FT DISULFID 497 690 BY SIMILARITY.
 FT DISULFID 507 521 BY SIMILARITY.
 FT DISULFID 518 532 BY SIMILARITY.
 FT DISULFID 589 603 BY SIMILARITY.
 FT DISULFID 641 645 BY SIMILARITY.
 FT METAL 81 81 IRON 1 (BY SIMILARITY).
 FT METAL 113 113 IRON 1 (BY SIMILARITY).
 FT METAL 211 211 IRON 1 (BY SIMILARITY).
 FT METAL 272 272 IRON 1 (BY SIMILARITY).
 FT METAL 414 414 IRON 2 (BY SIMILARITY).
 FT METAL 449 449 IRON 2 (BY SIMILARITY).
 FT METAL 543 543 IRON 2 (BY SIMILARITY).
 FT METAL 611 611 IRON 2 (BY SIMILARITY).
 FT BINDING 142 142 ANION (POTENTIAL).
 FT BINDING 479 479 ANION (POTENTIAL).
 FT CARBOHYD 514 514 N-LINKED (GLCNAC... (POTENTIAL).
 SQ SEQUENCE 704 AA; 77753 MW; D87BB2AFE46C708D CRC64;

Query Match 70.6%; Score 36; DB 1; Length 704;
 Best Local Similarity 66.7%; Pred. No. 24;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GPPVSCIKR 9
 |||:
 Db 52 GPFVSCVKK 60

RESULT 12

TRFL CAMDR STANDARD; PRT; 708 AA.

AC Q9TUM0; Q9MZS5; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Lactotransferrin precursor (Lactoferrin).

GN LfP.

OS Camelus dromedarius (Dromedary) (Arabic camel).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.

OX NCBI_TaxID=9838;

RN [1]

RN SEQUENCE FROM N.A.

RP STRAIN=Somali; TISSUE=Lactating mammary gland;

RA Kappeler S.R., Ackermann M., Farah Z., Puhon Z.;

RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";

RN Int. Dairy J. 9:481-486(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Mammary gland;

RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).

CC -!- SUBUNIT: MONOMER (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.

CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

CC -----

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CC -----

CC EMBL; AJ131674; CAB53387.1; "

CC EMBL; AF165879; AAP82241.1; "

CC HSP; 077811; 181X.

CC InterPro; IPR001156; Transferrin.

CC Pfam; PF00405; transferrin; 2.

CC PRINTS; PR00422; TRANSFERRIN.

CC SMART; SM00094; TR_FER; 2.

CC PROSITE; PS00205; TRANSFERRIN_1; 2.

CC PROSITE; PS00206; TRANSFERRIN_2; 2.

CC PROSITE; PS00207; TRANSFERRIN_3; 2.

CC transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal.

KW SIGNAL.

FT CHAIN 1 19

FT CHAIN 20 708

FT REPEAT 20 363

FT REPEAT 364 708

FT DISULFID 28 64

FT DISULFID 38 55

FT DISULFID 134 217

FT DISULFID 176 192

FT DISULFID 189 200

FT DISULFID 250 264

FT DISULFID 367 399

FT DISULFID 377 390

FT DISULFID 424 703

FT DISULFID 444 666

FT DISULFID 476 551

FT DISULFID 500 694

FT DISULFID 510 524

FT DISULFID 521 534

FT DISULFID 592 606

FT DISULFID 644 649

FT METAL 79 79

FT METAL 111 111

FT METAL 211

FT METAL 272

FT METAL 414

FT METAL 452

FT METAL 545

FT METAL 614

FT BINDING 140 140

FT BINDING 482 482

FT CARBOHYD 252 252

FT CARBOHYD 385 385

FT CARBOHYD 537 537

FT CARBOHYD 594 594

FT CONFLICT 261 261

FT CONFLICT 304 304

FT CONFLICT 330 330

FT CONFLICT 492 494

FT CONFLICT 506 506

FT CONFLICT 609 609

FT CONFLICT 642 642

SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 708;

Best Local Similarity 55.6%; Pred. No. 24;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9

DB 50 GPSVTCVKK 58

RESULT 13

INA4 MOUSE

ID INA4 MOUSE STANDARD; PRT; 186 AA.

AC P07351;

DT 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Interferon alpha-4 precursor.

GN IFNA4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RN SEQUENCE FROM N.A.

RX MEDLINE=85215516; PubMed=2987811;

RA Kelly K.A., Pitha P.M.;

RT "Characterization of a mouse interferon gene locus I. Isolation of a cluster of four alpha interferon genes."

RL Nucleic Acids Res. 13:805-823(1985).

CC -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES: A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.

CC -----

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CC -----

CC EMBL; X01973; CAA26005.1; "

CC FIR; B23087; IYMSA4.

CC HSSP; P01563; 2HIE.

CC MGD; MGI:107664; Ifna4.

CC InterPro; IPR000471; Interferon_abd.

CC Pfam; PF00143; interferon; 1.

CC PRINTS; PR00266; INTERFERONAB.

CC ProDom; PD000550; Interferon_abd; 1.


```
DR SMART: SM00076; IPAbd: 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Antiviral; Multigene family; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 186 INTERFERON ALPHA-4.
FT DISULFID 25 123 BY SIMILARITY.
FT DISULFID 53 158 BY SIMILARITY.
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 186 AA; 21524 MW; FCS4D46D73741794 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 186;
Best Local Similarity 71.4%; Pred. No. 10;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPVSCIJK 8
DB 49 PPLUSCLK 55

RESULT 14
LORI HUMAN
ID LORI HUMAN STANDARD; PRT; 316 AA.
AC P23430;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lorcrin.
GN LOR OR LRN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Forebrain; PubMed=2007607;
RX MEDLINE=91177926; PubMed=2007607;
RA Hohl D., Mehrel T., Ichtai U., Turner M.L., Roop D.R., Steinert P.M.;
RT "Characterization of human lorcrin. Structure and function of a new
class of epidermal cell envelope proteins.";
RL J. Biol. Chem. 266:6626-6636(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92388173; PubMed=1355480;
RA Yoneda K., Hohl D., McBride O.W., Wang M., Cehrs K.U., Idler W.W.,
RT Steinert P.M.;
RA "The human lorcrin gene.";
RL J. Biol. Chem. 267:18060-18066(1992).
CC -1- FUNCTION: MAJOR KERATINOCYTE CELL ENVELOPE PROTEIN.
CC -1- SUBUNIT: MONOMERS ARE CROSSLINKED BY DISULFIDE AND N-(GAMMA-
GLUTAMYL) LYSINE ISODIPEPTIDE BONDS.
CC
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```
DB 12 PPVDCVK 18

RESULT 15
VE2_HPV54
ID VE2_HPV54 STANDARD; PRT; 367 AA.
AC Q81021;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Regulatory protein E2.
GN E2.
OS Human papillomavirus type 54.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=37113;
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACNNNNNGGT-3') PRESENT
IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
REPLICATION.
CC -1- SUBUNIT: BINDS DNA AS A DIMER.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC
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```

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:44:43 ; Search time 16.2558 Seconds
(without alignments)
114.078 Million cell updates/sec

Title: US-09-743-107b-101
Perfect score: 51
Sequence: 1 GPPVSCIKR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	711	4	Q8TCD2
2	46	90.2	1245	4	Q9ULD2
3	39	76.5	1521	4	Q9UQ02
4	39	76.5	1924	4	Q9UPY3
5	38	74.5	244	10	Q94JK1
6	38	74.5	823	4	Q8WY18
7	37	72.5	41	5	Q9NGM7
8	37	72.5	148	11	Q5CR70
9	37	72.5	148	11	Q8R2R7
10	37	72.5	184	4	Q9P0D5
11	37	72.5	223	5	Q9VJM2
12	37	72.5	499	5	Q960G4
13	37	72.5	576	15	Q55604
14	37	72.5	591	5	Q866U1
15	37	72.5	591	5	Q5SR88
16	37	72.5	704	5	Q9VVT8

17	37	72.5	718	4	Q05850
18	37	72.5	3895	12	Q9P297
19	36	70.6	64	6	Q97942
20	36	70.6	189	16	Q8UGB5
21	36	70.6	396	12	Q58869
22	36	70.6	551	4	Q9UK95
23	36	70.6	723	5	O16775
24	36	70.6	3989	12	Q9PYB2
25	35	68.6	203	4	Q9NUD3
26	35	68.6	204	4	Q9GZP1
27	35	68.6	282	16	Q9ZCN7
28	35	68.6	331	5	O16367
29	35	68.6	338	4	O60354
30	35	68.6	439	10	Q9SWS2
31	35	68.6	443	10	Q9SWS3
32	35	68.6	450	10	Q9LME9
33	35	68.6	466	5	Q8T282
34	35	68.6	479	10	Q9LMF0
35	35	68.6	481	10	Q8W4G1
36	35	68.6	481	10	Q9ZWJ3
37	35	68.6	487	10	Q9LME8
38	35	68.6	489	10	Q9M9E7
39	35	68.6	489	10	Q9SK82
40	35	68.6	830	10	Q9ZT06
41	34	66.7	121	16	Q8YC23
42	34	66.7	123	5	Q8WRN9
43	34	66.7	132	3	Q8XOD2
44	34	66.7	197	16	Q98AK3
45	34	66.7	243	5	Q8TIY6

ALIGNMENTS

RESULT 1
Q8TCD2 PRELIMINARY; PRT; 711 AA.
ID Q8TCD2 PRELIMINARY; PRT; 711 AA.
AC Q8TCD2; 2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE Lactotransferrin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022347, AAH2347.1; -
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7E907C45FAF CRC64;

Query Match	100.0%;	Score 51;	DB 4;	Length 711;
Best Local Similarity	100.0%;	Pred. No. 0.072;	0;	Mismatches 0;
Matches	9;	Conservative	0;	Indels 0;
Gaps	0;			
Qy	1	GPPVSCIKR	9	
Db	51	GPPVSCIKR	59	
RESULT 2				
Q9ULD2				
ID Q9ULD2				
AC Q9ULD2				
DT 01-MAY-2000 (Tremblrel. 13, Created)				
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)				
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)				
DE KIAA1288 protein (Fragment).				
GN KIAA1288.				
OS Homo sapiens (Human).				

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20039619; PubMed=10574462;
RA Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:337-345(1999).
DR EMBL; AB033114; BAA86602.1; -
FT NON TER 1
SQ SEQUENCE 1245 AA; 138533 MW; AB446CC36AC30ED4 CRC64;

Query Match 90.2%; Score 46; DB 4; Length 1245;
Best Local Similarity 77.8%; Pred. No. 1.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
DB 705 GPPVSCILRR 713

RESULT 3
ID Q9UQ02 PRELIMINARY; PRT; 1521 AA.
AC Q9UQ02, 2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE KIAA0928 protein (Fragment).
GN KIAA0928.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=99246063; PubMed=10231032;
RA Nagase T., Ishikawa K., Suyama H., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:63-70(1999).
DR EMBL; AB023145; BAA76772.1; -
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001159; DS_RBD.
DR InterPro; IPR005034; DUF283.
DR InterPro; IPR000532; Glucagon.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR003100; PAZ.
DR InterPro; IPR003999; RNase_3.
DR Pfam; PF00035; GERM; 1.
DR Pfam; PF03368; DUF283; 1.
DR Pfam; PF0271; helicase_C; 1.
DR Pfam; PF02170; PAZ; 1.
DR Pfam; PF00636; Ribonuclease_3; 2.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00358; DSRM; 1.
DR SMART; SM00490; HELICC; 1.
DR SMART; SM00535; RIBOC; 2.
DR PROSITE; PS0137; DS_RBD; 1.
DR PROSITE; PS00517; RNASE_3_1; 1.
DR PROSITE; PS0142; RNASE_3_2; 2.
KW ATP-binding; Helicase.
FT NON TER 1
SQ SEQUENCE 1521 AA; 172818 MW; D566C31E65081C19 CRC64;

Query Match 76.5%; Score 39; DB 4; Length 1521;
Best Local Similarity 77.8%; Pred. No. 1.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Best Local Similarity 62.5%; Pred. No. 33;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIK 8
DB 280 GPPMSCVR 287

RESULT 4
ID Q9UPY3 PRELIMINARY; PRT; 1924 AA.
AC Q9UPY3, 2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Helicase-MOI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20246304; PubMed=10786632;
RA Matsuda S., Ichigotani Y., Okuda T., Irimura T., Nakatsugawa S.;
RT "Molecular cloning and characterization of a novel human gene (HERNA)
RL Biochim. Biophys. Acta 1490:163-169(2000).
DR EMBL; AB028449; BAA78691.1; -
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001159; DS_RBD.
DR InterPro; IPR005034; DUF283.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR003100; PAZ.
DR InterPro; IPR000999; RNase_3.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00035; GERM; 1.
DR Pfam; PF03368; DUF283; 1.
DR Pfam; PF00271; helicase_C; 1.
DR Pfam; PF02170; PAZ; 1.
DR Pfam; PF00636; Ribonuclease_3; 2.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00358; DSRM; 1.
DR SMART; SM00490; HELICC; 1.
DR PROSITE; PS0137; DS_RBD; 1.
DR PROSITE; PS00517; RNASE_3_1; 1.
DR PROSITE; PS0142; RNASE_3_2; 2.
KW ATP-binding; Helicase.
SQ SEQUENCE 1924 AA; 218811 MW; BA5D3020995B5F89 CRC64;

Query Match 76.5%; Score 39; DB 4; Length 1924;
Best Local Similarity 62.5%; Pred. No. 4;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIK 8
DB 683 GPPMSCVR 690

RESULT 5
ID Q94JK1 PRELIMINARY; PRT; 244 AA.
AC Q94JK1, 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE P0434B04.22 protein.
GN P0434B04.22.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
```

OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 RT clone: P0434B04.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF002540; BAB44001.1; -;
 DR InterPro: IPR003902; GCM motif.
 SQ SEQUENCE 244 AA; 27252 MW; 445B5CEBA06064FA CRC64;

Query Match 74.5%; Score 38; DB 10; Length 244;
 Best Local Similarity 55.6%; Pred. No. 11;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPPVSCIIR 9
 |||||
 Db 81 GPPAACLR 89

RESULT 6
 ID Q8WV18 PRELIMINARY; PRT; 823 AA.
 AC Q8WV18;
 DT 01-MAR-2002 (TREMELrel. 20, Created)
 DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
 DE MSTP018.
 GN MST018.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=AORTA;
 RA Xu Y.Y., Sun L.Z., Wu Q.Y., Liu Y.Q., Liu B., Zhao B., Wang X.Y.,
 RA Song L., Ye J.J., Sheng H., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
 RA Sun Y.H., Jiang Y.X., Zhao X.W., Liu S., Liu L.S., Ding J.F.,
 RA Gao R.L., Qiang B.Q., Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF111799; AAL39001.1; -;
 DR InterPro: IPR000413; Integrin_alpha.
 DR Pfam: PF01839; FG-GAP; 4.
 DR PRINTS; PRO1185; INTEGRINA.
 DR SMART; SM00191; Int_alpha; 4.
 SQ SEQUENCE 823 AA; 92672 MW; D54E78079DCD4925 CRC64;

Query Match 74.5%; Score 38; DB 4; Length 823;
 Best Local Similarity 77.8%; Pred. No. 3;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPPVSCIIR 9
 |||||
 Db 618 GPPFSCIIR 626

RESULT 7
 ID Q9NGM7 PRELIMINARY; PRT; 41 AA.
 AC Q9NGM7;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
 DE Myosin-like protein MipB (Fragment).
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20440049; PubMed=10984411;
 RA Sirotkin V., Seipel S., Krendel M., Bonder E.M.;
 RT "Characterization of sea urchin unconventional myosins and analysis of
 RT their patterns of expression during early embryogenesis.";
 RL Mol. Reprod. Dev. 57:111-126(2000).
 DR EMBL; AF247514; AAF17126.1; -;
 FT NON TER 1
 FT NON TER 41
 SQ SEQUENCE 41 AA; 4693 MW; 54CD7BF60626D599 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 41;
 Best Local Similarity 75.0%; Pred. No. 3.6;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PPVSCIIR 9
 |||||
 Db 25 PPVECIER 32

RESULT 8
 ID Q9CR70 PRELIMINARY; PRT; 148 AA.
 AC Q9CR70;
 DT 01-JUN-2001 (TREMELrel. 17, Created)
 DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
 DE 110049G11Rik protein.
 GN 110049G11Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=CS7BL/6J; TISSUE=EMBRYO, AND KIDNEY;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Hono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Straubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AK004210; BAB23222.1; -;
 DR EMBL; AK002539; BAB22174.1; -;
 DR MGD; MGI:1913442; 110049G11Rik.
 SQ SEQUENCE 148 AA; 15824 MW; 17C28868F75064CC CRC64;

Query Match 72.5%; Score 37; DB 11; Length 148;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSC 6
 |||||
 Db 143 GPPVSC 148

RESULT 9
 ID Q8R2R7 PRELIMINARY; PRT; 148 AA.

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AC Q8R2R7;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 1110049G11 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
OX NCBI_TaxID=1090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027305; AAB27305.1; -.
SQ SEQUENCE 148 AA; 15857 MW; 19DD1C9A5FE81D83 CRC64;

Query Match 72.5%; Score 37; DB 11; Length 148;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSC 6
Db 143 GPPVSC 148

RESULT 10
Q9P0D5 PRELIMINARY; PRT; 184 AA.
ID Q9P0D5
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE HSPC101 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Q.H., Ye M., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
RA Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RT "Human partial CDS cloned from c334+ stem cells.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161364; AAF28924.1; -.
FT NON_TER
SQ SEQUENCE 184 AA; 20857 MW; 05D569073D334F5D CRC64;

Query Match 72.5%; Score 37; DB 4; Length 184;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PVPVSCIKR 9
Db 149 PVPVSCIKR 156

RESULT 11
Q9VJM2 PRELIMINARY; PRT; 223 AA.
ID Q9VJM2
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE BG:DS04095.2 protein.
GN BG:DS04095.2 OR CG4892.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
```

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RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod W.F., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wasmann D.A., Weinstock G.M., Weissbach J., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AB003650; AAF53502.1; -.
DR FlyBase; FBgn0028884; BG:DS04095.2.
SQ SEQUENCE 223 AA; 25233 MW; C72A405F7BEF981E CRC64;

Query Match 72.5%; Score 37; DB 5; Length 223;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PVPVSCIKR 9
Db 25 PVPVSCIKR 32

RESULT 12
Q960G4 PRELIMINARY; PRT; 499 AA.
ID Q960G4
OC Q960G4
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE SD02971P.
GN CG3961.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
```

RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY052074; RA039498.1; -
 DR Flybase: FBgn0036821; CG3961.
 DR InterPro: IPR000873; AMP-Bind.
 DR Pfam: PF00501; AMP-binding; 1.
 DR PROSITE: PS00455; AMP BINDING; UNKNOWN 1.
 SQ SEQUENCE 499 AA; 55517 MW; CAD577FC98873421 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 499;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSC 6
 |||||
 Db 283 GPPVSC 288

RESULT 13

Q65604 PRELIMINARY; PRT; 576 AA.

ID Q65604;
 AC Q65604;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE Surface envelope protein (Fragment).
 OS Bovine immunodeficiency-like virus.
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11647;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FL491;
 RX MEDLINE=96010247; PubMed=7571444;
 RA Suarez D.L., Whetstone C.A.;
 RT "Identification of hypervariable and conserved regions in the surface
 envelope gene in the bovine lentivirus.";
 RL Virology 212:728-733 (1995).
 DR EMBL: L43127; AAC42157.1; -
 KW Envelope protein.
 FT NON TER 576
 SQ SEQUENCE 576 AA; 64168 MW; 5690B759A5FC51C7 CRC64;

Query Match 72.5%; Score 37; DB 15; Length 576;
 Best Local Similarity 55.6%; Pred. No. 36;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPPVSCIKR 9
 |||||
 Db 475 GRPISCVKX 483

RESULT 14

Q966U1 PRELIMINARY; PRT; 591 AA.

ID Q966U1;
 AC Q966U1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Transcription factor ems/emx.
 GN HREMx.
 OS Halocynthia roretzi (sea squirt).
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Pyrosidae; Halocynthia.
 OX NCBI_TaxID=7729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21359114; PubMed=11466524;
 RA Oda I., Saiga H.;
 RT "Hremx, the ascidian homologue of ems/emx, is expressed in the
 anterior and posterior-lateral epidermis but not in the central
 nervous system during embryogenesis.";
 RL Dev. Genes Evol. 211:291-298 (2001).
 DR EMBL: AB055144; BAB61733.1; -

DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; homeobox; 1.
 DR ProDom: PD000010; Homeobox; 1.
 DR PROSITE: PS00027; HOMEBOX_1; UNKNOWN 1.
 DR PROSITE: PSS0071; HOMEBOX_2; 1.
 SQ SEQUENCE 591 AA; 65943 MW; 11E74AA8237CC33B CRC64;

Query Match 72.5%; Score 37; DB 5; Length 591;
 Best Local Similarity 85.7%; Pred. No. 36;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPPVSCI 7
 |||||
 Db 326 GPPVSCI 332

RESULT 15

Q95R88 PRELIMINARY; PRT; 691 AA.

ID Q95R88;
 AC Q95R88;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE S001152p.
 GN CG3961.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY061568; AAL29116.1; -
 DR Flybase: FBgn0036821; CG3961.
 DR InterPro: IPR000873; AMP-bind.
 DR Pfam: PF00501; AMP-binding; 1.
 DR PROSITE: PS00455; AMP BINDING; UNKNOWN 1.
 SQ SEQUENCE 691 AA; 77346 MW; FBB4EAB69BC7C6B9 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 691;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSC 6
 |||||
 Db 475 GPPVSC 480

Search completed: February 21, 2003, 08:00:52
 Job time : 18.2558 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds
(without alignments)
56,502 Million cell updates/sec

Title: US-09-743-107B-47

Perfect score: 71

Sequence: 1 CFQWQNRKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	12	21	AAV78038 Human lactoferrin
2	71	100.0	12	21	AAV78046 Human lactoferrin
3	71	100.0	12	21	AAV78047 Human lactoferrin
4	71	100.0	13	21	AAV78037 Human lactoferrin
5	71	100.0	13	21	AAV78048 Human lactoferrin
6	71	100.0	13	21	AAV78049 Human lactoferrin
7	71	100.0	14	21	AAV78036 Human lactoferrin
8	71	100.0	14	21	AAV78050 Human lactoferrin
9	71	100.0	14	21	AAV78051 Human lactoferrin
10	71	100.0	15	17	AAV98554 Peptide for anti-u

11	71	100.0	15	21	AAV78035 Human lactoferrin
12	71	100.0	15	21	AAV78062 Human lactoferrin
13	71	100.0	15	21	AAV78063 Human lactoferrin
14	71	100.0	16	21	AAV78031 Human lactoferrin
15	71	100.0	16	21	AAV78064 Human lactoferrin
16	71	100.0	16	21	AAV78065 Human lactoferrin
17	71	100.0	17	21	AAV78034 Human lactoferrin
18	71	100.0	17	21	AAV78066 Human lactoferrin
19	71	100.0	17	21	AAV78067 Human lactoferrin
20	71	100.0	18	15	AAV69352 Human lactoferrin
21	71	100.0	18	17	AAV13397 Advanced glycosyla
22	71	100.0	18	21	AAV78033 Human lactoferrin
23	71	100.0	19	21	AAV68867 Amino acid sequenc
24	71	100.0	19	21	AAV78032 Human lactoferrin
25	71	100.0	20	13	AAV21810 Anti microbial pep
26	71	100.0	20	14	AAV44841 Lactoferrin-relate
27	71	100.0	20	15	AAV48530 Lactoferrin derive
28	71	100.0	20	15	AAV48531 Lactoferrin derive
29	71	100.0	20	15	AAV57461 Lactoferrin derive
30	71	100.0	20	15	AAV57462 Lactoferrin derive
31	71	100.0	20	16	AAV84598 Bovine lactoferrin
32	71	100.0	20	16	AAV84599 Bovine lactoferrin
33	71	100.0	20	16	AAV80263 Anti-parasitic lac
34	71	100.0	20	16	AAV80264 Anti-parasitic lac
35	71	100.0	20	17	AAV98553 Peptide for anti-u
36	71	100.0	20	17	AAV91852 Lactoferrin-derive
37	71	100.0	20	17	AAV03045 Lactoferrin derive
38	71	100.0	20	17	AAV90607 Lactoferrin-derive
39	71	100.0	20	17	AAV87621 Lactoferrin-derive
40	71	100.0	20	17	AAV87622 Lactoferrin-derive
41	71	100.0	20	18	AAV26150 Lactoferrin derive
42	71	100.0	20	18	AAV14036 Anti-parasitic pep
43	71	100.0	20	19	AAV70310 Thrombus formation
44	71	100.0	20	19	AAV53224 Lactoferrin hydrol
45	71	100.0	20	19	AAV53225 Lactoferrin hydrol

ALIGNMENTS

RESULT 1

AAV78038
ID AAV78038 standard; Peptide; 12 AA.
XX
AC AAV78038;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:38.

Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; candida infection; fungicidal;
bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Matthey-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

DR

XX PT New peptides used for treatment and prevention of infections, -
PT inflammations and tumors and for use in infant formula food -
XX PS Claim 12; Page 70; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX SQ Sequence 12 AA;
SQ Query Match 100.0%; Score 71; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKVR 12
DB |||||
1 CFQWQRNMRKVR 12

RESULT 2
AAY78046
ID AAY78045 standard; Peptide; 12 AA.
XX AC AAY78046;
XX DT 25-APR-2000 (first entry)
XX DE Human lactoferrin derived peptide SEQ ID NO:46.
XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX KW urinary tract infection; colitis; Candida infection; fungicidal;
XX KW bactericidal; preservative.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200001730-A1.
XX PD 13-JAN-2000.
XX PF 06-JUL-1999; 99WO-SE01230.
XX PR 06-JUL-1998; 98SE-0002441.
XX PR 17-JUL-1998; 98SE-0002562.
XX PR 29-DEC-1998; 98SE-0004614.
XX PA (ASCI-) A+ SCI INVEST AB.
XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX DR New peptides used for treatment and prevention of infections, -
XX PT inflammations and tumors and for use in infant formula food -
XX PS Claim 15; Page 35; 102pp; English.
XX CC AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX SQ Sequence 12 AA;
SQ Query Match 100.0%; Score 71; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKVR 12
DB |||||
1 CFQWQRNMRKVR 12

RESULT 3
AAY78047
ID AAY78047 standard; Peptide; 12 AA.
XX AC AAY78047;
XX DT 25-APR-2000 (first entry)
XX DE Human lactoferrin derived peptide SEQ ID NO:47.
XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX KW urinary tract infection; colitis; Candida infection; fungicidal;
XX KW bactericidal; preservative.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200001730-A1.
XX PD 13-JAN-2000.
XX PF 06-JUL-1999; 99WO-SE01230.
XX PR 06-JUL-1998; 98SE-0002441.
XX PR 17-JUL-1998; 98SE-0002562.
XX PR 29-DEC-1998; 98SE-0004614.
XX PA (ASCI-) A+ SCI INVEST AB.
XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX DR New peptides used for treatment and prevention of infections, -
XX PT inflammations and tumors and for use in infant formula food -
XX PS Claim 18; Page 73; 102pp; English.
XX CC AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 71; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKVR 12
 DB 1 CFQWQNRMRKVR 12
 |||||

RESULT 4
 AAY78037
 ID AAY78037 standard; Peptide; 13 AA.
 XX
 AC AAY78037;
 XX
 XX 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:37.
 DE
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200001730-A1.
 XX 13-JAN-2000.
 PD
 XX 06-JUL-1999; 99WO-SE01230.
 PF
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 PA (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 DR WPI; 2000-147388/13.
 XX
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 XX Claim 12; Page 70; 102pp; English.

CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 71; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKVR 12
 DB 2 CFQWQNRMRKVR 13
 |||||

RESULT 5
 AAY78048
 ID AAY78048 standard; Peptide; 13 AA.
 XX
 AC AAY78048;
 XX
 XX 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:48.
 DE
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200001730-A1.
 XX 13-JAN-2000.
 PD
 XX 06-JUL-1999; 99WO-SE01230.
 PF
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 PA (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 DR WPI; 2000-147388/13.
 XX
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 XX Claim 15; Page 74; 102pp; English.

CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 71; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12
 DB 2 CFQWQNNRKVR 13

RESULT 6

AAAY78049
 ID AAY78049 standard; Peptide; 13 AA.

XX AC AAY78049;
 XX DT 25-APR-2000 (first entry)
 XX DE Human lactoferrin derived peptide SEQ ID NO:49.
 XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,

XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 18; Page 74; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 13 AA;
 Query Match 100.0%; Score 71; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12

DB 2 CFQWQNNRKVR 13

RESULT 7

AAAY78036

ID AAY78036 standard; Peptide; 14 AA.

XX AC AAY78036;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:36.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,

XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 12; Page 69; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 14 AA;
 Query Match 100.0%; Score 71; DB 21; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12

DB 3 CFQWQNNRKVR 14

RESULT 8

AAAY78050

ID AAY78050 standard; Peptide; 14 AA.

XX AC AAY78050;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:50.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX 13-JAN-2000.
 PD
 XX 06-JUL-1999; 99WO-SE01230.
 XX
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 XX (ASCI-) A+ SCI INVEST AB.
 PA
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX
 DR New peptides used for treatment and prevention of infections, -
 PT inflammations and tumors and for use in infant formula food
 XX Claim 15; Page 75; 102pp; English.
 PS
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 71; DB 21; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFQWQRNMRKVR 12
 DB 3 CFQWQRNMRKVR 14
 RESULT 9
 AAY78051
 ID AAY78051 standard; Peptide; 14 AA.
 XX
 AC AAY78051;
 XX
 DT 25-APR-2000 (first entry)
 DE Human lactoferrin derived peptide SEQ ID NO:51.
 XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.

OS Synthetic.
 XX WO200001730-A1.
 PN
 XX 13-JAN-2000.
 PD
 XX 06-JUL-1999; 99WO-SE01230.
 XX
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 XX (ASCI-) A+ SCI INVEST AB.
 PA
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX
 DR New peptides used for treatment and prevention of infections, -
 PT inflammations and tumors and for use in infant formula food
 XX Claim 18; Page 75; 102pp; English.
 PS
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 71; DB 21; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFQWQRNMRKVR 12
 DB 3 CFQWQRNMRKVR 14
 RESULT 10
 AAR98554
 ID AAR98554 standard; Peptide; 15 AA.
 XX
 AC AAR98554;
 XX
 DT 12-NOV-1996 (first entry)
 DE Peptide for anti-ulcer agent.
 XX
 KW anti-ulcer agent; low toxicity; stable; heat-resistant.
 XX
 OS Synthetic.
 XX JP08143468-A.
 PN
 XX 04-JUN-1996.
 PD
 XX 17-NOV-1994; 94JP-0283869.
 XX
 PR 17-NOV-1994; 94JP-0283869.
 XX
 PA (MORG) MORINAGA MILK IND CO LTD.

XX WPI; 1996-318857/32.
 XX Anti-ulcer agent contg. peptide - has low toxicity, is
 PT heat-resistant and water-soluble
 XX
 PS Claim 1; Page 11; 11pp; Japanese.
 XX
 CC AAs98531-54 are peptides used in an anti-ulcer agent. The agent is low
 CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be
 CC administered orally and be produced in large amounts.
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 71; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFQWQRNMRKVR 12
 Db 2 CFQWQRNMRKVR 13
 RESULT 11
 AAY78035
 ID AAY78035 standard; Peptide; 15 AA.
 XX
 AC AAY78035;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human lactoferrin derived peptide SEQ ID NO:35.
 XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 PF 06-JUL-1999; 99WO-SE01230.
 XX
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 PA (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX
 DR WPI; 2000-147388/13.
 XX
 PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 PS Claim 12; Page 69; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations, colitis, and Candida infection on a mucosal
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 71; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFQWQRNMRKVR 12
 Db 4 CFQWQRNMRKVR 15
 RESULT 12
 AAY78062
 ID AAY78062 standard; Peptide; 15 AA.
 XX
 AC AAY78062;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human lactoferrin derived peptide SEQ ID NO:62.
 XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 PF 06-JUL-1999; 99WO-SE01230.
 XX
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 PA (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX
 DR WPI; 2000-147388/13.
 XX
 PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 PS Claim 15; Page 81; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations, colitis, and Candida infection on a mucosal
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 15 AA;

CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 71; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNNRKR 12
 DB 4 CFQWQNNRKR 15

RESULT 13
 AAY78063
 ID AAY78063 standard; Peptide; 15 AA.
 AC AAY78063;
 DT 25-APR-2000 (first entry)
 DE Human lactoferrin derived peptide SEQ ID NO:63.

Human; lactoferrin; modification; infection; inflammation; tumour;
 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 urinary tract infection; colitis; Candida infection; fungicidal;
 bactericidal; preservative.

OS Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 PF 06-JUL-1999; 99WO-SE01230.
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 18; Page 81; 102pp; English.

AAV78001 to AAV78100 represent peptides having sequences based on human
 lactoferrin. The peptides are taken up in the intestine through
 binding to specific lactoferrin receptors and are then transported
 through the circulation. A medicinal product of the peptide or fragment
 can be used for treating and/or prevention of infections (such as
 urinary tract infections, colitis, and Candida infection on a mucosal
 membrane), inflammations and/or tumours. The peptides can also be used
 in food stuffs such as infant formula food. The peptides are also
 fungicidal and bactericidal and may also be used as preservatives.
 Even though native human lactoferrin have been shown to have desired
 anti-inflammatory anti-infectious and anti-tumoural properties they
 cannot be used clinically on a broad basis because of high production
 costs. Therefore, provision of peptides based on lactoferrin would
 enable them to be used for the same purposes as lactoferrin at lower
 cost.

QY Sequence 15 AA;

Query Match 100.0%; Score 71; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNNRKR 12
 DB 4 CFQWQNNRKR 15

RESULT 14
 AAY78031
 ID AAY78031 standard; Peptide; 16 AA.

XX AAY78031;
 AC AAY78031;
 DT 25-APR-2000 (first entry)
 DE Human lactoferrin derived peptide SEQ ID NO:31.

Human; lactoferrin; modification; infection; inflammation; tumour;
 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 urinary tract infection; colitis; Candida infection; fungicidal;
 bactericidal; preservative.

OS Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 PF 06-JUL-1999; 99WO-SE01230.
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 11; Page 68; 102pp; English.

AAV78001 to AAV78100 represent peptides having sequences based on human
 lactoferrin. The peptides are taken up in the intestine through
 binding to specific lactoferrin receptors and are then transported
 through the circulation. A medicinal product of the peptide or fragment
 can be used for treating and/or prevention of infections (such as
 urinary tract infections, colitis, and Candida infection on a mucosal
 membrane), inflammations and/or tumours. The peptides can also be used
 in food stuffs such as infant formula food. The peptides are also
 fungicidal and bactericidal and may also be used as preservatives.
 Even though native human lactoferrin have been shown to have desired
 anti-inflammatory anti-infectious and anti-tumoural properties they
 cannot be used clinically on a broad basis because of high production
 costs. Therefore, provision of peptides based on lactoferrin would
 enable them to be used for the same purposes as lactoferrin at lower
 cost.

QY Sequence 16 AA;

Query Match 100.0%; Score 71; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNNRKR 12
 DB 5 CFQWQNNRKR 16

RESULT 15
 AAY78064
 ID AAY78064 standard; Peptide; 16 AA.

XX AAY78064;

Tue Dec 9 06:51:21 2003

XX 25-APR-2000 (first entry)
DT Human lactoferrin derived peptide SEQ ID NO:64.
DE
XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX WO200001730-A1.
XX
XX 13-JAN-2000.
PD
XX 06-JUL-1999; 99WO-SE01230.
PF
XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
FA
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
PI WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections, -
PT inflammations and tumors and for use in infant formula food
XX
XX Claim 15; Page 82; 102pp; English.
PS
XX AAV78001 to AAV78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX SQ Sequence 16 AA;

Query Match 100.0%; Score 71; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQENNEKVR 12
DB 5 CFQWQENNEKVR 16

Search completed: February 21, 2003, 07:37:10
Job time : 29.35 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 seconds
(without alignments)
40.818 Million cell updates/sec

Title: US-09-743-107B-47

Perfect score: 71

Sequence: 1 CFOWQRMKRV 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
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6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	18	1	US-08-204-487-3
2	71	100.0	18	2	US-08-485-948-8
3	71	100.0	18	2	US-08-628-380-8
4	71	100.0	18	2	US-08-475-055-8
5	71	100.0	20	1	US-07-755-161A-3
6	71	100.0	20	1	US-07-891-174-3
7	71	100.0	20	1	US-08-204-487-1
8	71	100.0	20	1	US-08-256-771-24
9	71	100.0	20	1	US-08-256-771-25
10	71	100.0	20	1	US-08-381-984-24
11	71	100.0	20	1	US-08-381-984-25
12	71	100.0	22	4	US-09-508-734-4
13	71	100.0	24	4	US-09-508-734-6
14	71	100.0	25	1	US-07-755-161A-10
15	71	100.0	25	1	US-07-891-174-10
16	71	100.0	25	1	US-08-204-487-7
17	71	100.0	29	4	US-09-508-734-8
18	71	100.0	36	1	US-07-755-161A-8
19	71	100.0	36	1	US-07-891-174-8
20	71	100.0	36	1	US-08-256-771-30
21	71	100.0	36	1	US-08-381-984-29
22	71	100.0	47	2	US-08-464-182A-6
23	71	100.0	47	2	US-08-406-271-6
24	71	100.0	50	2	US-08-693-274A-7
25	71	100.0	52	4	US-09-017-043A-3
26	71	100.0	53	2	US-08-464-182A-5
27	71	100.0	53	2	US-08-406-271-5

28 71 100.0 54 2 US-08-464-182A-2 Sequence 2, Appli
29 71 100.0 54 2 US-08-406-271-2 Sequence 2, Appli
30 71 100.0 694 3 US-08-724-586-2 Sequence 2, Appli
31 71 100.0 694 4 US-09-421-632-2 Sequence 2, Appli
32 71 100.0 694 4 US-09-932-190-2 Sequence 2, Appli
33 71 100.0 705 2 US-08-655-640-2 Sequence 2, Appli
34 71 100.0 708 2 US-08-655-640-4 Sequence 4, Appli
35 71 100.0 711 1 US-08-154-019-4 Sequence 4, Appli
36 71 100.0 711 1 US-08-461-333-4 Sequence 4, Appli
37 71 100.0 711 3 US-08-464-167-4 Sequence 4, Appli
38 71 100.0 711 3 US-09-158-313-4 Sequence 4, Appli
39 71 100.0 711 4 US-08-476-798-4 Sequence 4, Appli
40 68 95.8 711 1 US-08-145-681-2 Sequence 2, Appli
41 68 95.8 711 1 US-08-250-308-2 Sequence 2, Appli
42 68 95.8 711 1 US-08-453-703-2 Sequence 2, Appli
43 68 95.8 711 2 US-08-456-106-2 Sequence 2, Appli
44 68 95.8 711 3 US-08-456-108-2 Sequence 2, Appli
45 68 95.8 711 4 US-09-265-577-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-204-487-3
Sequence 3, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHIGEKI
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: UCHIDA, TOSHIKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAMPELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: RJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37) "
US-08-204-487-3

Query Match 100.0%; Score 71; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.1e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKV 12
||| |||||
DB 1 CFQWQNRMRKV 12

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882

GENERAL INFORMATION:

APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,948

FILING DATE:

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/488,217

FILING DATE: JUNE 7, 1995

APPLICATION NUMBER: 08/418,642

FILING DATE: APRIL 7, 1995

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 947-1-008A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

DESCRIPTION: LF-Cl, 8-25

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

US-08-485-948-8

Query Match 100.0%; Score 71; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.1e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKV 12
||| |||||
DB 1 CFQWQNRMRKV 12

RESULT 3

US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341

GENERAL INFORMATION:

APPLICANT: LI, YONG MING
APPLICANT: VLASSARA, HELEN
APPLICANT: CERAMI, ANTHONY
TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/628,380

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/418,642

FILING DATE: APRIL 7, 1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 947-1-008 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

DESCRIPTION: LF-Cl, 8-25

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

US-08-628-380-8

Query Match 100.0%; Score 71; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 7.1e-06;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKV 12

DB 1 CFQWQNRMRKV 12

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245

GENERAL INFORMATION:

APPLICANT: YONG MING LI

APPLICANT: HELEN VLASSARA

APPLICANT: ANTHONY CERAMI

TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE

NUMBER OF SEQUENCES: 9


```
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Klauber & Jackson
;; STREET: 411 Hackensack Avenue
;; CITY: Hackensack
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07601
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/475,055
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/485,948
;; FILING DATE:
;; APPLICATION NUMBER: 08/489,217
;; FILING DATE: JUNE 7, 1995
;; APPLICATION NUMBER: 08/418,642
;; FILING DATE: APRIL 7, 1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 947-1-008A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; DESCRIPTION: LF-C1, 8-25
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
;; US-08-475-055-8
;;
;; Query Match 100.0%; Score 71; DB 2; Length 18;
;; Best Local Similarity 100.0%; Pred. No. 7.1e-06;
;; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;;
Qy 1 CFQWRNNRKVR 12
Db 1 CFQWRNNRKVR 12
;;
RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KB
COMPUTER: IBM Compatible
;;
OPERATING SYSTEM: MS-DOS
SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3
Query Match 100.0%; Score 71; DB 1; Length 20;
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Best Local Similarity 100.0%, Pred. No. 7.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWQRNMRKVR 12
    |||||
Db 2 CFQWQRNMRKVR 13

RESULT 6
US-07-891-174-3
; Sequence 3, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Porack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8950
; TELEFAX: 202-371-8956
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 100.0%; Score 71; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWQRNMRKVR 12
    |||||
Db 2 CFQWQRNMRKVR 13

RESULT 7
US-08-204-487-1
; Sequence 1, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGRAKI
; APPLICANT: DOSAKO, SHUN ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: EUN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
```

```
TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 20 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: 1..20
;   OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
;   DERIVED FROM HUMAN LACTOFERRIN"
US-08-204-487-1

Query Match      100.0%; Score 71; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWRNMRKVR 12
   |||||
DB 2 CFQWRNMRKVR 13

RESULT 8
US-08-256-771-24
; Sequence 24, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,771
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 20 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are linked by
; OTHER INFORMATION: disulfide bond"
```

```
US-08-256-771-24

Query Match      100.0%; Score 71; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWRNMRKVR 12
   |||||
DB 2 CFQWRNMRKVR 13

RESULT 9
US-08-256-771-25
; Sequence 25, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,771
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 20 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are protected to
; OTHER INFORMATION: prevent disulfide bond"
US-08-256-771-25

Query Match      100.0%; Score 71; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWRNMRKVR 12
   |||||
DB 2 CFQWRNMRKVR 13

RESULT 10
US-08-381-984-24
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; Sequence 24, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues as well as
; OTHER INFORMATION: and 19 are bonded by disulfide linkage"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
; US-08-381-984-24

Query Match 100.0%; Score 71; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNRKVR 12
Db 2 CFQWQRNRKVR 13

RESULT 11
US-08-381-984-25
; Sequence 25, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at positions 2
; OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
; US-08-381-984-25

Query Match 100.0%; Score 71; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNRKVR 12
Db 2 CFQWQRNRKVR 13

RESULT 12
US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; TITLE OF INVENTION: useful microorganism thereof
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KRI998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 4

; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4

Query Match 100.0%; Score 71; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12
| | | | | | | | | | | | | | | | | | | | | |
DB 2 CFQWQNNRKVR 13

RESULT 13

US-09-508-734-6

; Sequence 6, Application US/09508734

; Patent No. 6433509

; GENERAL INFORMATION:

; APPLICANT: Samyang Genex Corporation

; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SYG/00139

; CURRENT APPLICATION NUMBER: US/09/508,734

; CURRENT FILING DATE: 2000-06-01

; PRIOR APPLICATION NUMBER: PCT/KR99/00373

; PRIOR FILING DATE: 1999-07-14

; PRIOR APPLICATION NUMBER: KR1998-29351

; PRIOR FILING DATE: 1998-07-13

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Kopatentin 1.71

; SEQ ID NO 6

; LENGTH: 24

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-508-734-6

Query Match

100.0%; Score 71; DB 4; Length 24;

Best Local Similarity 100.0%; Pred. No. 9.4e-06;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12
| | | | | | | | | | | | | | | | | | | | | |
DB 3 CFQWQNNRKVR 14

RESULT 14

US-07-755-161A-10

; Sequence 10, Application US/07755161A

; Patent No. 5304633

; GENERAL INFORMATION:

; APPLICANT: Mamoru TOMITA et al.

; TITLE OF INVENTION: Antimicrobial Peptides and an

; TITLE OF INVENTION: Antimicrobial Agent

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500KB

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: DisplayWrite

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/755,161A

; FILING DATE: 19910905

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 25 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE:

; HYPOTHETICAL:

; ANTI-SENSE:

; FRAGMENT TYPE:

; ORIGINAL SOURCE:

; ORGANISM:

; STRAIN:

; INDIVIDUAL ISOLATE:

; DEVELOPMENTAL STAGE:

; HAPLOTYPE:

; TISSUE TYPE:

; CELL TYPE:

; CELL LINE:

; ORGANELLE:

; IMMEDIATE SOURCE:

; LIBRARY:

; CLONE:

; POSITION IN GENOME:

; CHROMOSOME/SEGMENT:

; MAP POSITION:

; UNITS:

; FEATURE:

; NAME/KEY: modified site

; LOCATION: 4

; IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "thiol group of

; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with

; OTHER INFORMATION: thiol group of Cys residue at location 21"

; FEATURE:

; NAME/KEY: modified site

; LOCATION: 21

; IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "thiol group of

; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with

; OTHER INFORMATION: thiol group of Cys residue at location 4"

; PUBLICATION INFORMATION:

; AUTHORS:

; TITLE:

; JOURNAL:

; VOLUME:

; ISSUE:

; PAGES:

; DATE:

; DOCUMENT NUMBER:

; FILING DATE:

; PUBLICATION DATE:

; RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10

Query Match 100.0%; Score 71; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 9.8e-06;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12

| | | | | | | | | | | | | | | | | | | | | |

DB 4 CFQWQNNRKVR 15

| | | | | | | | | | | | | | | | | | | | | |

RESULT 15
US-07-891-174-10
Sequence 10, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
LOCATION: 21

IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
Query Match 100.0%; Score 71; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFQWQNRKVR 12
DB 4 CFQWQNRKVR 15
Search completed: February 21, 2003, 07:50:32
Job time : 9.7 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds
(without alignments)
35.508 Million cell updates/sec

Title: US-09-743-107B-47
Perfect score: 71
Sequence: 1 CFQWQNNRKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	15	9	US-09-798-869-2
2	71	100.0	25	9	US-09-798-869-20
3	71	100.0	694	9	US-10-023-096-2
4	63	88.7	15	9	US-09-798-869-6
5	54	76.1	15	9	US-09-798-869-3
6	54	76.1	25	9	US-09-798-869-23
7	46	64.8	15	9	US-09-798-869-7
8	45	63.4	15	9	US-09-798-869-4
9	45	63.4	25	9	US-09-798-869-22
10	42	59.2	15	9	US-09-798-869-8
11	42	59.2	15	9	US-09-798-869-29
12	42	59.2	15	9	US-09-798-869-30
13	38	53.5	489	9	US-09-888-320-2
14	37	52.1	21	10	US-09-864-761-47985
15	37	52.1	747	9	US-10-066-500-58
16	37	52.1	747	9	US-10-002-796-58
17	37	52.1	747	9	US-10-066-273-58
18	37	52.1	747	9	US-10-066-494-58
19	36	50.7	86	9	US-09-738-626-5715

20	36	50.7	209	10	US-09-904-536-8	Sequence 8, Appli
21	36	50.7	209	10	US-09-904-536-9	Sequence 9, Appli
22	36	50.7	209	10	US-09-904-536-11	Sequence 11, Appli
23	36	50.7	209	10	US-09-904-536-12	Sequence 12, Appli
24	36	50.7	209	10	US-09-904-536-13	Sequence 13, Appli
25	36	50.7	209	10	US-09-904-536-14	Sequence 14, Appli
26	36	50.7	209	10	US-09-904-536-15	Sequence 15, Appli
27	36	50.7	209	10	US-09-904-536-16	Sequence 16, Appli
28	36	50.7	209	10	US-09-904-536-17	Sequence 17, Appli
29	36	50.7	209	10	US-09-904-536-18	Sequence 18, Appli
30	36	50.7	212	10	US-09-904-536-10	Sequence 10, Appli
31	36	50.7	235	9	US-10-035-449-6	Sequence 6, Appli
32	36	50.7	235	10	US-09-448-378-1	Sequence 1, Appli
33	36	50.7	235	10	US-09-983-806-6	Sequence 1, Appli
34	36	50.7	235	10	US-09-904-536-1	Sequence 1, Appli
35	36	50.7	338	9	US-09-978-295A-119	Sequence 119, App
36	36	50.7	338	9	US-09-978-697-119	Sequence 119, App
37	36	50.7	338	9	US-09-978-192A-119	Sequence 119, App
38	36	50.7	338	9	US-09-998-822A-119	Sequence 119, App
39	36	50.7	338	9	US-09-978-189-119	Sequence 119, App
40	36	50.7	553	9	US-09-796-753-14	Sequence 14, App
41	36	50.7	553	10	US-09-981-649A-6	Sequence 6, Appli
42	36	50.7	553	10	US-09-981-649A-24	Sequence 24, Appli
43	36	50.7	554	10	US-09-981-649A-30	Sequence 30, Appli
44	36	50.7	554	10	US-09-981-649A-32	Sequence 32, Appli
45	36	50.7	559	10	US-09-981-649A-28	Sequence 28, Appli

ALIGNMENTS

RESULT 1
US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINER (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2

Query Match 100.0%; Score 71; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12
Db 3 CFQWQNNRKVR 14

RESULT 2
US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINER (RNSON

```
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match      100.0%; Score 71; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CFQWQRNMRKVR 12
      |||||
DB      3 CFQWQRNMRKVR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; TITLE OF INVENTION: Lactoferrin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-023-096-2
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Query Match      100.0%; Score 71; DB 9; Length 694;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CFQWQRNMRKVR 12
      |||||
DB      22 CFQWQRNMRKVR 33

RESULT 4
US-09-798-869-6
; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJARNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-6

Query Match      88.7%; Score 63; DB 9; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CFQWQRNMRKVR 12
      |||||
DB      3 CFQWQRNMRKVR 14

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJARNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-3

Query Match      76.1%; Score 54; DB 9; Length 15;
Best Local Similarity 72.7%; Pred. No. 0.0041;
```


Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRMRKV 11
|:|||||:
Db 3 CYQWRMRKL 13

RESULT 6
US-09-798-869-23
; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23

Query Match 76.1%; Score 54; DB 9; Length 25;
Best Local Similarity 72.7%; Pred. No. 0.0066;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRMRKV 11
|:|||||:
Db 3 CYQWRMRKL 13

RESULT 7
US-09-798-869-7
; Sequence 7, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-7

Query Match 64.8%; Score 46; DB 9; Length 15;
Best Local Similarity 63.8%; Pred. No. 0.0086;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWRMRKV 11
|:|||||:
Db 3 CYQWRMRKL 13

RESULT 8
US-09-798-869-4
; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4

Query Match 63.4%; Score 45; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.13;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWRMRKV 11
|:|||||:
Db 3 CLRQWRMRKV 13

RESULT 9
US-09-798-869-22
; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-22

Query Match 63.4%; Score 45; DB 9; Length 25;
Best Local Similarity 63.6%; Pred. No. 0.2;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWRMRKV 11
|:|||||:
Db 3 CLRQWRMRKV 13

```
RESULT 10
US-09-798-869-8
; Sequence 8, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine
; OTHER INFORMATION: sequence)
US-09-798-869-8
```

```
Query Match          59.2%; Score 42; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.39; Indels 3; Gaps 0;
Matches 7; Conservative 1; Mismatches 3; Indels 3; Gaps 0;
```

```
QY 1 CFQWQRMNRKV 11
|:|:|:|:|
Db 3 CLRWQWEMRKV 13
```

```
RESULT 11
US-09-798-869-29
; Sequence 29, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29
```

```
Query Match          59.2%; Score 42; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.39; Indels 2; Gaps 0;
Matches 6; Conservative 3; Mismatches 3; Indels 2; Gaps 0;
```

```
QY 1 CFQWQRMNRKV 11
|:|:|:|:|
Db 3 CLRWQWEMRKV 13
```

```
RESULT 12
US-09-798-869-30
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; Sequence 30, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-30
```

```
Query Match          59.2%; Score 42; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.39; Indels 2; Gaps 0;
Matches 6; Conservative 3; Mismatches 3; Indels 2; Gaps 0;
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```
QY 1 CFQWQRMNRKV 11
|:|:|:|:|
Db 3 CLRWQWEMRKV 13
```

```
RESULT 13
US-09-888-320-2
; Sequence 2, Application US/09888320
; Publication No. US20030013090A1
; GENERAL INFORMATION:
; APPLICANT: Barry III, Clifton E.
; APPLICANT: DeBarber, Andrea E.
; APPLICANT: Mdluli, Khisimuzi
; APPLICANT: Bekker, Linda-Gail
; APPLICANT: as represented by The Government of the United States of America
; APPLICANT: Department of Health and Human Services
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
; FILE REFERENCE: 015280-413100US
; CURRENT APPLICATION NUMBER: US/09/888,320
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/214,187
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
US-09-888-320-2
```

```
Query Match          53.5%; Score 38; DB 9; Length 489;
Best Local Similarity 54.5%; Pred. No. 47; Indels 3; Gaps 0;
Matches 6; Conservative 2; Mismatches 3; Indels 3; Gaps 0;
```

```
QY 1 CFQWQRMNRKV 11
|:|:|:|:|
Db 253 CQWFRMRKRM 263
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```
RESULT 14
US-09-864-761-47985
; Sequence 47985, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
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; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-02-04
; PRIOR FILING DATE: 2000-02-04
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
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; PRIOR FILING DATE: 2001-01-29
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; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
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; RESULT 15
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; Sequence 58, Application US/10066500
; Patent No. US2002017165A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C7
; CURRENT APPLICATION NUMBER: US/10/066,500
; CURRENT FILING DATE: 2002-02-01
; PRIOR FILING DATE: 2001-11-15
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8	PRIOR FILING DATE: 2000-09-18	
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37	PRIOR APPLICATION NUMBER: PCT/US98/25108	
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39	PRIOR APPLICATION NUMBER: PCT/US98/25190	
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41	PRIOR APPLICATION NUMBER: PCT/US99/05028	
42	PRIOR FILING DATE: 1999-03-08	
43	PRIOR APPLICATION NUMBER: PCT/US99/12252	
44	PRIOR FILING DATE: 1999-06-02	
45	PRIOR APPLICATION NUMBER: PCT/US99/20111	
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50	PRIOR FILING DATE: 1999-09-15	
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Query Match 52.1%; Score 37; DB 9; Length 747;

Qy 1 CFQWQRNMRKV 11
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Db 311 CVRWQINSRRI 321

Search completed: February 21, 2003, 08:08:02
Job time : 10.55 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 seconds
(without alignments)
120.168 Million cell updates/sec

Title: US-09-743-107b-47

Perfect score: 71

Sequence: 1 CFQQRNMRKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	711	1	TFHUL
2	54	76.1	708	2	lactotransferrin p
3	51	71.8	33	2	JC2323
4	45	63.4	707	1	lactoferrin - goat
5	44	62.0	4568	2	lactoferrin - sheep
6	42	59.2	298	2	lactoferrin precursor
7	42	59.2	511	2	dynein beta heavy
8	41	57.7	275	2	hypothetical prote
9	41	57.7	932	2	hypothetical prote
10	40	56.3	681	2	hypothetical prote
11	39	54.9	584	2	hypothetical prote
12	38	53.5	121	2	hypothetical prote
13	38	53.5	205	2	hypothetical prote
14	38	53.5	274	2	26S proteasome SU
15	38	53.5	282	2	apolipoprotein B-1
16	38	53.5	489	2	hypothetical prote
17	38	53.5	515	2	probable monooxyge
18	38	53.5	543	2	probable cytochrom
19	38	53.5	1432	2	cytochrome P450 ho
20	37	52.1	206	2	trichonyalin like
21	37	52.1	206	2	pyridoxamine 5'-ph
22	37	52.1	208	2	pyridoxamine 5'-ph
23	37	52.1	202	2	probable pyridoxam
24	37	52.1	222	2	hypothetical prote
25	37	52.1	275	1	interleukin-2 rece
26	37	52.1	275	1	interleukin-2 rece
27	37	52.1	289	2	33.3K hypothetical
28	37	52.1	361	2	hypothetical prote
29	37	52.1	365	2	MHC class I histoc
30	37	52.1	500	2	protein kinase (BC

ALIGNMENTS

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000

C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S741

R:Cho, Y.

submitted to the EMBL Data Library, March 1994

A:Reference number: G06820

A:Accession: G01394

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-711 <CHO>

A:Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237

R:Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A:Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A:Reference number: S11228; MUID:90384839; PMID:2402455

A:Accession: S11228

A:Molecule type: mRNA

A:Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>

A:Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R:Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A:Title: Differential molecular mechanism of the estrogen action that regulates lactoferrin

A:Reference number: A45401; MUID:93125571; PMID:1480183

A:Accession: A45401

A:Molecule type: DNA

A:Residues: 1-15 <TEN>

A:Cross-references: GB:S52659; NID:G263311; PIDN:AAB24877.1; PID:G263312

A:Experimental source: Placenta

A:Note: sequence extracted from NCBI backbone (NCBIP:122202)

R:Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A:Title: Nucleotide sequence of human lactoferrin cDNA.

A:Reference number: S10324; MUID:90326549; PMID:2374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <POW>

A:Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A:Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A:Reference number: S15853; MUID:91264786; PMID:2049066

A:Accession: S15853

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 20-31 <ST1>

A:Accession: S20841

A:Molecule type: protein

A:Residues: 20-28, 'X', 30-31 <ST2>

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
 Blood 70, 989-993, 1987
 A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
 A;Reference number: S07160; MUID:86001031; PMID:3477300
 A;Accession: S07160
 A;Molecule type: mRNA
 A;Residues: 436-487, 'A', 489-711 <RAD>
 A;Cross-references: EMBL:M18642; NID:G186815; PIDN:AAA86665.1; PID:G386855
 R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
 Cancer Res. 51, 3037-3043, 1991
 A;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
 A;Reference number: A61169; MUID:91235214; PMID:1674448
 A;Accession: A61169
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 3-701, 'SWKPVN' <PAN>
 A;Experimental source: normal breast tissue
 R;Mez-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.; Eur. J. Biochem. 145, 659-666, 1984
 A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with other
 A;Reference number: A31000; MUID:85076667; PMID:6510420
 A;Accession: A31000
 A;Molecule type: protein
 A;Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-400
 A;Note: this is the final paper in a series
 R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
 Eur. J. Biochem. 241, 303-308, 1996
 A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity
 A;Reference number: S74119; MUID:97054624; PMID:8899921
 A;Accession: S74119
 A;Molecule type: protein
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 A;Cross-references: GDB:119368; OMIM:150210
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 C;Keywords: duplication; glycoprotein; iron binding; milk
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 F;20-711/Product: lactotransferrin #status experimental <MAT>
 F;21-356/Domain: transferrin repeat homology <TRH1>
 F;360-699/Domain: transferrin repeat homology <TRH2>
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 F;157-498/Binding site: carbohydrate (Asn) (covalent) #status experimental
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 DB 39 CFQWQNRMRKV 50
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 JC2323
 lactoferrin - goat
 C;Species: Capra aegagrus hircus (domestic goat)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 C;Accession: JC2323
 R;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
 A;Reference number: JC2323; MUID:94380047; PMID:8093048
 A;Accession: JC2323
 A;Molecule type: mRNA
 A;Residues: 1-708 <LEP>
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication; glycoprotein
 F;359-696/Domain: transferrin repeat homology <TRH2>
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 DB 38 CYQWQNRMRKV 48

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S52107

lactoferrin - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997

A;Accession: S52107

R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.

Biochim. Biophys. Acta 1243, 25-32, 1995

A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet a

A;Reference number: S52107; MUID:95127729; PMID:7827104

A;Accession: S52107

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-33 <QIA>

C;Superfamily: transferrin; transferrin repeat homology

C;Keywords: duplication

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 DB 19 CYQWQNRMRKV 29

RESULT 4

A28438

lactoferrin precursor - mouse

N;Alternate names: lactotransferrin

C;Species: Mus musculus (house mouse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

A;Accession: A28438; A41205

R;Pentecost, B.T.; Teng, C.T.

J. Biol. Chem. 262, 10134-10139, 1987

A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret

A;Reference number: A92596; MUID:87280033; PMID:3611056

A;Accession: A28438

A;Molecule type: mRNA

A;Residues: 3-707 <PEN>

A;Cross-references: EMBL:J03298

R;Liu, Y.; Teng, C.T.

J. Biol. Chem. 266, 21880-21895, 1991

A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.

A;Reference number: A41205; MUID:92042099; PMID:1939212

A;Accession: A41205

A;Molecule type: DNA

A;Residues: 1-15 <LIU>

A;Cross-references: GB:M74778

C;Superfamily: transferrin; transferrin repeat homology

C;Keywords: duplication; glycoprotein

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-707/Product: lactotransferrin #status predicted <MAT>

F;358-695/Domain: transferrin repeat homology <TRH2>

F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.4%; Score 45; DB 1; Length 707;
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 DB 37 CLRQWNRMRKV 47

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C/Species: Chlamydomonas reinhardtii
C/Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C/Accession: T08030
R/Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A/Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A/Reference number: Z16302; MUID:94274778; PMID:8006077
A/Accession: T08030
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-4568 <MIT>
A/Cross-references: EMBL:U02963; NID:G409965; PIDN:AA19956.1; PID:G514215
A/Experimental source: strain 21gr
C/Genetics:
A/Gene: ODA4
A/Map position: IX
A/Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 359/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;
334/3; 3686/3; 3892/3; 4240/3
C/Superfamily: dynein heavy chain, ciliary
C/Keywords: nucleotide binding; P-loop
F/1919-1926/Region: nucleotide-binding motif A (P-loop)
F/202-2209/Region: nucleotide-binding motif A (P-loop)
F/2530-2537/Region: nucleotide-binding motif A (P-loop)

Query Match 62.0%; Score 44; DB 2; Length 4568;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKVR 12
Db 1852 CFQWQSLRVIQ 1863

RESULT 6
AD2346
hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)
C/Species: Nostoc sp.
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C/Accession: AD2346
R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AD2346
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-298 <KUR>
A/Cross-references: GB:BA000019; PIDN:BA876022.1; PID:G17133459; GSPDB:GN00179
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: alr4323

Query Match 59.2%; Score 42; DB 2; Length 298;
Best Local Similarity 77.8%; Pred. No. 7.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQRMNRK 10
Db 163 FHWQRMNRK 171

RESULT 7
AB0858
hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Ty
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi

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C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C/Accession: AB0858
 R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Conner, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A/Reference number: AB0502; PMID:11677608
 A/Accession: AB0858
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-511 <PAR>
 A/Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:G16504016; GSPDB:GN00176
 C/Genetics:
 A/Gene: STY3070

Query Match 59.2%; Score 42; DB 2; Length 511;
 Best Local Similarity 58.3%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKVR 12
 Db 350 CFQWQRMNRKVR 361

RESULT 8
 T22597
 hypothetical protein F53H4.4 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C/Accession: T22597
 R/Dobson, R.
 submitted to the EMBL Data Library, October 1996
 A/Reference number: Z19587
 A/Accession: T22597
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-275 <WIL>
 A/Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
 A/Experimental source: clone F53H4
 C/Genetics:
 A/Gene: CESP:F53H4.4
 A/Map position: X
 A/Introns: 67/1; 153/1
 C/Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4

Query Match 57.7%; Score 41; DB 2; Length 275;
 Best Local Similarity 63.6%; Pred. No. 10;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQRMNRKVR 12
 Db 262 FQWQRMNRKVR 272

RESULT 9
 T28820
 hypothetical protein F07C3.1 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C/Accession: T28820
 R/Favella, A.; Gartung, S.
 submitted to the EMBL Data Library, March 1996
 A/Description: The sequence of C. elegans cosmid F07C3.
 A/Reference number: Z20528
 A/Accession: T28820
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-932 <FAV>
 A/Cross-references: EMBL:U50308; PIDN:AAC48001.1; GSPDB:GN00023; CESP:F07C3.1
 A/Experimental source: strain Bristol N2; clone F07C3
 C/Genetics:

A:Gene: CESP:F07C3.1
A:Map position: 5
A:Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 599/3

Query Match 57.7%; Score 41; DB 2; Length 932;
Best Local Similarity 63.6%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQRMKRV 12
|||||:
Db 579 FQWQSRALVK 599
|||||:
|||||:

RESULT 10
T19429
hypothetical protein C24H11.8 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19429
R:Lloyd, C.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19123
A:Accession: T19429
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-681 <WIL>
A:Cross-references: EMBL:Z81475; PIDN:CAB03914.1; GSPDB:GN00021; CESP:C24H11.8
A:Experimental source: clone C24H11
C:Genetics:
A:Gene: CESP:C24H11.8
A:Map position: 3
A:Introns: 18/3; 65/3; 108/1; 138/1; 177/3; 256/2; 303/2; 343/1; 409/3; 484/3; 532/2; 568/3

Query Match 56.3%; Score 40; DB 2; Length 681;
Best Local Similarity 60.0%; Pred. No. 38;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWQRMKRV 12
|||||:
Db 192 RWQKRRVR 201
|||||:
|||||:

RESULT 11
C84325
hypothetical protein Vng1732c [imported] - *Halobacterium* sp. NRC-1
C:Species: *Halobacterium* sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: C84325
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo, Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of *Halobacterium* species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: C84325
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-584 <STO>
A:Cross-references: GB:AE004437; NID:g10581192; PIDN:AA319967.1; GSPDB:GN00138
C:Genetics:
A:Gene: VNG1732C

Query Match 54.9%; Score 39; DB 2; Length 584;
Best Local Similarity 41.7%; Pred. No. 49;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 12
|||||:
Db 445 CFTWRKDMERK 456
|||||:
|||||:

RESULT 12

AH3147
hypothetical protein Atu4804 [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C:Species: *Agrobacterium tumefaciens*
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AH3147
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I.; Wager, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, K.; P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AH3147
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-121 <KUR>
A:Cross-references: GB:AE008689; PIDN:AAL45598.1; PID:g17743317; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu4804
A:Map position: linear chromosome

Query Match 53.5%; Score 38; DB 2; Length 121;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 11
|||||:
Db 14 CLAWQRRNRV 24
|||||:
|||||:

RESULT 13
E90094
26S proteasome SU B5 [imported] - *Guillardia theta* nucleomorph
C:Species: nucleomorph *Guillardia theta*
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: E90094
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reil, Nature 410, 1091-1096, 2001
A:Title: The highly reduced genome of an enslaved algal nucleus.
A:Reference number: A99082; MUID:11323671; PMID:11323671
A:Accession: E90094
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-205 <DOU>
A:Cross-references: GB:AF165818; NID:g13794510; PIDN:AAK39885.1; GSPDB:GN00150
C:Genetics:
A:Gene: prsB5
A:Map position: 1
A:Genome: nucleomorph
C:Keywords: nucleomorph

Query Match 53.5%; Score 38; DB 2; Length 205;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 8
|||||:
Db 63 CFFWRNL 70
|||||:
|||||:

RESULT 14
B60950
apolipoprotein B-100 - rat (fragment)
C:Species: *Rattus norvegicus* (Norway rat)
C>Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 07-Oct-1994
C:Accession: B60950
R:Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
A:Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
A:Reference number: A60950; MUID:90324804; PMID:2373961

A;Accession: B60950
 A;Molecule type: mRNA
 A;Residues: 1-274 <IAW>
 A;Note: authors translated the codon ATA for residue 8 as Val
 C;Superfamily: apolipoprotein B
 C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match 53.5%; Score 38; DB 2; Length 274;
 Best Local Similarity 66.7%; Pred. No. 35;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 WQRMNRKV 12
 | | | | |
 DB 39 WDRNRKFR 47

RESULT 15

F90580
 Hypothetical protein MYPU_5500 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
 C;Species: Mycoplasma pulmonis
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
 C;Accession: F90580
 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
 Nucleic Acids Res. 29, 2145-2153, 2001
 A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
 A;Reference number: A99512; MUID:21267165; PMID:11353084
 A;Accession: F90580
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-282 <KUR>
 A;Cross-references: GB:AL445566; PID:G14089965; PIDN:CAC13723.1; GSPDB:GN00153
 A;Experimental source: strain UAB CTIP
 C;Genetics:
 A;Gene: MYPU_5500
 A;Genetic code: SGC3

Query Match 53.5%; Score 38; DB 2; Length 282;
 Best Local Similarity 50.0%; Pred. No. 36;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWRNRKV 11
 | | | | |
 DB 20 FAWQNNIKI 29

Search completed: February 21, 2003, 07:47:34
 Job time : 12.65 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds
(without alignments)
108.199 Million cell updates/sec

Title: US-09-743-107B-47

Perfect score: 71

Sequence: 1 CFQWQNNMRKVR 12

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	71	100.0	711	1	TRFL_HUMAN
2	54	76.1	708	1	TRFL_CAMDR
3	54	76.1	708	1	TRFL_CAPHI
4	46	64.8	695	1	TRFL_HORSE
5	45	63.4	707	1	TRFL_MOUSE
6	44	62.0	4568	1	DYHB_CHLRE
7	39	54.9	292	1	NLA_DROME
8	38	53.5	146	1	RPOB_LIBAF
9	37	52.1	62	1	RL28_THETN
10	37	52.1	275	1	IL2A_BOVIN
11	37	52.1	275	1	IL2A_SHEEP
12	37	52.1	385	1	IA34_HUMAN
13	37	52.1	455	1	YKYL_CABEL
14	37	52.1	749	1	VP4_ROTGA
15	37	52.1	783	1	YNR2_CABEL
16	36	50.7	214	1	VIF_SIVS4
17	36	50.7	235	1	FL3L_HUMAN
18	36	50.7	306	1	BUB2_YEAST
19	36	50.7	1135	1	PHYC_SORBI
20	36	50.7	2671	1	IP3T_HUMAN
21	35	49.3	85	1	PMRD_SALTY
22	35	49.3	211	1	LOLB_VIBCH
23	35	49.3	238	1	YBM9_SCHPO
24	35	49.3	428	1	SVH_CHLMU
25	35	49.3	435	1	DCOR_PANRE
26	35	49.3	502	1	C911_ARATH
27	35	49.3	663	1	PD11_HUMAN
28	35	49.3	665	1	YL14_CABEL
29	35	49.3	708	1	TRFL_BUBBU
30	35	49.3	728	1	KDGI_ARATH
31	35	49.3	765	1	Y008_HUMAN
32	35	49.3	962	1	YBX7_SCHPO
33	34	47.9	60	1	RL28_BACST

RESULT 1

ID	TRFL_HUMAN	STANDARD;	PRT;	711 AA.
AC	P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96KZ4;			
AC	Q96KZ5;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrroxin A;			
DE	Lactoferrroxin B; Lactoferrroxin C]			
GN	LTF OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RC	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woioshuk S.L., de Boer H.A., Pieper F.R.;			
RT	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RL	Nucleic Acids Res. 18:5288-5288(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cho Y.Y.;			
RL	Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Connely O.M.;			
RL	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RT	"Molecular cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Rado T.A.;			
RT	"Human neutrophil lactoferrin coding and 5' flanking region DNA			
RL	sequences.";			
RN	[6]			
RP	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cheng H., Chen X., Huan L.;			
RT	"cDNA cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[8]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			

34	34	47.9	62	1	RL28_LISMO
35	34	47.9	62	1	RL28_STAAM
36	34	47.9	152	1	YE83_METJA
37	34	47.9	215	1	VIF_HV2SB
38	34	47.9	215	1	VIF_HV2ST
39	34	47.9	246	1	Y495_SYNY3
40	34	47.9	267	1	Y125_MYCCA
41	34	47.9	272	1	IL2A_HUMAN
42	34	47.9	316	1	NORC_CHLTR
43	34	47.9	334	1	CATL_MOUSE
44	34	47.9	334	1	CATL_RAT
45	34	47.9	369	1	SP11_MYXVL

ALIGNMENTS

Q92aj2	listeria mo
Q99up4	staphylococ
Q58878	methanococc
P24452	human immun
P20878	human immun
Q55185	synchocyst
P53661	mycoplasma
P01589	homo sapien
O84281	chlamydia t
P06797	mus musculu
P07154	rattus norv
P12393	myxoma viru

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE-Mammary Gland.
RX MEDLINE=9036549; PubMed=2374734;
RA Powell M.J., Ogden J.E.;
RT "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=8507667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
RT "Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1984).
RN [10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
Jolles P.;
RT "The present state of the human lactotransferrin sequence. Study and
alignment of the cyanogen bromide fragments and characterization of
N- and C-terminal domains.";
RL Biochim. Biophys. Acta 670:243-254(1981).
RN [11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
lactotransferrin.";
RL FEBS Lett. 142:107-110(1982).
RN [12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
RN [13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
Gao L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
Sagripanti J.L.;
RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2555506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human diferric lactoferrin refined at 2.2-A
resolution.";
RL Acta Crystallogr. D 51:629-646(1995).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
binding properties and crystal structure of the histidine-
253-->methionine mutant.";
RL Biochemistry 36:341-346(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in Aspergillus
awamori.";
RL Acta Crystallogr. D 55:403-407(1999).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
and analysis of ligand-induced conformational change.";
RL Acta Crystallogr. D 54:1319-1335(1998).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of opioid antagonist peptides derived
from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810(1990).
RN [20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
Qumsiyeh M.B., Lin P.-Y., Batti S., Reddy M.K., Kanai A., Hotta Y.,
Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
El Matri L., Iwata F., Kalsner-Kupfer M., Nagata M., Nakayasu K.,
Hejtmancik J.F., Teng C.T.;
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RL Mol. Vision 4:31-32(1998).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
CC -1- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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DR EMBL; X53961; CAA37914.1; -
DR EMBL; U07643; AAB60324.1; -
DR EMBL; M93150; AAA36159.1; -
DR EMBL; M83202; AAA59511.1; -
DR EMBL; M83205; AAA58656.1; -
DR EMBL; M18642; AAA86665.1; -
DR EMBL; AF332168; AAG48753.1; -
DR EMBL; BC015822; AAH15822.1; -
DR EMBL; BC015823; AAH15823.1; -
DR EMBL; M73700; AAA59479.1; -
DR EMBL; X52941; CAA37116.1; -
DR EMBL; U95626; AAB57795.1; -
DR PIR; S11228; TTHUL.
DR PDB; 1LCF; 31-AUG-94.
DR PDB; 1LCT; 31-OCT-93.
DR PDB; 1LFG; 31-JUL-94.
DR PDB; 1LFH; 31-OCT-93.
DR PDB; 1LFI; 31-OCT-93.
DR PDB; 1LGB; 31-AUG-94.
DR PDB; 1LGC; 31-AUG-94.
DR PDB; 1BKA; 08-NOV-96.
DR PDB; 1DSN; 08-VAR-96.
DR PDB; 1HSE; 12-VAR-97.
DR PDB; 1VFD; 21-APR-97.

Query Match 100.0%; Score 71; DS 1; Length 711;
Best Local Similarity 100.0%; Pred. No. 4.9e-05; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 1 CFQWQRNKKVR 12
| | | | | | | | | | | | | |
DB 39 CFQWQRNKKVR 50

RESULT 2

TRFL_CAMDR STANDARD; PRT; 708 AA.
AC Q9TUMG; Q9MZS5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (lactoferrin).
GN LTF.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Somali; TISSUE=Lactating mammary gland;
RA Kappeler S.R., Ackermann M., Farah Z., Puhon Z.;
RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
RL Int. Dairy J. 9:481-486(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC
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CC
CC EMBL; AJ131674; CAB53387.1; -
CC EMBL; AF165879; AAF82241.1; -
CC HSP; 077811; IBI.
CC InterPro; IPR001156; Transferrin.
CC Pfam; PF00405; transferrin; 2.
CC PRINTS; PR00422; TRANSFERRIN.
CC SMART; SM00094; TR_FER_2.
CC PROSITE; PS00205; TRANSFERRIN 1; 2.
CC PROSITE; PS00206; TRANSFERRIN_2; 2.
CC PROSITE; PS00207; TRANSFERRIN 3; 2.
CC Signal.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
Signal.
FT CHAIN 1 19 BY SIMILARITY.
FT CHAIN 20 708 LACTOTRANSFERRIN.
FT REPEAT 20 363 1.
FT REPEAT 364 708 2.
FT DISULFID 28 64 BY SIMILARITY.
FT DISULFID 38 55 BY SIMILARITY.
FT DISULFID 134 217 BY SIMILARITY.
FT DISULFID 176 192 BY SIMILARITY.
FT DISULFID 189 200 BY SIMILARITY.
FT DISULFID 250 264 BY SIMILARITY.
FT DISULFID 367 399 BY SIMILARITY.

Query Match 76.1%; Score 54; DB 1; Length 708;
Best Local Similarity 75.0%; Pred. No. 0.048;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRNKKVR 12
| | | | | | | | | | | | | |
DB 38 CAQWQRNKKVR 49

RESULT 3

TRFL_CAPHI STANDARD; PRT; 708 AA.
ID TRFL_CAPHI
AC Q29477; Q29479;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (lactoferrin).
GN LTF.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Lee T., Yu S., Kim S., Lee K., Yu D.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=94380047; PubMed=9093048;
RA Le Provost F., Nocart M., Guerin G., Martin P.;
RT "Characterization of the goat lactoferrin cDNA. Assignment of the
RT relevant locus to bovine U12 syntenic group."
CC Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.


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RESULT 6
DYHB CHLRE
ID QY9565; STANDARD; PRT; 4568 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Dynein beta chain, flagellar outer arm.
GN ODA4 OR ODA-4 OR SUP1
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=219F;
RX MEDLINE=94274778; PubMed=8006077;
RA Mitchell D.R., Brown K.S.;
RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
chain genes";
RL J. Cell Sci. 107:635-644(1994).
CC -!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC DYNEIN HAS ATPASE ACTIVITY.
CC -!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
CC -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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CC -----
DR EMBL; U02963; AAA19556.1; -
DR InterPro; IPR004273; Dynein heavy.
DR Pfam; PF03028; Dynein heavy; 1.
KW Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
KW Coiled coil.
FT DOMAIN 277 293 COILED COIL (POTENTIAL).
FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).
FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
FT DOMAIN 2017 2045 COILED COIL (POTENTIAL).
FT DOMAIN 2831 2848 MICROTUBULE-BINDING (POTENTIAL).
FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
FT DOMAIN 3239 3425 COILED COIL (POTENTIAL).
FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
FT NP_BIND 1919 1926 ATP (POTENTIAL).
FT NP_BIND 2202 2209 ATP (POTENTIAL).
FT NP_BIND 2530 2537 ATP (POTENTIAL).
FT NP_BIND 2879 2886 ATP (POTENTIAL).
SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;

Query Match 62.0%; Score 44; DB 1; Length 4568;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
Db 1852 CFQWQSLRYIQ 1863

RESULT 7
NLA DROME
ID NLA DROME
AC Q9XZL8; Q9V391; PRT; 292 AA.
DT 30-MAY-2000 (Rel. 39, Created)

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DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nebula protein.
GN NLA OR CG6072.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA McCormick A.V., Goldberg M.L.;
RT "Gene required for elongation of meiosis I spindle in Drosophila
females";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Dones M., Dugan-Rocha S., Dunn P.,
Dustin K., Evans G., Gabor C., Garg N.S., Gelbart W.M., Glasser K.,
Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hoskins D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhu H.O.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zou S., Smith H.O.,
Zhang R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
CC -!- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.
CC -----
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CC -----
DR EMBL; AF147700; AAD33987.1; -
DR EMBL; AE003712; AAF55285.1; -
DR FlyBase; FBgn0026629; nla.
DR SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;

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Query Match 54.9%; Score 39; DB 1; Length 292;
 Best Local Similarity 54.5%; Pred. No. 8.4;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNRKVR 12
 DB 150 FQWLSFRRLR 160

RESULT 8
 ID PROB LIBAF STANDARD; PRT; 146 AA.
 AC P41187; 1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (transcriptase
 beta chain) (RNA polymerase beta subunit) (fragment).
 GN PROB
 OS Liberibacter africanus (Liberibacter africanus).
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Rhizobiaceae; Candidatus Liberibacter.
 CC NCBI_TaxID=34020;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=Nelepruit;
 CC Planet P., Jagoueix S., Bove J.M., Garnier M.;
 CC "Detection and characterization of the African Citrus Greening
 CC RT Liberibacter by amplification, cloning and sequencing of the rplKJL-
 CC RT rpoBC operon";
 CC Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA}(N).
 CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
 CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
 CC BETA' CHAIN.
 CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.

Query Match 53.5%; Score 38; DB 1; Length 146;
 Best Local Similarity 60.0%; Pred. No. 6.2;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNRK 10
 DB 10 CFQWQNRGARK 19

RESULT 9
 ID RL28_THETN STANDARD; PRT; 62 AA.
 AC Q8R9U1;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE 50S ribosomal protein L28.
 GN RPMB OR TTE1495.
 OS Thermoanaerobacter tengcongensis.
 CC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
 CC Thermoanaerobacteriaceae; Thermoanaerobacter.
 CC NCBI_TaxID=119072;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=MB4 / JCM 11007;
 CC MEDLINE=21992816; PubMed=11997336;
 CC Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 CC Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 CC Tan H., Chen R., Wang J., Yu J., Yang H.;
 CC "A complete sequence of T. tengcongensis genome";
 CC Genome Res. 12:689-700(2002).
 CC -1- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.

Query Match 52.1%; Score 37; DB 1; Length 62;
 Best Local Similarity 60.0%; Pred. No. 3.9;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWQNRKVR 12
 DB 27 RWKPNRKVR 36

RESULT 10
 ID IL2A_BOVIN STANDARD; PRT; 275 AA.
 AC P12342;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
 DE subunit) (P85) (TAC antigen) (CD25).
 GN IL2RA.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=88212503; PubMed=2835311;
 CC Weinberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S.,
 CC Reeves R., Magnuson J.A.;
 CC "Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";
 CC Immunology 63:603-610(1988).
 CC [2]
 CC SEQUENCE OF 1-21 FROM N.A.
 CC MEDLINE=96116968; PubMed=8563178;
 CC Yoo J., de Leon F.A., Stone R.T., Beattie C.W.;
 CC "Cloning and chromosomal assignment of the bovine interleukin-2
 CC receptor alpha (IL-2R alpha) gene";
 CC Mamm. Genome 6:751-753(1995).
 CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
 CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
 CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
 CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
 CC WITH A GAMMA CHAIN.


```

CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC DR EMBL; M20818; AAA51414.1; -.
CC DR EMBL; U24226; AAC48487.1; -.
CC DR PIR; S07442; S07442.
CC DR HSP; P01589; IILM.
CC DR InterPro; IPR000436; Sush1_SCR_CCP.
CC DR Pfam; PF00084; sush1; 2.
CC DR SMART; SM00032; CCP; 2.
CC KW Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sush1.
CC FT SIGNAL 1 21
CC FT CHAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
CC FT DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 244 262 POTENTIAL.
CC FT DOMAIN 263 275 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 23 78 SUSHI 1.
CC FT DOMAIN 122 185 SUSHI 2.
CC FT DISULFID 24 64 BY SIMILARITY.
CC FT DISULFID 751 77 BY SIMILARITY.
CC FT DISULFID 123 168 BY SIMILARITY.
CC FT DISULFID 152 184 BY SIMILARITY.
CC FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 109 109 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 275 AA; 31238 MW; 4901BBF9A4862390 CRC64;
Query Match 52.1%; Score 37; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 CFQWQRMNRKVR 12
DB 261 CLTWQREKKNR 272
RESULT 11
ID IL2A SHEEP STANDARD; PRT; 275 AA.
AC P26998;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
DE subunit) (P55) (TAC antigen) (CD25).
GN IL2RA.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RA Verhagen A.A.;
RL Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92241682; PubMed=1572550;
RA Bujdoso R., Sargan D.R., Williamson M.L., McConnell I.;
RT "Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa
RT protein, CD25."
RL Gene 113:283-284 (1992).
CC -!- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
CC -!- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE

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CC CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CC CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
CC CC WITH A GAMMA CHAIN.
CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC DR EMBL; Z11560; CAA77652.1; -.
CC DR EMBL; X60149; CAA42723.1; -.
CC DR EMBL; A19167; CAA01447.1; -.
CC DR PIR; S18910; S18910.
CC DR PIR; S18899; S18899.
CC DR PIR; JC1113; JC1113.
CC DR HSP; P01589; IILM.
CC DR InterPro; IPR000436; Sush1_SCR_CCP.
CC DR Pfam; PF00084; sush1; 2.
CC DR SMART; SM00032; CCP; 2.
CC KW Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sush1.
CC FT SIGNAL 1 21
CC FT CHAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
CC FT DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 244 262 POTENTIAL.
CC FT DOMAIN 263 275 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 23 78 SUSHI 1.
CC FT DOMAIN 122 185 SUSHI 2.
CC FT DISULFID 24 64 BY SIMILARITY.
CC FT DISULFID 751 77 BY SIMILARITY.
CC FT DISULFID 123 168 BY SIMILARITY.
CC FT DISULFID 152 184 BY SIMILARITY.
CC FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 166 166 S -> T (IN REF. 2).
CC SQ SEQUENCE 275 AA; 30904 MW; 1101A2DE5A5A088 CRC64;
Query Match 52.1%; Score 37; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 CFQWQRMNRKVR 12
DB 261 CLTWQREKKNR 272
RESULT 12
ID 1A34 HUMAN STANDARD; PRT; 365 AA.
AC P30453; P30454;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, A*34(A-10) alpha chain
DE precursor.
DE HLA-A OR HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (A*3401/A*3402).
RX MEDLINE=93056508; PubMed=1431115;
RA Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
RA Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
RA Martell R.W., du Toit E.D., Parham P.;
RT "Distinctive HLA-A,B antigens of black populations formed by
RT interallelic conversion."
RL J. Immunol. 149:3411-3415 (1992).
RN [2]

```

RP SEQUENCE FROM N.A. (A*3401/A*3402).
 RX MEDLINE-93235211; PubMed-8475492;
 RA Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,
 RA Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzi-Erler M.L.,
 RA du Toit E.D., Farham P.;
 RT "Structural diversity in the HLA-A10 family of alleles: correlations
 RT with serology.";
 RL Tissue Antigens 41:72-80(1993).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC -!- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401
 CC (AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
 CC A*3401.
 CC -----
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 CC -----
 DR EMBL; X61704; CAA43873.1; -;
 DR EMBL; X61705; CAA43874.1; -;
 DR PIR; S16767; S16767.
 DR PIR; S16771; S16771.
 DR HSP; Q19673; 1H8B.
 DR MIM; 142800; -;
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGC1; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 365
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 365
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT VARIANT 3 3
 FT VARIANT 90 90
 FT VARIANT 121 121
 FT VARIANT 129 129
 FT VARIANT 138 138
 FT VARIANT 180 180
 FT VARIANT 312 312
 FT SEQUENCE 365 AA; 41055 MW; 063BF63E6E01F6 CRC64;
 SQ
 Query Match 52.1%; Score 37; DB 1; Length 365;
 Best Local Similarity 66.7%; Pred. No. 24;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 WQNRKRV 12
 | | | | |

Db 84 WDRNTRKVK 92
 RESULT 13
 YKYL_CABEL STANDARD; PRT; 455 AA.
 ID YKYL_CABEL
 AC Q19910;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein F30B5.4 in chromosome IV.
 DE F30B5.4.
 GN Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Miller N., Bradshaw H.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP REVISIONS.
 RP Waterston R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE OKL38 FAMILY.
 CC -----
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 CC -----
 DR EMBL; U42437; AAA83493.2; -;
 DR WormPep; F30B5.4; CE28552.
 DR Hypothetical protein.
 KW SEQUENCE 455 AA; 51148 MW; D8E6909408FD6C69 CRC64;
 SQ
 Query Match 52.1%; Score 37; DB 1; Length 455;
 Best Local Similarity 50.0%; Pred. No. 30;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWRNWK 10
 | | | | |
 Db 102 CIQWELNRR 111
 RESULT 14
 VP4_ROTGA STANDARD; PRT; 749 AA.
 ID VP4_ROTGA
 AC Q04916;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).
 DE S4.
 GN Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
 OX NCBI_TaxID=12705;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE-93233240; PubMed-8386274;
 RA Mackow E.R., Werner-Eckert R., Fay M.B., Tao H., Chen G.-M.;
 RT "Identification and baculovirus expression of the VP4 protein of the
 RT human group B rotavirus ADRV.";
 RL J. Virol. 67:2730-2738(1993).
 CC -!- SUBCELLULAR LOCATION: Outer capsid.
 CC -!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
 CC -----
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CC -----
DR EMBL; M91434; AAA47338.1; -;
DR InterPro; IPR000416; Cap_VP4.
DR Pfam; PF00426; VP4; 1.
KW Coat protein; Glycoprotein.
FT CARBOHYD 29 29 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 527 527 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 568 568 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 681 681 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 698 698 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 749 AA; 84362 MW; D1223527DEAE0F21 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 749;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CFQWORNMRKVR 12
Db 195 CFTWDMNCANVR 206

RESULT 15

YNR2 CAEEL STANDARD; PRT; 783 AA.
AC Q21988;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein R13G10.2 in chromosome III.
GN R13G10.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gardner A.E.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Durbin R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- COFACTOR: FAD (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
CC -----
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CC -----
DR EMBL; Z35602; CAAB4671.2; -;
DR WormPep; R13G10.2; CE25088.
DR InterPro; IPR002937; Amino_oxidase.
DR Pfam; PF01593; Amino_oxidase; 1.
KW Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.
FT NP_BIND 311 366 FAD (ADP PART) (POTENTIAL).
SQ SEQUENCE 783 AA; 88799 MW; 8DC87E96464DC908 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 783;

Best Local Similarity 50.0%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWORNMRKVR 12
Db 540 CIDWGRDRKVK 551

Search completed: February 21, 2003, 07:27:38
Job time : 7.6 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds
(without alignments)
118.873 Million cell updates/sec

Title: US-09-743-107b-47
Perfect score: 71
Sequence: 1 CFQWQRNMRKV 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL.21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	93.0	711	4 Q8TCD2	Q8Tcd2 homo sapien
2	62	87.3	38	4 Q9UCY5	Q9ucy5 homo sapien
3	51	71.8	33	6 Q9TR80	Q9tr80 ovis aries
4	42	59.2	298	16 Q8IP77	Q8yp77 anabaena sp
5	42	59.2	511	16 Q8Z462	Q8z462 salmorella
6	41	57.7	148	10 Q9XHP1	Q9xhp1 sesamum ind
7	41	57.7	275	5 Q93780	Q93780 caenorhabdi
8	41	57.7	932	5 Q19153	Q19153 caenorhabdi
9	40	56.3	279	16 Q8XSE2	Q8xse2 ralstonia s
10	40	56.3	469	9 Q38115	Q38115 bacterioph
11	40	56.3	681	5 Q9XVD1	Q9xvd1 caenorhabdi
12	39	54.9	105	10 Q9XFD5	Q9xkd5 oryza sativ
13	39	54.9	273	2 Q31090	Q31090 rhizobium l
14	39	54.9	274	4 Q96M21	Q96m21 homo sapien
15	39	54.9	306	4 Q8TAX2	Q8tax2 homo sapien
16	39	54.9	372	10 Q81653	Q81653 hemerocalli

Q9nu2 homo sapien
Q8s934 diospyros k
Q9hpa3 halobacteri
Q77855 human immun
Q77856 human immun
Q8u8k3 agrobacteri
Q98rr2 guillardi
Q98ql9 mycoplasma
Q8r2a4 mus musculu
Q9nzw0 homo sapien
Q9nzw3 homo sapien
P96223 mycobacteri
Q22185 arabidopsis
Q22188 arabidopsis
Q94937 homo sapien
Q8s487 zea mays (m
Q62582 encephalito
Q8srq3 encephalito
Q8sq16 encephalito
Q9fhi9 arabidopsis
Q23230 arabidopsis
Q9n906 trypanosoma
Q8r9u1 thermonaer
Q9ygc1 human immun
Q9ygc0 human immun
Q9yqb9 human immun
Q9yqb8 human immun
Q9yji7 human immun
Q9yji2 human immun

39 54.9 466 4 Q9NUS2
39 54.9 488 10 Q8S934
39 54.9 584 17 Q9HPA3
38 53.5 91 15 Q77855
38 53.5 91 15 Q77856
38 53.5 121 16 Q8U8K3
38 53.5 205 8 Q98RR2
38 53.5 282 16 Q98Q19
38 53.5 341 11 Q8R2A4
38 53.5 459 4 Q9NZW0
38 53.5 460 4 Q9NZW3
38 53.5 489 16 P96223
38 53.5 515 10 Q22185
38 53.5 543 10 Q22188
38 53.5 570 10 Q8S487
38 53.5 632 4 Q94937
38 53.5 864 5 Q62582
38 53.5 864 5 Q8SRG3
38 53.5 864 5 Q8SQ16
38 53.5 866 10 Q9FHI9
38 53.5 1432 10 Q23230
38 53.5 2186 5 Q9N906
37 52.1 62 16 Q8R9U1
37 52.1 109 15 Q9YQC1
37 52.1 109 15 Q9YQC0
37 52.1 109 15 Q9YQB9
37 52.1 109 15 Q9YQB8
37 52.1 109 15 Q9YJI7
37 52.1 109 15 Q9YJI2

ALIGNMENTS

RESULT 1
Q8TCD2 PRELIMINARY; PRT; 711 AA.
ID Q8TCD2
AC Q8TCD2;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Lactotransferrin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022347; AAH22347.1; -
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;

Query Match 93.0%; Score 66; DB 4; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWQRNMRKV 11
Db 39 CFQWQRNMRKV 49

RESULT 2
Q9UCY5 PRELIMINARY; PRT; 38 AA.
ID Q9UCY5
AC Q9UCY5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Lactoferrin homolog (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]_SEQUENCE FROM N.A.
 RP MEDLINE=96081613; PubMed=8551695;
 RA Sato I.;
 RT "Characterization of the 84-kDa protein with ABH activity in human
 seminal plasma";
 RL Jpn. J. Legal Med. 49:281-293(1995).
 DR HSP, P02788; 13XA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5BDDDBB CRC64;

Query Match 87.3%; Score 62; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FQWQNRKVR 12
 Db 21 FQWQNRKVR 31
 |||||
 |||||

RESULT 3
 Q9TR80 PRELIMINARY; PRT; 33 AA.
 ID Q9TR80;
 AC Q9TR80;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Lactoferrin (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]_SEQUENCE.
 RP MEDLINE=95127729; PubMed=7827104;
 RX Qian Z.Y., Jolles P., Migliore-Samcor D., Fiat A.M.;
 RA Biochim. Biophys. Acta 1243:25-32(1995).
 RL HSP; O77698; 1CE2.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 33 AA; 3514 MW; D1904CAE15A73961 CRC64;

Query Match 71.8%; Score 51; DB 6; Length 33;
 Best Local Similarity 63.6%; Pred. No. 0.017;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 11
 Db 19 CFQWQNRKVR 29
 |||||
 |||||

RESULT 4
 Q9YP77 PRELIMINARY; PRT; 298 AA.
 ID Q9YP77;
 AC Q9YP77;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein Alr4323.
 GN Alr4323.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]_SEQUENCE FROM N.A.
 RP MEDLINE=21595285; PubMed=11759840;
 RX Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
 Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120";
 RL DNA Res. 8:205-213(2001).
 DR EMBL; AF003596; BAB76022.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 298 AA; 34513 MW; 64036B6B5229A9F CRC64;

Query Match 59.2%; Score 42; DB 16; Length 298;
 Best Local Similarity 77.8%; Pred. No. 8.2;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNRKVR 10
 Db 163 FQWQNRKVR 171
 |||||
 |||||

RESULT 5
 Q8Z462 PRELIMINARY; PRT; 511 AA.
 ID Q8Z462;
 AC Q8Z462;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein STY3070.
 GN STY3070.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=601;
 RN [1]_SEQUENCE FROM N.A.
 RP STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.F., Holroyd S., Jagals K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 enterica serovar Typhi CT18";
 RL Nature 413:848-852(2001).
 DR EMBL; AL627276; CAD06049.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;

Query Match 59.2%; Score 42; DB 16; Length 511;
 Best Local Similarity 58.3%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12
 Db 350 CFQWQNRKVR 361
 |||||
 |||||

RESULT 6
 Q9XHP1 PRELIMINARY; PRT; 148 AA.
 ID Q9XHP1;
 AC Q9XHP1;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE 2S albumin.
 OS Sesamum indicum (Oriental sesame) (Gingelly).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
 OX NCBI_TaxID=4182;
 RN [1]_SEQUENCE FROM N.A.

```

RP SEQUENCE FROM N.A.
RC STRAIN=TAINAN 1;
RX MEDLINE=20074970; PubMed=10606554;
RA Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;
RT "Molecular cloning of 11S globulin and 2S albumin, the two major seed
RL J. Agric. Food Chem. 47:4932-4938(1999).
DR EMBL; AF091841; AAD42943.1; -.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR000617; Napin.
DR InterPro; IPR001768; try/amy1 inhbr.
DR Pfam; PF00234; try2_alpha_ami1; 1.
DR PRINTS; PR00496; NAPIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;

Query Match 57.7%; Score 41; DB 10; Length 148;
Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFOWQRNMR 9
| | | | |
Db 54 CFQWRSMR 62

RESULT 7
Q93780
ID Q93780 PRELIMINARY; PRT; 275 AA.
AC Q93780;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F53H4.4 protein.
GN F53H4.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Dobson R.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81089; CAB03137.1; -.
SQ SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;

Query Match 57.7%; Score 41; DB 5; Length 275;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQRNMRKVR 12
| | | | |
Db 262 FQWISMRKTR 272

RESULT 8
Q19153
ID Q19153 PRELIMINARY; PRT; 932 AA.
AC Q19153;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 105.1 kDa protein.
GN F07C3.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.

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OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Favell A., Gattung S.;
RT "The sequence of C. elegans cosmid F07C3.";
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U50308; ARG24025.1; -.
DR InterPro; IPR000731; HMGCR/patch_5TM.
DR PROSITE; PS50156; SSD; 1.
KW Hypothetical protein.
SQ SEQUENCE 932 AA; 105144 MW; 66680619ADACBFDS CRC64;

Query Match 57.7%; Score 41; DB 5; Length 932;
Best Local Similarity 63.6%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQRNMRKVR 12
| | | | |
Db 579 FQWQRNMRKVR 589

RESULT 9
Q8XSE2
ID Q8XSE2 PRELIMINARY; PRT; 279 AA.
AC Q8XSE2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative ICC protein homolog.
GN ICC OR RSP0534 OR RS00414.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler N., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguiet P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646079; CAD17685.1; -.
DR InterPro; IPR004843; Mppstrase.
DR InterPro; IPR004844; S/T_phosphatase.
DR Pfam; PF00149; Metallophos; 1.
KW Plasmid; Complete proteome.
SQ SEQUENCE 279 AA; 31541 MW; ABB38818004B2EDA CRC64;

Query Match 56.3%; Score 40; DB 16; Length 279;
Best Local Similarity 41.7%; Pred. No. 18;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Query Match          56.3%; Score 40; DB 5; Length 681;
Best Local Similarity 60.0%; Pred.No. 47;
Matches 6; Conservative 3; Mismatches 0; Gaps 0;

QY 3 QWQWRNRKVR 12
   |||:|:|
DB 192 RWQKRRRVR 201

RESULT 12
Q9XFD5 PRELIMINARY; PRT; 105 AA.
ID Q9XFD5;
AC Q9XFD5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome P450 (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=PANICLE;
RA Liu J., Yang J.;
RT "suppression subtractive hybridization (SSH) identified candidate
RT genes that are differentially expressed at rice young panicle.";
RRL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AF140486; AAD29699.1; -.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
FT NCN_TER 1
FT SEQUENCE 105 AA; 11912 MW; B0EFCD487E19F9 CRC64;

Query Match          54.9%; Score 39; DB 10; Length 105;
Best Local Similarity 60.0%; Pred.No. 9.5;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWRNRKX 10
   |||:|:|
DB 61 CFQWRLGKX 70

RESULT 13
O31090 PRELIMINARY; PRT; 273 AA.
ID O31090;
AC O31090;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical 31.0 kDa protein.
OS Rhizobium leguminosarum (biovar viciae).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=387;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VF39;
RA Ivashina T.V., Sadykov M.R., Kanapin A.A., Ksenzenko V.N.;
RRL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=VF39;
RC MEDLINE=99113394; PubMed=9914965;
RA Sadykov M.R., Ivashina T.V., Kanapin A.A., Shlyapnikov M.G.,
RA Ksenzenko V.N.;
RT "structural and functional organization of the exopolysaccharide
RT biosynthesis genes in Rhizobium leguminosarum bv. viciae VF39.";

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RL Mcl. Biol. (Mosc) 32:797-804(1998).
DR EMBL; AF028810; AAB8891.1; -
KW Hypothetical protein.
SQ SEQUENCE 273 AA; 30986 MW; F195D2FEF7AD44D3 CRC64;

Query Match 54.9%; Score 39; DB 2; Length 273;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 QWQNRNKR 12
DB 245 RWLRNKR 254

RESULT 14

Q96M21 PRELIMINARY; PRT; 274 AA.
AC Q96M21;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CDNA FLJ32891 fis, clone TESTI2004929.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahori K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK057453; BAB71493.1; -
SQ SEQUENCE 274 AA; 30083 MW; 1DD43654D4135B2F CRC64;

Query Match 54.9%; Score 39; DB 4; Length 274;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 CFQWRNKR 12
DB 66 CFQWRNKR 77

RESULT 15

Q8TAX2 PRELIMINARY; PRT; 306 AA.
AC Q8TAX2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to hypothetical protein FLJ11175.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PANCREAS;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025708; AAH25708.1; -
KW Hypothetical protein.
SQ SEQUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;

Query Match 54.9%; Score 39; DB 4; Length 306;
Best Local Similarity 55.6%; Pred. No. 30;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 CFQWRNKR 9
DB 269 CFQWRNKR 277

Search completed: February 21, 2003, 07:44:14
Job time : 23.8 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds
(without alignments)
56.502 Million cell updates/sec

Title: US-09-743-107b-68

Perfect score: 66

Sequence: 1 AFGQWRNKKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	12	21	AAV78068 Human lactoferrin
2	62	93.9	11	21	AAV57318 Human lactoferrin
3	62	93.9	11	21	AAV78039 Human lactoferrin
4	62	93.9	11	21	AAV78044 Human lactoferrin
5	62	93.9	11	21	AAV78045 Human lactoferrin
6	62	93.9	11	22	AAV78038 Human lactoferrin
7	62	93.9	12	21	AAV78038 Human lactoferrin
8	62	93.9	12	21	AAV78046 Human lactoferrin
9	62	93.9	12	21	AAV78047 Human lactoferrin
10	62	93.9	13	21	AAV78037 Human lactoferrin

11	62	93.9	13	21	AAV78048 Human lactoferrin
12	62	93.9	13	21	AAV78049 Human lactoferrin
13	62	93.9	14	21	AAV78036 Human lactoferrin
14	62	93.9	14	21	AAV78050 Human lactoferrin
15	62	93.9	14	21	AAV78051 Human lactoferrin
16	62	93.9	14	21	AAV78056 Human lactoferrin
17	62	93.9	14	21	AAV78057 Human lactoferrin
18	62	93.9	14	21	AAV78098 Human lactoferrin
19	62	93.9	15	17	AAV78055 Peptide for anti-u
20	62	93.9	15	20	AAV04008 Antibacterial lact
21	62	93.9	15	21	AAV57317 Human lactoferrin
22	62	93.9	15	21	AAV78035 Human lactoferrin
23	62	93.9	15	21	AAV78062 Human lactoferrin
24	62	93.9	15	21	AAV78063 Human lactoferrin
25	62	93.9	16	21	AAV78031 Human lactoferrin
26	62	93.9	16	21	AAV78064 Human lactoferrin
27	62	93.9	16	21	AAV78065 Human lactoferrin
28	62	93.9	17	21	AAV78034 Human lactoferrin
29	62	93.9	17	21	AAV78066 Human lactoferrin
30	62	93.9	17	21	AAV78067 Human lactoferrin
31	62	93.9	18	15	AAV69352 Human lactoferrin
32	62	93.9	18	17	AAV13397 Advanced glycosyla
33	62	93.9	18	21	AAV78033 Human lactoferrin
34	62	93.9	19	21	AAV68867 Amino acid sequenc
35	62	93.9	19	21	AAV78032 Human lactoferrin
36	62	93.9	20	13	AAV21810 Anti microbial pep
37	62	93.9	20	13	AAV21811 Anti microbial pep
38	62	93.9	20	14	AAV44841 Lactoferrin-relate
39	62	93.9	20	15	AAV48530 Lactoferrin derive
40	62	93.9	20	15	AAV48531 Lactoferrin derive
41	62	93.9	20	15	AAV57461 Lactoferrin derive
42	62	93.9	20	15	AAV57462 Lactoferrin derive
43	62	93.9	20	16	AAV44698 Bovine lactoferrin
44	62	93.9	20	16	AAV44699 Bovine lactoferrin
45	62	93.9	20	16	AAV80263 Anti-parasitic lac

ALIGNMENTS

RESULT 1
AAV78068
ID AAV78068 standard; Peptide; 12 AA.
XX AAV78068;
AC AAV78068;
DT 25-APR-2000 (first entry)
DE Human lactoferrin derived peptide SEQ ID NO:68.
XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
DR

XX New peptides used for treatment and prevention of infections, -
PT inflammations and tumors and for use in infant formula food -
XX PS Claim 22; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX Sequence 12 AA;
SQ Query Match 100.0%; Score 66; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APOQQRNMRKVR 12
Db 1 APOQQRNMRKVR 12

RESULT 2
AAY57318
ID AAY57318 standard; peptide; 11 AA.
XX AC AAY57318;
XX DT 13-JUN-2000 (first entry)
XX DE Human lactoferrin partial peptide sequence.
XX KW Lactoferrin; anti-microbial; adhesive; coating material; clothing;
XX KW waste water treatment; leather; fiber; human.
XX OS Homo sapiens.
XX PN JP2000045182-A.
XX PD 15-FEB-2000.
XX PF 23-JUL-1998; 98JP-0207751.
XX PR 23-JUL-1998; 98JP-0207751.
XX PA (PEPU-) PEPUCHIDO SCI YG.
XX PA (FUJI-) FUJII KAIHATSU KENKYUSHO YG.
XX PA (MARU-) MARUJU KK.
XX WPI; 2000-306598/27.
XX Antimicrobial fiber for bandage, guaze, sheet and fiber goods comprises
PT anti-microbial component fixed to fiber by water soluble resin -
XX PS Claim 3; Page 2; 10pp; Japanese.

XX The invention provides water soluble resin-based fixing agent which
CC dissociates the anionic polymer component in water, fixes cationic anti-
CC microbial component into a fiber to form anti-microbial fiber. Cow or
CC human lactoferrin peptides may be used as the anti-microbial component
CC in the anti-microbial fiber of the invention. The agent is useful as
CC adhesive, coating material, waste water treatment and in fixing

CC antimicrobial component to a fiber to form antimicrobial fiber useful as
CC a bandage, guaze, sheet, clothing others or leathers, and fiber goods.
CC The antimicrobial activity is measured against S. coli, S. aureus,
CC methicillin-resistant S. aureus and P. aeruginosa. The antimicrobial
CC fiber formed has excellent antimicrobial activity and wash durability.
CC The leather used has excellent antimicrobial processing agent. Fixing of
CC lactoferrin to the fiber is reliable. The present sequence represents a
CC human lactoferrin partial peptide fragment.

XX Sequence 11 AA;
SQ Query Match 93.9%; Score 62; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FQWRNMRKVR 12
Db 1 FQWRNMRKVR 11

RESULT 3
AAY78039
ID AAY78039 standard; Peptide; 11 AA.
XX AC AAY78039;
XX DT 25-APR-2000 (first entry)
XX DE Human lactoferrin derived peptide SEQ ID NO:39.
XX KW Human, lactoferrin; modification; infection; inflammation; tumour;
XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX KW urinary tract infection; colitis; Candida infection; fungicidal;
XX KW bactericidal; preservative.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200001730-A1.
XX PD 13-JAN-2000.
XX PF 06-JUL-1999; 99WO-SE01230.
XX PR 06-JUL-1998; 98SE-0002441.
XX PR 17-JUL-1998; 98SE-0002562.
XX PR 29-DEC-1998; 98SE-0004614.
XX PA (ASCI-) A+ SCI INVEST AB.
XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX PS Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower

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CC cost.
XX Sequence 11 AA;
SQ

Query Match 93.9%; Score 62; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FQWRNMRKVR 12
Db 1 FQWRNMRKVR 11

RESULT 4
AAV78044
ID AAV78044 standard; Peptide; 11 AA.
XX
AC AAV78044;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:44.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
PS Claim 15; Page 72; 102pp; English.
XX
CC AAV78001 to AAV78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 11 AA;

Query Match 93.9%; Score 62; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 FQWRNMRKVR 12
Db 1 FQWRNMRKVR 11

RESULT 5
AAV78045
ID AAV78045 standard; Peptide; 11 AA.
XX
AC AAV78045;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:45.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
PS Claim 18; Page 72; 102pp; English.
XX
CC AAV78001 to AAV78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 11 AA;

Query Match 93.9%; Score 62; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6

AAB97384
 ID AAB97384 standard; peptide; 11 AA.
 XX
 AC AAB97384;
 XX
 DT 17-AUG-2001 (first entry)
 XX
 DE Human lactoferrin fragment hLF (21-3).
 XX
 KW Human; lactoferrin; hLF; N-terminal; antimicrobial; heparin;
 inflammatory response; cytokine production reduction;
 neutrophil degranulation; myelopoiesis inhibition.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200134641-A2.
 XX
 PD 17-MAY-2001.
 XX
 PF 10-NOV-2000; 2000WO-NL00821.
 XX
 PR 11-NOV-1999; 99BP-0203775.
 PR 11-NOV-1999; 99US-0164975.
 XX
 FA (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.
 XX
 PI Van Berkel PHC, Nibbering PH, Nuijens JH;
 XX
 DR WPI; 2001-335909/35.
 XX
 FT New polypeptides comprising the N-terminal region of human lactoferrin
 PT protein exhibit higher antimicrobial activity than the full length
 PT protein and are useful to treat bacterial infections
 XX
 PS Example 1; Page 22; 59pp; English.
 XX
 CC This invention relates to fragments (between 6 and 26 amino acids) of the
 human lactoferrin hLF protein, such as that represented in the present
 CC sequence. N-terminal hLF peptides have antimicrobial activity. The
 CC peptides of the invention are used to treat microbial infections,
 CC especially infections by gram positive or negative bacteria, particularly
 CC Listeria, Staphylococcus, Klebsiella or E. coli. Other uses include reducing
 CC L. monocytogenes, S. aureus and E. coli. Other uses include reducing
 CC inflammatory response by neutralising heparin or lipopolysaccharide or by
 CC reducing cytokine production and neutrophil degranulation, inhibiting
 CC entry of viruses such as cytomegalovirus, herpes simplex virus 1 or HIV
 CC into cells, inhibiting myelopoiesis and reducing production of GM-CSF
 CC (granulocyte/macrophage colony stimulating factor).
 XX
 SQ Sequence 11 AA;
 Query Match 93.9%; Score 62; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00026;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FQWRNMRKVR 12
 DB 1 FQWRNMRKVR 11
 RESULT 7
 AAY78038
 ID AAY78038 standard; Peptide; 12 AA.
 XX
 AC AAY78038;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human lactoferrin derived peptide SEQ ID NO:38.
 XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 urinary tract infection; colitis; Candida infection; fungicidal;
 KW

KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 PF 06-JUL-1999; 99WO-SB01230.
 XX
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 PA (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX
 DR WPI; 2000-147388/13.
 XX
 PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food
 XX
 PS Claim 12; Page 70; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 12 AA;
 Query Match 93.9%; Score 62; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00028;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FQWRNMRKVR 12
 DB 2 FQWRNMRKVR 12
 RESULT 8
 AAY78046
 ID AAY78046 standard; Peptide; 12 AA.
 XX
 AC AAY78046;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human lactoferrin derived peptide SEQ ID NO:46.
 XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX

PD 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

XX inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

XX lactoferrin. The peptides are taken up in the intestine through

XX binding to specific lactoferrin receptors and are then transported

XX through the circulation. A medicinal product of the peptide or fragment

XX can be used for treating and/or prevention of infections (such as

XX urinary tract infections, colitis, and Candida infection on a mucosal

XX membrane), inflammations and/or tumors. The peptides can also be used

XX in food stuffs such as infant formula food. The peptides are also

XX fungicidal and bactericidal and may also be used as preservatives.

XX Even though native human lactoferrin have been shown to have desired

XX anti-inflammatory anti-infectious and anti-tumoural properties they

XX cannot be used clinically on a broad basis because of high production

XX costs. Therefore, provision of peptides based on lactoferrin would

XX enable them to be used for the same purposes as lactoferrin at lower

XX cost.

XX Sequence 12 AA;

XX Query Match 93.9%; Score 62; DB 21; Length 12;

XX Best Local Similarity 100.0%; Pred.No. 0.00028;

XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 2 FQWQNRMKVR 12

XX Db 2 FQWQNRMKVR 12

XX RESULT 9

XX AAY78047

XX ID AAY78047 standard; Peptide; 12 AA.

XX AC AAY78047;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:47.

XX Human; lactoferrin; modification; infection; inflammation; tumour;

XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

XX urinary tract infection; colitis; Candida infection; fungicidal;

XX bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

XX inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

XX lactoferrin. The peptides are taken up in the intestine through

XX binding to specific lactoferrin receptors and are then transported

XX through the circulation. A medicinal product of the peptide or fragment

XX can be used for treating and/or prevention of infections (such as

XX urinary tract infections, colitis, and Candida infection on a mucosal

XX membrane), inflammations and/or tumors. The peptides can also be used

XX in food stuffs such as infant formula food. The peptides are also

XX fungicidal and bactericidal and may also be used as preservatives.

XX Even though native human lactoferrin have been shown to have desired

XX anti-inflammatory anti-infectious and anti-tumoural properties they

XX cannot be used clinically on a broad basis because of high production

XX costs. Therefore, provision of peptides based on lactoferrin would

XX PA

XX PI

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XX DR

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XX PI

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PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PS Claim 12; Page 70; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX SQ Sequence 13 AA;
 SQ Query Match 93.9%; Score 62; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00031;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FQWQNNRKVR 12
 DB 3 FQWQNNRKVR 13
 RESULT 11
 AAY78048
 ID AAY78048 standard; Peptide; 13 AA.
 AC AAY78048;
 XX
 DT 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:48.
 DE
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 OS WO200001730-A1.
 XX 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 74; 102pp; English.
 PS AAY78001 to AAY78100 represent peptides having sequences based on human
 XX lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX SQ Sequence 13 AA;
 SQ Query Match 93.9%; Score 62; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00031;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FQWQNNRKVR 12
 DB 3 FQWQNNRKVR 13
 RESULT 12
 AAY78049
 ID AAY78049 standard; Peptide; 13 AA.
 AC AAY78049;
 XX
 DT 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:49.
 DE
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 OS WO200001730-A1.
 XX 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 18; Page 74; 102pp; English.
 PS AAY78001 to AAY78100 represent peptides having sequences based on human
 XX lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 13 AA;

Query Match 93.9%; Score 62; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00031;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FQWRNMRKVR 12
 |||||
 Db 3 FQWRNMRKVR 13

RESULT 13

AAV78036
 ID AAY78036 standard; Peptide; 14 AA.

XX AC AAY78036;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:36.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX urinary tract infection; colitis; Candida infection; fungicidal;
 XX bactericidal; preservative.

XX OS Homo sapiens.
 XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-S01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Matthey-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
 XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 12; Page 69; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX

SQ Sequence 14 AA;

Query Match 93.9%; Score 62; DB 21; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FQWRNMRKVR 12
 |||||
 Db 4 FQWRNMRKVR 14

RESULT 14

AAV78050
 ID AAY78050 standard; Peptide; 14 AA.

XX AC AAY78050;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:50.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX urinary tract infection; colitis; Candida infection; fungicidal;
 XX bactericidal; preservative.

XX OS Homo sapiens.
 XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-S01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Matthey-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
 XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 15; Page 75; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 14 AA;

Query Match 93.9%; Score 62; DB 21; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FQWRNMRKVR 12

Db 4 FQWRNRKVR 14

RESULT 15

AAV78051
 ID AAV78051 standard; Peptide; 14 AA.
 AC AAV78051;
 XX
 DT 25-APR-2000 (first entry)
 DE Human lactoferrin derived peptide SEQ ID NO:51.
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 PF 06-JUL-1999; 99WO-SE01230.
 XX
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 PA (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Mattesby-Baltzer I, Baltzer L, Dolphin GT;
 XX
 DR WPI; 2000-147388/13.
 XX
 PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 PS Claim 18; Page 75; 102pp; English.
 XX
 CS AAV78001 to AAV78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 14 AA;

Query Match 93.9%; Score 62; DB 21; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FQWRNRKVR 12
 DB 4 FQWRNRKVR 14

Search completed: February 21, 2003, 07:37:10
 Job time : 28.35 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 seconds
(without alignments)

56.502 Million cell updates/sec

Title: US-09-743-107B-70

Perfect score: 70

Sequence: 1 CFAWRNRKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

1:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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19:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	12	21	AAV78070 Human lactoferrin
2	66	94.3	12	21	AAV78094 Human lactoferrin
3	65	92.9	12	21	AAV78038 Human lactoferrin
4	65	92.9	12	21	AAV78046 Human lactoferrin
5	65	92.9	12	21	AAV78047 Human lactoferrin
6	65	92.9	13	21	AAV78037 Human lactoferrin
7	65	92.9	13	21	AAV78048 Human lactoferrin
8	65	92.9	13	21	AAV78049 Human lactoferrin
9	65	92.9	14	21	AAV78036 Human lactoferrin
10	65	92.9	14	21	AAV78050 Human lactoferrin

11	65	92.9	14	21	AAV78051 Human lactoferrin
12	65	92.9	15	17	AAV78054 Peptide for anti-u
13	65	92.9	15	21	AAV78035 Human lactoferrin
14	65	92.9	15	21	AAV78062 Human lactoferrin
15	65	92.9	15	21	AAV78063 Human lactoferrin
16	65	92.9	16	21	AAV78031 Human lactoferrin
17	65	92.9	16	21	AAV78064 Human lactoferrin
18	65	92.9	16	21	AAV78065 Human lactoferrin
19	65	92.9	17	21	AAV78034 Human lactoferrin
20	65	92.9	17	21	AAV78066 Human lactoferrin
21	65	92.9	17	21	AAV78067 Human lactoferrin
22	65	92.9	18	15	AAV78067 Human lactoferrin
23	65	92.9	18	17	AAV78033 Advanced glycosyla
24	65	92.9	18	21	AAV78033 Human lactoferrin
25	65	92.9	19	21	AAV78067 Amino acid sequenc
26	65	92.9	19	21	AAV78032 Human lactoferrin
27	65	92.9	20	13	AAV78032 Anti microbial pep
28	65	92.9	20	14	AAV78032 Lactoferrin-relate
29	65	92.9	20	15	AAV78032 Lactoferrin derive
30	65	92.9	20	15	AAV78032 Lactoferrin derive
31	65	92.9	20	15	AAV78032 Lactoferrin derive
32	65	92.9	20	15	AAV78032 Lactoferrin derive
33	65	92.9	20	16	AAV78032 Bovine lactoferrin
34	65	92.9	20	16	AAV78032 Bovine lactoferrin
35	65	92.9	20	16	AAV78032 Anti-parasitic lac
36	65	92.9	20	16	AAV78032 Anti-parasitic lac
37	65	92.9	20	16	AAV78032 Peptide for anti-u
38	65	92.9	20	17	AAV78032 Lactoferrin-derive
39	65	92.9	20	17	AAV78032 Lactoferrin-derive
40	65	92.9	20	17	AAV78032 Lactoferrin-derive
41	65	92.9	20	17	AAV78032 Lactoferrin-derive
42	65	92.9	20	17	AAV78032 Lactoferrin-derive
43	65	92.9	20	18	AAV78032 Lactoferrin deriva
44	65	92.9	20	18	AAV78032 Anti-parasitic pep
45	65	92.9	20	19	AAV78032 Thrombus formation

ALIGNMENTS

RESULT 1

AAV78070

ID AAV78070 standard; Peptide; 12 AA.

XX AAV78070;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:70.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.

OS Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

PD 13-JAN-2000.

PF 06-JUL-1999; 99WO-SE01230.

PR 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

PA (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

DR WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
PT Inflammations and tumors and for use in infant formula food -
XX
PS Claim 22; Page 35; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 70; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFAWQNRNKKVR 12
Db |||||:
1 CFAWQNRNKKVR 12
RESULT 2
AAY78094
ID AAY78094 standard; Peptide; 12 AA.
XX
AC AAY78094;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:94.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
XX
PR 17-JUL-1998; 98SE-0002562.
XX
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 22; Page 38; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 12 AA;
Query Match 94.3%; Score 66; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 8.6e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFAWQNRNKKVR 12
Db |||||:
1 CFAWQNRNKKVR 12
RESULT 3
AAY78038
ID AAY78038 standard; Peptide; 12 AA.
XX
AC AAY78038;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:38.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
XX
PR 17-JUL-1998; 98SE-0002562.
XX
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 12; Page 70; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;
 Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00013;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQNRNKRVR 12
 |||||
 Db 1 CFQWQNRNKRVR 12

RESULT 4

AA78046
 ID AAY78046 standard; Peptide; 12 AA.
 XX
 AC AAY78046;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human lactoferrin derived peptide SEQ ID NO:46.
 XX
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX

OS Homo sapiens.
 OS Synthetic.

PN WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

XX inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;
 Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00013;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQNRNKRVR 12
 |||||
 Db 1 CFQWQNRNKRVR 12

RESULT 5

AA78047
 ID AAY78047 standard; Peptide; 12 AA.

XX

AC AAY78047;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:47.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

PN WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 XX inflammations and tumors and for use in infant formula food -

XX Claim 18; Page 73; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00013;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQRMKVR 12
 |||||
 Db 1 CFQWQRMKVR 12

RESULT 6

AAV78037
 ID AAV78037 standard; Peptide; 13 AA.

XX AAV78037;
 XX 25-APR-2000 (first entry)
 DE Human lactoferrin derived peptide SEQ ID NO:37.
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 70; 102pp; English.

XX AAV78001 to AAV78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 0.00014;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQRMKVR 12
 |||||
 Db 2 CFQWQRMKVR 13

RESULT 7

AAV78048

ID AAV78048 standard; Peptide; 13 AA.

XX AAV78048;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:48.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 74; 102pp; English.

XX AAV78001 to AAV78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 0.00014;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQRMKVR 12
 |||||
 Db 2 CFQWQRMKVR 13

RESULT 8

AAV78049

ID AAV78049 standard; Peptide; 13 AA.

XX AAV78049;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:49.

XX Human, lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

OS Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food -

XX Claim 18; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. No. 0.00014;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFAWQRNMRKVR 12

Db 2 CFQWQRNMRKVR 13

RESULT 9

AAY78036

ID AAY78036 standard; Peptide; 14 AA.

XX AAY78036;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:36.

XX Human; lactoferrin; modification; infection; inflammation; tumour;

KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

KW urinary tract infection; colitis; Candida infection; fungicidal;

KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 69; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 14 AA;

Query Match 92.9%; Score 65; DB 21; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.00015;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFAWQRNMRKVR 12

Db 3 CFQWQRNMRKVR 14

RESULT 10

AAY78050

ID AAY78050 standard; Peptide; 14 AA.

XX AAY78050;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:50.

KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 75; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX SQ Sequence 14 AA;
 Query Match 92.9%; Score 65; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00015;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFAWQRNRKVR 12
 DB 3 CFQWQRNRKVR 14
 RESULT 11
 AAY78051
 ID AAY78051 standard; Peptide; 14 AA.
 AC AAY78051;
 XX 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:51.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 PN 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 75; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 18; Page 75; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX SQ Sequence 14 AA;
 Query Match 92.9%; Score 65; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00015;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFAWQRNRKVR 12
 DB 3 CFQWQRNRKVR 14
 RESULT 12
 AAR98554
 ID AAR98554 standard; Peptide; 15 AA.
 XX AC AAR98554;
 XX 12-NOV-1996 (first entry)
 XX Peptide for anti-ulcer agent.
 DE anti-ulcer agent; low toxicity; stable; heat-resistant.
 KW Synthetic.
 OS JP08143468-A.
 XX 04-JUN-1996.
 PD 17-NOV-1994; 94JP-0283869.
 XX 17-NOV-1994; 94JP-0283869.
 PR (MORG) MORINAGA MILK IND CO LTD.
 XX WPI; 1996-318857/32.
 DR Anti-ulcer agent contg. peptide - has low toxicity, is
 PT heat-resistant and water-soluble
 XX Claim 1; Page 11; 11pp; Japanese.
 PS AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
 CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be
 CC administered orally and be produced in large amounts.
 XX SQ Sequence 15 AA;

Query Match 92.9%; Score 65; DB 17; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.00016;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12
 |||||
 Db 2 CFQWQNNRKVR 13

RESULT 13
 AAY78035
 ID AAY78035 standard; Peptide; 15 AA.
 XX AC AAY78035;
 XX DT 25-APR-2000 (first entry)
 XX DE Human lactoferrin derived peptide SEQ ID NO:35.
 XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX OS Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX PD 13-JAN-2000.
 XX PF 06-JUL-1999; 99WO-SE01230.
 XX PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX PA (ASCI-) A+ SCI INVEST AB.
 XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 12; Page 69; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX SQ Sequence 15 AA;

Query Match 92.9%; Score 65; DB 21; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.00016;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12
 |||||
 Db 4 CFQWQNNRKVR 15

RESULT 15
 AAY78063
 ID AAY78063 standard; Peptide; 15 AA.
 XX AC AAY78063;

RESULT 14
 AAY78062
 ID AAY78062 standard; Peptide; 15 AA.
 XX AC AAY78062;
 XX DT 25-APR-2000 (first entry)
 XX DE Human lactoferrin derived peptide SEQ ID NO:62.
 XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX OS Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX PD 13-JAN-2000.
 XX PF 06-JUL-1999; 99WO-SE01230.
 XX PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX PA (ASCI-) A+ SCI INVEST AB.
 XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 81; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX SQ Sequence 15 AA;

Query Match 92.9%; Score 65; DB 21; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.00016;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12
 |||||
 Db 4 CFQWQNNRKVR 15

RESULT 15
 AAY78063
 ID AAY78063 standard; Peptide; 15 AA.
 XX AC AAY78063;

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XX 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:63.
DE Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-SE01230.
XX
XX 06-JUL-1998; 98SE-0002441.
XX 17-JUL-1998; 98SE-0002562.
XX 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
PI
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food. -
XX
XX Claim 18; Page 81; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX
SQ Sequence 15 AA;
Query Match 92.9%; Score 65; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.00016;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFAWQENMRKVR 12
Db 4 CFWQENMRKVR 15

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Search completed: February 21, 2003, 07:37:11
Job time : 28.35 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 seconds
(without alignments)
40.818 Million cell updates/sec

Title: US-09-743-107B-70

Perfect score: 70

Sequence: 1 CFAWQNMKRV 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
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4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCtus_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	92.9	18	1 US-08-204-487-3	Sequence 3, Appli
2	65	92.9	18	2 US-08-485-948-8	Sequence 8, Appli
3	65	92.9	18	2 US-08-628-380-8	Sequence 8, Appli
4	65	92.9	18	2 US-08-475-055-8	Sequence 8, Appli
5	65	92.9	20	1 US-07-755-161A-3	Sequence 3, Appli
6	65	92.9	20	1 US-07-891-174-3	Sequence 3, Appli
7	65	92.9	20	1 US-08-204-487-1	Sequence 1, Appli
8	65	92.9	20	1 US-08-256-771-25	Sequence 24, Appl
9	65	92.9	20	1 US-08-771-25	Sequence 25, Appl
10	65	92.9	20	1 US-08-381-984-24	Sequence 24, Appl
11	65	92.9	20	1 US-08-381-984-25	Sequence 25, Appl
12	65	92.9	22	4 US-09-508-734-4	Sequence 25, Appl
13	65	92.9	24	4 US-09-508-734-6	Sequence 4, Appli
14	65	92.9	25	1 US-07-755-161A-10	Sequence 6, Appli
15	65	92.9	25	1 US-07-891-174-10	Sequence 10, Appl
16	65	92.9	25	1 US-08-204-487-7	Sequence 7, Appli
17	65	92.9	29	4 US-09-508-734-8	Sequence 8, Appli
18	65	92.9	36	1 US-07-755-161A-8	Sequence 8, Appli
19	65	92.9	36	1 US-07-891-174-8	Sequence 8, Appli
20	65	92.9	36	1 US-08-256-771-30	Sequence 30, Appl
21	65	92.9	36	1 US-08-381-984-29	Sequence 29, Appl
22	65	92.9	47	2 US-08-464-182A-6	Sequence 6, Appli
23	65	92.9	47	2 US-08-406-271-6	Sequence 6, Appli
24	65	92.9	50	2 US-08-693-274A-7	Sequence 7, Appli
25	65	92.9	52	4 US-09-017-043A-3	Sequence 3, Appli
26	65	92.9	53	2 US-08-464-182A-5	Sequence 5, Appli
27	65	92.9	53	2 US-08-406-271-5	Sequence 5, Appli

28	65	92.9	54	2 US-08-454-182A-2	Sequence 2, Appli
29	65	92.9	54	2 US-08-406-271-2	Sequence 2, Appli
30	65	92.9	694	3 US-08-724-586-2	Sequence 2, Appli
31	65	92.9	694	4 US-09-421-632-2	Sequence 2, Appli
32	65	92.9	694	4 US-09-932-190-2	Sequence 2, Appli
33	65	92.9	705	2 US-08-655-640-2	Sequence 2, Appli
34	65	92.9	708	2 US-08-655-640-4	Sequence 4, Appli
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36	65	92.9	711	1 US-08-481-333-4	Sequence 4, Appli
37	65	92.9	711	3 US-08-464-167-4	Sequence 4, Appli
38	65	92.9	711	3 US-09-158-313-4	Sequence 4, Appli
39	65	92.9	711	4 US-08-476-798-4	Sequence 4, Appli
40	62	88.6	711	1 US-08-145-681-2	Sequence 2, Appli
41	62	88.6	711	1 US-08-250-308-2	Sequence 2, Appli
42	62	88.6	711	1 US-08-453-703-2	Sequence 2, Appli
43	62	88.6	711	2 US-08-456-106-2	Sequence 2, Appli
44	62	88.6	711	3 US-08-456-108-2	Sequence 2, Appli
45	62	88.6	711	4 US-09-265-577-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FJN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37)"
US-08-204-487-3

Query Match 92.9%; Score 65; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 6.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQNRMKVR 12
||| |||||
Db 1 CFQWQNRMKVR 12

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,948
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,217
; FILING DATE: JUNE 7, 1995
; APPLICATION NUMBER: 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-485-948-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 6.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQNRMKVR 12
||| |||||
Db 1 CFQWQNRMKVR 12

RESULT 3

US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341
; GENERAL INFORMATION:
; APPLICANT: LI, YONG MING
; APPLICANT: VLASSARA, HELEN
; APPLICANT: CERAMI, ANTHONY
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,380
; FILING DATE: April 4, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-628-380-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 6.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQNRMKVR 12
||| |||||
Db 1 CFQWQNRMKVR 12

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9

```

CORRESPONDENCE ADDRESS:
ADDRESS: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LP-CL, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8

Query Match          92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. NO. 6.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKVR 12
DB 1 CFQWQNRMRKVR 12

RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

Query Match          92.9%; Score 65; DB 1; Length 20;
```

Best Local Similarity 91.7%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFAWQRNRKVR 12
Db 2 CFQWRNRKVR 13

RESULT 6

US-07-891-174-3
; Sequence 3, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992

CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991

ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.

REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:

TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856

TELEX:
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE:
HYPOTHETICAL:

ANTI-SENSE:
FRAGMENT TYPE:

ORGANISM:
STRAIN:

INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:

HAPLOTYPE:
TISSUE TYPE:

CELL TYPE:
CELL LINE:

ORGANELLE:
IMMEDIATE SOURCE:

LIBRARY:
CLONE:

POSITION IN GENOME:
CHROMOSOME/SEGMENT:

MAP POSITION:
UNITS:

FEATURE:
NAME/KEY: modified site

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFAWQRNRKVR 12
Db 2 CFQWRNRKVR 13

RESULT 7

US-08-204-487-1
; Sequence 1, Application US/08204487
; Patent No. 5565425

GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NAOKI

APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOTOCHI, WATARU

APPLICANT: TANAKA, SHIGEKI
APPLICANT: DOSAKO, SHUN'ICHI

APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: UCHIDA, TOSHIKI

TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT

STREET: 53 STATE STREET
CITY: BOSTON

STATE: MA
COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487

FILING DATE: 02-MAR-1994
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.

REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: RJN-019

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
US-08-204-487-1

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAQWRNMRKVR 12
DB 2 CFQWRNMRKVR 13

RESULT 8

US-08-256-771-24
Sequence 24, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"

US-08-256-771-24

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAQWRNMRKVR 12
DB 2 CFQWRNMRKVR 13

RESULT 9

US-08-256-771-25
Sequence 25, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are protected to
OTHER INFORMATION: prevent disulfide bond"
US-08-256-771-25

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAQWRNMRKVR 12
DB 2 CFQWRNMRKVR 13

RESULT 10

US-08-381-984-24

```

; Sequence 24, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at positions 2
; OTHER INFORMATION: and 19 are bonded by disulfide linkage"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
; US-08-381-984-24

```

```

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 CFAWQRNMRKVR 12
Db 2 CFQWQRNMRKVR 13

```

```

RESULT 11
US-08-381-984-25
; Sequence 25, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack

```

```

; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at positions 2
; OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
; US-08-381-984-25

```

```

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 CFAWQRNMRKVR 12
Db 2 CFQWQRNMRKVR 13

```

```

RESULT 12
US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; TITLE OF INVENTION: useful microorganism thereof
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 4

```

LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
US-09-508-734-4

Query Match 92.9%; Score 65; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNNRKVR 12
Db 2 CFQWQNNRKVR 13

RESULT 13

US-09-508-734-6
Sequence 6, Application US/09508734
Patent No. 6423509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: KopatentIn 1.71
SEQ ID NO 6
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
US-09-508-734-6

Query Match 92.9%; Score 65; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 8.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNNRKVR 12
Db 3 CFQWQNNRKVR 14

RESULT 14

US-07-755-161A-10
Sequence 10, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE:

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM:

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE:

CELL LINE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY: modified site

LOCATION: 4

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of

OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with

OTHER INFORMATION: thiol group of Cys residue at location 21"

FEATURE:

NAME/KEY: modified site

LOCATION: 21

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of

OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with

OTHER INFORMATION: thiol group of Cys residue at location 4"

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10

Query Match 92.9%; Score 65; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNNRKVR 12
Db 4 CFQWQNNRKVR 15

```
RESULT 15
US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21

; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
Query Match 92.9%; Score 65; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CFAWQNNRKVR 12
Db 4 CFAWQNNRKVR 15
Search completed: February 21, 2003, 07:50:33
Job time : 9.7 secs
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds
(without alignments)
35.508 Million cell updates/sec

Title: US-09-743-107B-70
Perfect score: 70
Sequence: 1 CFQWRNNRKR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 3109816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	15	9	US-09-798-869-2
2	65	92.9	25	9	US-09-798-869-20
3	65	92.9	694	9	US-10-023-096-2
4	57	81.4	15	9	US-09-798-869-6
5	48	68.6	15	9	US-09-798-869-3
6	48	68.6	25	9	US-09-798-869-23
7	43	61.4	15	9	US-09-798-869-4
8	43	61.4	25	9	US-09-798-869-22
9	40	57.1	15	9	US-09-798-869-7
10	40	57.1	15	9	US-09-798-869-8
11	40	57.1	15	9	US-09-798-869-29
12	40	57.1	15	9	US-09-798-869-30
13	38	54.3	338	9	US-09-978-295A-119
14	38	54.3	338	9	US-09-978-697-119
15	38	54.3	338	9	US-09-978-192A-119
16	38	54.3	338	9	US-09-999-832A-119
17	38	54.3	338	9	US-09-978-185-119
18	38	54.3	553	9	US-09-796-753-14
19	38	54.3	553	10	US-09-981-649A-6

20	38	54.3	553	10	US-09-981-649A-24	Sequence 24, Appl
21	38	54.3	554	10	US-09-981-649A-30	Sequence 30, Appl
22	38	54.3	554	10	US-09-981-649A-32	Sequence 32, Appl
23	38	54.3	559	10	US-09-981-649A-28	Sequence 28, Appl
24	38	54.3	2273	10	US-09-995-542-12	Sequence 12, Appl
25	38	54.3	2310	10	US-09-995-542-10	Sequence 10, Appl
26	37	52.9	34	9	US-09-510-332-68	Sequence 68, Appl
27	37	52.9	333	9	US-09-796-753-26	Sequence 26, Appl
28	37	52.9	607	9	US-09-81-579-10	Sequence 10, Appl
29	37	52.9	688	9	US-09-81-579-15	Sequence 15, Appl
30	36	51.4	210	9	US-09-738-626-4884	Sequence 4884, Ap
31	36	51.4	301	9	US-10-080-960-11	Sequence 11, Appl
32	36	51.4	302	10	US-09-948-078-2	Sequence 2, Appl
33	36	51.4	489	9	US-09-888-320-2	Sequence 2, Appl
34	35	50.0	97	9	US-09-738-626-5597	Sequence 5597, Ap
35	35	50.0	747	9	US-10-066-500-58	Sequence 58, Appl
36	35	50.0	747	9	US-10-002-796-58	Sequence 58, Appl
37	35	50.0	747	9	US-10-066-273-58	Sequence 58, Appl
38	35	50.0	747	9	US-10-066-494-58	Sequence 58, Appl
39	34	48.6	46	10	US-09-864-761-35744	Sequence 35744, A
40	34	48.6	69	10	US-09-804-969-17	Sequence 17, Appl
41	34	48.6	71	10	US-09-925-297-872	Sequence 872, App
42	34	48.6	77	10	US-09-864-761-41002	Sequence 41002, A
43	34	48.6	183	10	US-09-925-301-1013	Sequence 1013, Ap
44	34	48.6	209	10	US-09-904-536-8	Sequence 8, Appl
45	34	48.6	209	10	US-09-904-536-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GS99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2

Query Match 92.9%; Score 65; DB 9; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWRNNRKR 12
|||
DB 3 CFQWRNNRKR 14

RESULT 2
US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ RNSSON

<hr/>					
Query Match 92.9%; Score 65; DB 9; Length 25;					
Best Local Similarity 91.7%; Pred. No. 6.2e-05;					
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
<hr/>					
QY	1	CFAWQRNRKVR	12		
DB	22	CFQWRNRKVR	33		
<hr/>					
RESULT 4					
US-09-798-869-6					
; Sequence 6, Application US/09798869					
; Publication No. US20030022821A1					
; GENERAL INFORMATION:					
; APPLICANT: JOHN SIGURD SVENDSEN					
; APPLICANT: (VSTEIN REKDAL					
; APPLICANT: BALDUR SVEINBJ(RNSSON					
; APPLICANT: LARS VORLAND					
; TITLE OF INVENTION: BIOACTIVE PEPTIDES					
; FILE REFERENCE: A34049-PCT-USA-A					
; CURRENT APPLICATION NUMBER: US/09/798.869					
; CURRENT FILING DATE: 2001-02-27					
; PRIOR APPLICATION NUMBER: PCT/GB99/02851					
; PRIOR FILING DATE: 1999-08-31					
; PRIOR APPLICATION NUMBER: GB9818938.4					
; PRIOR FILING DATE: 1998-08-28					
; NUMBER OF SEQ ID NOS: 30					
; SOFTWARE: FastSEQ for Windows Version 4.0					
; SEQ ID NO 6					
; LENGTH: 15					
; TYPE: PRT					
; ORGANISM: Artificial Sequence					
; FEATURE:					
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens					
; OTHER INFORMATION: sequence)					
US-09-798-869-6					
<hr/>					
Query Match 81.4%; Score 57; DB 9; Length 15;					
Best Local Similarity 83.3%; Pred. No. 0.00086;					
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
<hr/>					
QY	1	CFAWQRNRKVR	12		
DB	3	CFQWRNRKVR	14		
<hr/>					
RESULT 5					
US-09-798-869-3					
; Sequence 3, Application US/09798869					
; Publication No. US20030022821A1					
; GENERAL INFORMATION:					
; APPLICANT: JOHN SIGURD SVENDSEN					
; APPLICANT: (VSTEIN REKDAL					
; APPLICANT: BALDUR SVEINBJ(RNSSON					
; APPLICANT: LARS VORLAND					
; TITLE OF INVENTION: BIOACTIVE PEPTIDES					
; FILE REFERENCE: A34049-PCT-USA-A					
; CURRENT APPLICATION NUMBER: US/09/798.869					
; CURRENT FILING DATE: 2001-02-27					
; PRIOR APPLICATION NUMBER: PCT/GB99/02851					
; PRIOR FILING DATE: 1999-08-31					
; PRIOR APPLICATION NUMBER: GB9818938.4					
; PRIOR FILING DATE: 1998-08-28					
; NUMBER OF SEQ ID NOS: 30					
; SOFTWARE: FastSEQ for Windows Version 4.0					
; SEQ ID NO 3					
; LENGTH: 15					
; TYPE: PRT					
; ORGANISM: CAPRINE					
US-09-798-869-3					
<hr/>					
Query Match 68.6%; Score 48; DB 9; Length 15;					
Best Local Similarity 63.6%; Pred. No. 0.029;					
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
<hr/>					
QY	1	CFAWQRNRKVR	12		
DB	22	CFQWRNRKVR	33		
<hr/>					
RESULT 4					
US-09-798-869-6					
; Sequence 6, Application US/09798869					
; Publication No. US20030022821A1					
; GENERAL INFORMATION:					
; APPLICANT: JOHN SIGURD SVENDSEN					
; APPLICANT: (VSTEIN REKDAL					
; APPLICANT: BALDUR SVEINBJ(RNSSON					
; APPLICANT: LARS VORLAND					
; TITLE OF INVENTION: BIOACTIVE PEPTIDES					
; FILE REFERENCE: A34049-PCT-USA-A					
; CURRENT APPLICATION NUMBER: US/09/798.869					
; CURRENT FILING DATE: 2001-02-27					
; PRIOR APPLICATION NUMBER: PCT/GB99/02851					
; PRIOR FILING DATE: 1999-08-31					
; PRIOR APPLICATION NUMBER: GB9818938.4					
; PRIOR FILING DATE: 1998-08-28					
; NUMBER OF SEQ ID NOS: 30					
; SOFTWARE: FastSEQ for Windows Version 4.0					
; SEQ ID NO 3					
; LENGTH: 15					
; TYPE: PRT					
; ORGANISM: CAPRINE					
US-09-798-869-6					
<hr/>					
Query Match 92.9%; Score 65; DB 9; Length 25;					
Best Local Similarity 91.7%; Pred. No. 6.2e-05;					
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
<hr/>					
QY	1	CFAWQRNRKVR	12		
DB	3	CFQWRNRKVR	14		
<hr/>					
RESULT 3					
US-10-023-096-2					
; Sequence 2, Application US/10023096					
; Patent No. US20020160941A1					
; GENERAL INFORMATION:					
; APPLICANT: Kruzel, Marian L.					
; APPLICANT: Kurecki, Tomasz					
; APPLICANT: Gollnick, Paul D.					
; APPLICANT: Doyle, Darrell J.					
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human					
; TITLE OF INVENTION: Lactoferrin					
; NUMBER OF SEQUENCES: 8					
; CORRESPONDENCE ADDRESS:					
; ADDRESSEE: Jacobson, Price, Holman & Stern					
; STREET: 400 Seventh St. N.W.					
; CITY: Washington D.C.					
; COUNTRY: U.S.A.					
; ZIP: 20004					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.25					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/10/023,096					
; FILING DATE:					
; CLASSIFICATION:					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: US/08/724,586					
; FILING DATE: 30-SEPT-1996					
; APPLICATION NUMBER: US 08/238,445					
; FILING DATE: 05-MAY-1994					
; ATTORNEY/AGENT INFORMATION:					
; NAME: Player, William E.					
; REGISTRATION NUMBER: 31,409					
; REFERENCE/DOCKET NUMBER: 10505/P58185C					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: (202) 638-6666					
; TELEFAX: (202) 393-5350					
; INFORMATION FOR SEQ ID NO: 2:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 694 amino acids					
; TYPE: amino acid					
; TOPOLOGY: linear					
; MOLECULE TYPE: protein					
US-10-023-096-2					

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQRMNRKV 11
| : ||| ||| :
Db 3 CYQWQRMNRKL 13

RESULT 6

US-09-798-869-23
; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23

Query Match 58.6%; Score 48; DB 9; Length 25;
Best Local Similarity 63.6%; Pred. No. 0.046;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQRMNRKV 11
| : ||| ||| :
Db 3 CYQWQRMNRKL 13

RESULT 7

US-09-798-869-4
; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4

Query Match 61.4%; Score 43; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.2;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWQRMNRKV 11
| : ||| ||| :
Db 3 CLRWQNMNRKV 13

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQRMNRKV 11
| : ||| ||| :
Db 3 CYQWQRMNRKL 13

RESULT 8

US-09-798-869-22
; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-22

Query Match 61.4%; Score 43; DB 9; Length 25;
Best Local Similarity 63.6%; Pred. No. 0.32;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWQRMNRKV 11
| : ||| ||| :
Db 3 CLRWQNMNRKV 13

RESULT 9

US-09-798-869-7
; Sequence 7, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-7

Query Match 57.1%; Score 40; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.64;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQRMNRKV 11
| : ||| ||| :
Db 3 CYQWQRMNRKL 13

RESULT 10
US-09-798-869-8
; Sequence 8, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine
; OTHER INFORMATION: sequence)
US-09-798-869-8

Query Match 57.1%; Score 40; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.64;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWQRMNRKV 11
| | | | |
Db 3 CLRQWEMRKV 13

RESULT 11
US-09-798-869-29
; Sequence 29, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29

Query Match 57.1%; Score 40; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.64;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQRMNRKV 11
| | | | |
Db 3 CFRQWEMRKV 13

RESULT 12
US-09-798-869-30

; Sequence 30, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-30

Query Match 57.1%; Score 40; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.64;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQRMNRKV 11
| | | | |
Db 3 CFRQWEMRKV 13

RESULT 13
US-09-978-295A-119
; Sequence 119, Application US/09978295A
; Patent No. US2002015606A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
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; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

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Best Local Similarity 45.5%; Pred. No. 27;
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Pacini, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Query Match 54.3%; Score 38; DB 9; Length 338;
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Db 50 CYGWRNSKGV 60

Search completed: February 21, 2003, 08:08:03
Job time : 10.55 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 Seconds
(without alignments)
120.168 Million cell updates/sec

Title: US-09-743-107B-70

Perfect score: 70

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Pir2:**

3: Pir3:**

4: Pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	47	67.1	511	2 AB0858	hypothetical prote
4	45	64.3	33	2 S52107	lactoferrin - shee
5	43	61.4	121	2 AH3147	hypothetical prote
6	43	61.4	282	2 F90580	hypothetical prote
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9	40	57.1	114	2 D33876	carcinoembryonic a
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15	39	55.7	274	2 B60350	apolipoprotein B-1
16	39	55.7	393	2 B64639	3-deoxy-manno-octu
17	39	55.7	681	2 T19429	hypothetical prote
18	38	54.3	196	2 T00702	hypothetical prote
19	38	54.3	275	1 JC1113	interleukin-2 rece
20	38	54.3	275	1 S07442	interleukin-2 rece
21	38	54.3	289	2 G86403	33.3K hypothetical
22	38	54.3	558	2 T17324	hypothetical prote
23	38	54.3	749	2 A45687	outer capsid prote
24	38	54.3	4568	2 T08030	dynamin beta heavy
25	37	52.9	236	2 A84666	hypothetical prote
26	37	52.9	365	2 I37477	MHC class I histoc
27	37	52.9	500	2 S42867	protein kinase (PC
28	37	52.9	500	2 G71833	ADP-ATP carrier pr
29	37	52.9	2700	2 D88450	protein F2H11.2 [

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 08-Dec-2000

C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74

R:Cho, Y.

submitted to the EMBL Data Library, March 1994

A:Reference number: G06820

A:Accession: G01394

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-711 <CHO>

A:Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237

R:Rev. M.W.; Woloshuk, S.L.; DeBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A>Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A:Reference number: S11228; MUID:90384839; PMID:2402455

A:Accession: S11228

A:Molecule type: mRNA

A:Residues: 1-148 'T', 150-422 'C', 424-711 <REV>

A:Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R:Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A>Title: Differential molecular mechanism of the estrogen action that regulates lactofer:

A:Reference number: A45401; MUID:93125571; PMID:1480183

A:Accession: A45401

A:Molecule type: DNA

A:Residues: 1-15 <TEN>

A:Cross-references: GB:S52659; NID:G263311; PIDN:AAB24877.1; PID:G263312

A:Experimental source: placenta

A>Note: sequence extracted from NCBI backbone (NCBIP:122202)

R:Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A>Title: Nucleotide sequence of human lactoferrin cDNA.

A:Reference number: S10324; MUID:9038549; PMID:12374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <POW>

A:Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A>Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A:Reference number: S15853; MUID:91264786; PMID:2049066

A:Accession: S15853

A:Molecule type: mRNA

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Residues: 20-31 <ST1>

A:Accession: S20841

A:Molecule type: protein

A:Residues: 20-28 'X', 30-31 <ST2>

hypothetical prote
sugar ABC transpor
conserved hypothet
hypothetical prote
hypothetical prote
serine/threonine k
conserved hypothet
histidyl-trNA synt
hypothetical prote
probable monooxyge
hypothetical prote
trichohyalin like
hypothetical prote
hypothetical prote
hypothetical prote
pyridoxamine 5'-ph
pyridoxamine 5'-ph

```

Query Match          58.6%; Score 48; DB 2; Length 708;
Best Local Similarity 63.6%; Pred. No. 1.4;
Matches 7; Conservative 2; Mismatches 2; Indels

Qy 1 CFQWQRNRKRV 11
   | | | | | |
Db 38 CYQWQRNRKRL 48

RESULT 3
AB0958
hypotheical protein STY3070 [imported] - Salmonella enterica s
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change
C/Accession: AB0958
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dow
, S.; Moule, S.; O'Gaora, P.,
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A/Title: Complete genome sequence of a multiple drug resistant
A/Reference number: AB0502; PMID:11677608
A/Accession: AB0958
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-511 <PAR>
A/Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:g16504016
C/Genetics:
A/Gene: STY3070

Query Match          67.1%; Score 47; DB 2; Length 511;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 4; Indels

Qy 1 CFQWQRNRKRV 12
   | | | | | |
Db 350 CFQWQNRKAKRV 361

RESULT 4
S52107
lactoferrin - sheep (fragment)
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic shu
C/Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change
C/Accession: S52107
R/Qian, Z.Y.; Jollies, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
A/Title: Isolation and characterization of sheep lactoferrin, a
A/Reference number: S52107; MUID:95127729; PMID:7827104
A/Accession: S52107
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-33 <QIA>
C/Superfamily: transferrin; transferrin repeat homology
C/Keywords: duplication

Query Match          64.3%; Score 45; DB 2; Length 33;
Best Local Similarity 54.5%; Pred. No. 0.25;
Matches 6; Conservative 3; Mismatches 2; Indels

Qy 1 CFQWQRNRKRV 11
   | | | | |
Db 19 CYQWQKMRKRL 29

RESULT 5
AH3147
hypotheical protein Atu4804 [imported] - Agrobacterium tumefac
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change
C/Accession: AH3147

```

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A;Reference number: AB2577; PMID:11743193
 A;Accession: AH3147
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-121 <KUR>
 A;Cross-references: GB:AE008689; PIDN:AAL45598.1; PID:gl7743317; GSPDB:GN00187
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu4804
 A;Map position: linear chromosome

Query Match 61.4%; Score 43; DB 2; Length 121;
 Best Local Similarity 63.6%; Pred. No. 2;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQNNRKV 11
 Db 14 CLAWQNNRV 24
 ||||| |

RESULT 6
 F90580
 hypothetical protein MYPU 5500 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
 C;Species: Mycoplasma pulmonis
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
 C;Accession: F90580
 R;Chamoud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
 Nucleic Acids Res. 29, 2145-2153, 2001
 A;Title: The complete genome sequence of the murine respiratory pathogen *Mycoplasma pulm*
 A;Reference number: A99512; MUID:21267165; PMID:11353084
 A;Accession: F90580
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-282 <KUR>
 A;Cross-references: GB:AL445566; PID:gl4089965; PIDN:CAC13723.1; GSPDB:GN00153
 A;Experimental source: strain UAB CTIP
 C;Genetics:
 A;Gene: MYPU 5500
 A;Genetic code: SGC3

Query Match 61.4%; Score 43; DB 2; Length 282;
 Best Local Similarity 60.0%; Pred. No. 4.4;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FAWQNNRKV 11
 Db 20 FAWQNNIKKI 29
 ||||| |

RESULT 7
 A28438
 lactoferrin precursor - mouse
 N;Alternate names: lactotransferrin
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A28438; A41205
 R;Pentecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre
 A;Reference number: A92596; MUID:87280033; PMID:3611056
 A;Accession: A28438
 A;Molecule type: mRNA
 A;Residues: 3-707 <PEN>
 A;Cross-references: EMBL:J03298
 R;Lin, Y.; Teng, C.T.
 J. Biol. Chem. 266, 21880-21885, 1991

A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
 A;Reference number: A41205; MUID:92042099; PMID:1939212
 A;Accession: A41205
 A;Molecule type: DNA
 A;Residues: 1-15 <LIU>
 A;Cross-references: GB:M74778
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication; glycoprotein
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-707/Product: lactotransferrin #status predicted <MAT>
 F;358-695/Domain: transferrin repeat homology <TRH2>
 F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.4%; Score 43; DB 1; Length 707;
 Best Local Similarity 63.6%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWQNNRKV 11
 Db 37 CLRWQNNRKV 47
 ||||| |

RESULT 8
 A39654
 cell cycle arrest protein BUB2 - yeast (*Saccharomyces cerevisiae*)
 N;Alternate names: protein YN9796.08c; protein YNR055c
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jul-2000
 C;Accession: A39654; S54555; S19034
 R;Hoyt, M.A.; Totis, L.; Roberts, B.T.
 Cell 66, 507-517, 1991
 A;Title: *Saccharomyces cerevisiae* genes required for cell cycle arrest in response to lo
 A;Reference number: A39654; MUID:91330299; PMID:1651171
 A;Accession: A39654
 A;Molecule type: DNA
 A;Residues: 1-306 <HOY>
 A;Cross-references: GB:M64706; NID:gl71133; PIDN:AAA16885.1; PID:gl71135
 R;Devlin, K.; Churcher, C.M.
 submitted to the EMBL Data Library, May 1995
 A;Reference number: S54558
 A;Accession: S54555
 A;Molecule type: DNA
 A;Residues: 1-306 <DEV>
 A;Cross-references: EMBL:Z49703; NID:9817880; PIDN:CAA89765.1; PID:9817888; GSPDB:GN0001
 C;Genetics:
 A;Gene: SGD:BUB2; MIPS:YMR055c
 A;Cross-references: SGD:S0004659; MIPS:YMR055c
 A;Map position: 13R
 C;Superfamily: cell cycle arrest protein BUB2
 C;Keywords: transmembrane protein
 F;232-248/Domain: transmembrane #status predicted <TM>

Query Match 58.6%; Score 41; DB 1; Length 306;
 Best Local Similarity 60.0%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQNNRK 10
 Db 108 CFAWQNNRK 117
 ||||| |

RESULT 9
 D33876
 carcinoembryonic antigen homolog 4 - rat (fragment)
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 23-Jul-1999
 C;Accession: D33876
 R;Kodelja, V.; Lucas, K.; Barnet, S.; von Kleist, S.; Thompson, J.A.; Zimmermann, W.
 J. Biol. Chem. 264, 6906-6912, 1989
 A;Title: Identification of a carcinoembryonic antigen gene family in the rat. Analysis of
 A;Reference number: A33876; MUID:89214106; PMID:2708349
 A;Accession: D33876
 A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-114 <KOD>
A;Cross-references: GB:M60026; NID:9203407; PIDN:AAA40911.1; PID:9554427; GB:J04626; GB:
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Query Match 57.1%; Score 40; DB 2; Length 114;
Best Local Similarity 60.0%; Pred. No. 6.2;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FAWQNRKRV 11
|||:|:|:
Db 42 FAWYGLRKI 51

RESULT 10
AD2346
hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AD2346
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2346
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-298 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA876022.1; PID:G17133459; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr4323

Query Match 57.1%; Score 40; DB 2; Length 298;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FAWQNRKRV 10
|||:|:|:
Db 163 FHWQNRKRV 171

RESULT 11
D71876
3-deoxy-manno-octulosonate cytidyltransferase [EC 2.7.7.38] [similarity] - Helicobacte
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 28-Jul-2000
C;Accession: D71876
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:99233682
A;Accession: D71876
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-393 <ARN>
A;Cross-references: GB:AE001518; GB:AE001439; NID:G4155454; PIDN:AAD06459.1; PID:G415545
A;Experimental source: strain J99
C;Genetics:
A;Gene: waaA
C;Superfamily: Chlamydia trachomatis 3-deoxy-manno-octulosonate cytidyltransferase
C;Keywords: nucleotidyltransferase

Query Match 57.1%; Score 40; DB 2; Length 393;
Best Local Similarity 36.4%; Pred. No. 21;
Matches 4; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 2 FAWQNRKRV 12
|||:|:|:|:
Db 163 FHWQNRKRV 171

Db 110 FAWKNLKRLK 120

RESULT 12
C84325
hypothetical protein Vng1732c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84325
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabc
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: C84325
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-584 <STO>
A;Cross-references: GB:AE004437; NID:G10581192; PIDN:AAG19967.1; GSPDB:GN00138
C;Genetics:
A;Gene: Vng1732C

Query Match 57.1%; Score 40; DB 2; Length 584;
Best Local Similarity 41.7%; Pred. No. 30;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQNRKRV 12
|||:|:|:|:
Db 445 CFTWRKMERK 456

RESULT 13
A96807
hypothetical protein T32E8.5 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A96807
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luo, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A96807
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-720 <STO>
A;Cross-references: GB:AE005173; NID:G6437532; PIDN:AAF08564.1; GSPDB:GN00141
C;Genetics:
A;Gene: T32E8.5
A;Map position: 1

Query Match 57.1%; Score 40; DB 2; Length 720;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQNRKRV 9
|||:|:|:|:
Db 616 CLAWDRNQR 624

RESULT 14
E90094
26S proteasome SU B5 [imported] - Guillardia theta nucleomorph
C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: E90094
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reil
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Accession: E90094
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-205 <DOU>
A;Cross-references: GB:AF165818; NID:gl3794510; PIDN:AAK39885.1; GSPDB:GN00150
C;Genetics:
A;Gene: prsB5
A;Map position: 1
A;Genome: nucleomorph
C;Keywords: nucleomorph

Query Match 55.7%; Score 39; DB 2; Length 205;
Best Local Similarity 62.5%; Pred.No. 16;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQRNM 8
Db 63 CFFWERNL 70

RESULT 15

B60950
apolipoprotein B-100 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 07-Oct-1994
C;Accession: B60950
R;Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
A;Reference number: A60950; MUID:90324804; PMID:2373961
A;Accession: B60950
A;Molecule type: mRNA
A;Residues: 1-274 <LAW>
A;Note: authors translated the codon ATA for residue 8 as Val
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match 55.7%; Score 39; DB 2; Length 274;
Best Local Similarity 60.0%; Pred.No. 22;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 AWQRNWKVR 12
Db 38 SWDRNLKFR 47

Search completed: February 21, 2003, 07:47:39
Job time : 11.65 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds
(without alignments)
108.199 Million cell updates/sec

Title: US-09-743-107B-70
Perfect score: 70
Sequence: 1 CFAWQNMRRKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	92.9	711	1 TRFL HUMAN	P02788 homo sapien
2	48	68.6	708	1 TRFL CAMDR	Q9tun0 camelus dro
3	48	68.6	708	1 TRFL CAPHI	Q29477 capra hircu
4	44	62.9	695	1 TRFL HORSE	O77811 equus cabal
5	43	61.4	707	1 TRFL MOUSE	P08071 mus musculu
6	41	58.6	306	1 BUB2 YEAST	P26448 saccharomyc
7	38	54.3	275	1 IL2A BOVIN	P12342 bos taurus
8	38	54.3	275	1 IL2A SHEEP	P26898 ovis aries
9	38	54.3	749	1 VP4 ROTGA	Q04916 rotavirus (
10	38	54.3	2273	1 ABCR HUMAN	P78163 homo sapien
11	38	54.3	4568	1 DYHB CHLRE	Q39565 chlamydomon
12	37	52.9	267	1 RS3A_DROME	P56830 drosophila
13	37	52.9	365	1 IA34 HUMAN	P30453 homo sapien
14	37	52.9	435	1 DHOM METGL	P37143 methylcobaci
15	37	52.9	500	1 TLCE RICPR	O05962 rickettsia
16	36	51.4	62	1 RL28 THETN	Q8-r9ul thermoanaer
17	36	51.4	267	1 Y125 MYCCA	P53661 mycoplasma
18	36	51.4	428	1 SYH CHLMU	Q991j9 chlamydia m
19	35	50.0	480	1 YQSI CABEL	Q09309 caenorhabdi
20	35	50.0	665	1 YL14 CABEL	Q11100 caenorhabdi
21	35	50.0	675	1 ZG20 XENLA	P18714 xenopus lae
22	35	50.0	783	1 YNR2 CABEL	Q21988 caenorhabdi
23	35	50.0	1179	1 ATX1 ARATH	Q91t02 arabidopsis
24	35	50.0	1574	1 RPOC AGUAE	P67763 aquifex aeo
25	35	50.0	1576	1 RPOC AGUPE	Q9x6y2 aquifex pyr
26	35	50.0	1592	1 YH05 YEAST	P38735 saccharomyc
27	35	50.0	1750	1 YH32 METJA	Q58242 methanococc
28	34	48.6	60	1 RL28 BACST	P23374 bacillus st
29	34	48.6	62	1 RL28 LISMO	Q92aj2 listeria mo
30	34	48.6	175	1 PAP1 HUMAN	Q06141 homo sapien
31	34	48.6	227	1 LIPE_SNY3	P74519 synecocyst
32	34	48.6	235	1 FL3L HUMAN	P49771 homo sapien
33	34	48.6	267	1 IL2A_RAT	P26897 rattus norv

ALIGNMENTS

RESULT 1
TRFL_HUMAN
ID TRFL_HUMAN STANDARD; PRT; 711 AA.
AC P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96KZ4;
AC Q96KZ5;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactoferrin precursor (Lactoferrin) [Contains: Lactoferrin A;
DE Lactoferrin B; Lactoferrin C]
GN LTF OR LF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90384839; PubMed=2402455;
RA Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";
RL Nucleic Acids Res. 18:5288-5288(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cho Y.Y.;
RL Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
RN [3]
RP SEQUENCE FROM N.A.
RA Conneely O.M.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Liang O., Jimenez-Flores R., Richardson T.;
RL "Molecular cloning and sequence analysis of human lactoferrin.";
RN Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Wei X., Han J., Rado T.A.;
RL "Human neutrophil lactoferrin coding and 5' flanking region DNA
sequences.";
RN Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cheng H., Chen X., Huan L.;
RL "cDNA cloning and sequence analysis of human lactoferrin.";
RN Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [8]

34 34 48.6 272 1 IL2A_HUMAN
35 34 48.6 334 1 CATL_MOUSE
36 34 48.6 334 1 CATL_RAT
37 34 48.6 360 1 HIS8_LACLA
38 34 48.6 369 1 SP11_MYXVL
39 34 48.6 413 1 CYCL_DROME
40 34 48.6 428 1 SYH_CHLTR
41 34 48.6 453 1 O83A_DROME
42 34 48.6 572 1 MAOX_HUMAN
43 34 48.6 572 1 MAOX_RAT
44 34 48.6 705 1 FRZ4_DROME
45 34 48.6 1293 1 XPC_DROME

P01589 homo sapien
P06797 mus musculu
P07154 rattus norv
Q02135 lactococcus
P12393 myxoma viru
O61734 drosophila
O84547 chlamydia t
Q9vnb3 drosophila
P48163 homo sapien
P13697 rattus norv
Q9nbw1 drosophila
Q24595 drosophila

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Osden J.B.,
RT "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
RX Legrand D., Spik G., Montreuil J., Jolles P.,
RT "Human lactoferrin: amino acid sequence and structural
RL comparisons with other transferrins.";
RN Eur. J. Biochem. 145:659-666(1984).
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RX Jolles P.;
RT "The present state of the human lactotransferrin sequence. Study and
RL alignment of the cyanogen bromide fragments and characterization of
RN N- and C-terminal domains.";
RX Biochim. Biophys. Acta 670:243-254(1981).
RN [11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J.,
RX Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
RL lactotransferrin.";
RN FEBS Lett. 142:1107-110(1982).
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.,
RT "Isolation of lactoferrin cDNA from a human myeloid library and
RL expression of mRNA during normal and leukemic myelopoiesis.";
RN Blood 70:989-993(1987).
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Khan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., La Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sagripanti J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
RL and refinement at 2.8-A resolution.";
RN J. Mol. Biol. 209:711-734(1989).
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Harias M., Anderson B.F., Baker E.N.;
RT "Structure of human diferric lactoferrin refined at 2.2-A
RL resolution.";
RN Acta Crystallogr. D 51:629-646(1995).
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
RA Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
RL binding properties and crystal structure of the histidine-
RN 253-->methionine mutant.";
RX Biochemistry 36:341-346(1997).
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in *Aspergillus*
RL *awamori*.";
RN Acta Crystallogr. D 55:403-407(1999).
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
RL and analysis of ligand-induced conformational change.";
RN Acta Crystallogr. D 54:1319-1335(1998).
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of opioid antagonist peptides derived
RL from human lactoferrin.";
RN Agric. Biol. Chem. 54:1803-1810(1990).
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
RA Omsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
RA Sugar J., Kumaramanickavel G., Munier P., Schorderet D.F.,
RA El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
RA Hejtmanek J.F., Teng C.T.;
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
RL corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RN Mol. Vision 4:31-32(1998).
RP FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
RP FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
RP SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
DR EMBL; X53961; CAA37914.1; -
DR EMBL; U07643; AAB60324.1; -
DR EMBL; M93150; AAA36159.1; -
DR EMBL; M83202; AAA59511.1; -
DR EMBL; M83205; AAA58656.1; -
DR EMBL; M18642; AAA86665.1; -
DR EMBL; AF332168; AAG48753.1; -
DR EMBL; BC015822; AHI15822.1; -
DR EMBL; SC015823; AHI15823.1; -
DR EMBL; M73700; AAA59479.1; -
DR EMBL; X52941; CAA37116.1; -
DR EMBL; U95626; AAB57795.1; -
DR PIR; S11228; TFHUL.
DR PDB; 1LCP; 31-AUG-94.
DR PDB; 1LCT; 31-OCT-93.
DR PDB; 1LFC; 31-JUL-94.
DR PDB; 1LFF; 31-OCT-93.
DR PDB; 1LFI; 31-OCT-93.
DR PDB; 1LGB; 31-AUG-94.
DR PDB; 1LGC; 31-AUG-94.
DR PDB; 1BKA; 08-NOV-96.
DR PDB; 1DSN; 08-MAR-96.
DR PDB; 1HSE; 12-MAR-97.
DR PDB; 1VFD; 21-APR-97.

Query Match 92.9%; Score 65; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.00028;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKKVR 12
 DB 39 CFQWQNNRKKVR 50

RESULT 2

TRFL CAMDR
 ID TRFL CAMDR STANDARD; PRT; 708 AA.
 AC QPTUMQ; Q3MZS5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;
 RA Kappeler S.R., Ackermann M., Farah Z., Puhon Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
 RL Int. Dairy J. 9:481-486(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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 or send an email to license@isb-sib.ch).

EMBL; AJ131674; CAB53387.1; -
 EMBL; AF165879; AAF82241.1; -
 HSP; 077811; IBLX.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SMC0094; TR_FER_2.
 DR PROSITE; PS00205; TRANSFERRIN 1; 2.
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.
 DR PROSITE; PS00207; TRANSFERRIN 3; 2.
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal.
 FT CHAIN 1 19 BY SIMILARITY.
 FT REPEAT 20 708 LACTOTRANSFERRIN.
 FT REPEAT 20 363 1.
 FT REPEAT 364 708 2.
 FT DISULFID 28 64 BY SIMILARITY.
 FT DISULFID 38 55 BY SIMILARITY.
 FT DISULFID 134 217 BY SIMILARITY.
 FT DISULFID 175 192 BY SIMILARITY.
 FT DISULFID 189 200 BY SIMILARITY.
 FT DISULFID 250 264 BY SIMILARITY.
 FT DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.
 FT DISULFID 424 703 BY SIMILARITY.
 FT DISULFID 444 666 BY SIMILARITY.
 FT DISULFID 476 551 BY SIMILARITY.
 FT DISULFID 500 694 BY SIMILARITY.
 FT DISULFID 510 524 BY SIMILARITY.
 FT DISULFID 521 534 BY SIMILARITY.
 FT DISULFID 592 606 BY SIMILARITY.
 FT DISULFID 644 649 BY SIMILARITY.
 FT METAL 79
 FT METAL 111
 FT METAL 211
 FT METAL 272
 FT METAL 414
 FT METAL 452
 FT METAL 545
 FT METAL 614
 FT BINDING 140
 FT BINDING 482
 FT CARBOHYD 252
 FT CARBOHYD 385
 FT CARBOHYD 537
 FT CARBOHYD 594
 FT CONFLICT 261
 FT CONFLICT 304
 FT CONFLICT 330
 FT CONFLICT 492
 FT CONFLICT 506
 FT CONFLICT 609
 FT CONFLICT 642
 SQ SEQUENCE 708 AA; 77211 MW; 080C175A0B69D430 CRC64;

Query Match 68.6%; Score 48; DB 1; Length 708;
 Best Local Similarity 66.7%; Pred. No. 0.34;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNNRKKVR 12
 DB 38 CAQWQNNRKKVR 49

RESULT 3

TRFL CAPHI
 ID TRFL CAPHI STANDARD; PRT; 708 AA.
 AC Q29477; Q29479;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA MEDLINE=94380047; PubMed=8093048;
 RX le Provost F., Nocard M., Guerin G., Martin P.;
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the
 RT relevant locus to bovine U12 syntenic group."
 EL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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 CC
 CC EMBL; U53857; AAA97958.1; -;
 CC EMBL; X78902; CAAS5517.1; -;
 CC HSSP; O77698; ICE2.
 CC InterPro; IPR001156; Transferrin.
 CC Pfam; PF00405; transferrin; 2.
 CC PRINTS; PR00422; TRANSFERRIN.
 CC SMART; SM00094; TR_FER; 2.
 CC PROSITE; PS00205; TRANSFERRIN_1; 2.
 CC PROSITE; PS00206; TRANSFERRIN_2; 2.
 CC PROSITE; PS00207; TRANSFERRIN_3; 2.
 CC Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal.
 KW
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 708 LACTOTRANSFERRIN.
 FT REPEAT 20 363 1.
 FT REPEAT 364 708 2.
 FT DISULFID 28 64 BY SIMILARITY.
 FT DISULFID 38 55 BY SIMILARITY.
 FT DISULFID 134 217 BY SIMILARITY.
 FT DISULFID 176 192 BY SIMILARITY.
 FT DISULFID 189 200 BY SIMILARITY.
 FT DISULFID 250 284 BY SIMILARITY.
 FT DISULFID 367 399 BY SIMILARITY.
 FT DISULFID 377 390 BY SIMILARITY.
 FT DISULFID 424 703 BY SIMILARITY.
 FT DISULFID 444 666 BY SIMILARITY.
 FT DISULFID 476 551 BY SIMILARITY.
 FT DISULFID 500 694 BY SIMILARITY.
 FT DISULFID 510 524 BY SIMILARITY.
 FT DISULFID 521 534 BY SIMILARITY.
 FT DISULFID 592 606 BY SIMILARITY.
 FT DISULFID 644 649 BY SIMILARITY.
 FT METAL 79 79 IRON 1 (BY SIMILARITY).
 FT METAL 111 111 IRON 1 (BY SIMILARITY).
 FT METAL 211 211 IRON 1 (BY SIMILARITY).
 FT METAL 272 272 IRON 2 (BY SIMILARITY).
 FT METAL 414 414 IRON 2 (BY SIMILARITY).
 FT METAL 452 452 IRON 2 (BY SIMILARITY).
 FT METAL 545 545 IRON 2 (BY SIMILARITY).
 FT METAL 614 614 IRON 2 (BY SIMILARITY).
 FT BINDING 140 140 ANION (BY SIMILARITY).
 FT BINDING 482 482 ANION (BY SIMILARITY).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 56 56 I -> V (IN REF. 2).
 FT CONFLICT 86 86 L -> R (IN REF. 2).
 FT CONFLICT 124 124 Q -> K (IN REF. 2).
 FT CONFLICT 154 154 F -> P (IN REF. 2).
 FT CONFLICT 304 304 S -> R (IN REF. 2).
 FT CONFLICT 414 414 D -> G (IN REF. 2).
 SQ SEQUENCE 708 AA; 77358 MW; F2EDA3C83539960D CRC64;

Query Match 68.6%; Score 48; DB 1; Length 708;
 Best Local Similarity 63.6%; Pred. No. 0.34;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFAMQNRKRV 11
 Db 38 CYQWQRVRL 48

RESULT 4
 TRFL HORSE
 ID TRFL HORSE STANDARD; PRT; 695 AA.
 AC O77811;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin) (Fragment).
 GN LIT.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN (1)
 RP SEQUENCE FROM N. A.
 RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "cDNA sequence of mare lactoferrin."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RC TISSUE=Milk;
 RX MEDLINE=92296631; PubMed=10366507;
 RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
 J. Mol. Biol. 289:303-317(1999).
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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 CC
 CC EMBL; AJ010930; CAA09407.1; -;
 CC PDB; 1B1X; 02-DEC-98.
 CC PDB; 1B7U; 02-FEB-99.
 CC PDB; 1B7Z; 02-FEB-99.
 CC InterPro; IPR001156; Transferrin.
 CC Pfam; PF00405; transferrin; 2.
 CC PRINTS; PR00422; TRANSFERRIN.
 CC SMART; SM00094; TR_FER; 2.
 CC PROSITE; PS00205; TRANSFERRIN_1; 2.
 CC PROSITE; PS00206; TRANSFERRIN_2; 2.
 CC PROSITE; PS00207; TRANSFERRIN_3; 1.
 CC Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal; 3D-structure.
 FT NON_TER 1 1
 FT SIGNAL <1 6
 FT CHAIN 7 695 LACTOTRANSFERRIN.
 FT REPEAT 7 350 1.
 FT REPEAT 351 695 2.
 FT DISULFID 15 51
 FT DISULFID 25 42
 FT DISULFID 121 204
 FT DISULFID 163 179
 FT DISULFID 166 189
 FT DISULFID 176 187
 FT DISULFID 237 251
 FT DISULFID 354 386
 FT DISULFID 364 377
 FT DISULFID 411 690
 FT DISULFID 431 653

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FT DISULFID 463 538
FT DISULFID 487 681
FT DISULFID 497 511
FT DISULFID 508 521
FT DISULFID 579 593
FT DISULFID 631 636
FT METAL 66 66
FT METAL 98 98
FT METAL 198 198
FT METAL 259 259
FT METAL 401 401
FT METAL 439 439
FT METAL 532 532
FT METAL 601 601
FT BINDING 127 127
FT BINDING 469 469
FT CARBOHYD 143 143
FT CARBOHYD 287 287
FT CARBOHYD 482 482
SQ SEQUENCE 695 AA; 75991 MW; 07B84D50E1B165D CRC64;

Query Match 62.9%; Score 44; DB 1; Length 695;
Best Local Similarity 66.7%; Pred. No. 1.8;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQNMKRV 12
DB 25 CAKFORNMKRV 36

RESULT 5
TRFL_MOUSE STANDARD; PRT: 707 AA.
AC P08071; P70690; Q61799; Q922P2;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN LTF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] _TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=87280033; PubMed=3611056;
RA Pentecost B.T., Teng C.T.;
RT "Lactotransferrin is the major estrogen inducible protein of mouse
RT uterine secretions.";
RL J. Biol. Chem. 262:10134-10139(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Morishashi K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=92042099; PubMed=1939212;
RA Liu Y., Teng C.T.;
RT "Characterization of estrogen-responsive mouse lactoferrin promoter.";
RL J. Biol. Chem. 266:21880-21885(1991).
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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EMBL; J03298; AAA40525.1; -;
EMBL; D88510; BAA13633.1; -;
EMBL; EC006904; AAH06904.1; -;
EMBL; M74778; AAA39427.1; -;
PIR; A28438; A28438.
HSP; P02788; 1CB6.
MGD; MGJ.96837; ltf.
InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SMC0094; TR_FER; 2.
PROSITE; PS00205; TRANSFERRIN_1; 1.
PROSITE; PS00206; TRANSFERRIN_2; 2.
PROSITE; PS00207; TRANSFERRIN_3; 2.
transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
Signal.
KW SIGNAL. 1 19
FT CHAIN 20 707 BY SIMILARITY.
FT REPEAT 20 357 LACTOTRANSFERRIN.
FT REPEAT 358 707 1.
FT DISULFID 27 63 BY SIMILARITY.
FT DISULFID 37 54 BY SIMILARITY.
FT DISULFID 133 216 BY SIMILARITY.
FT DISULFID 175 191 BY SIMILARITY.
FT DISULFID 188 199 BY SIMILARITY.
FT DISULFID 249 263 BY SIMILARITY.
FT DISULFID 366 398 BY SIMILARITY.
FT DISULFID 376 389 BY SIMILARITY.
FT DISULFID 423 702 BY SIMILARITY.
FT DISULFID 443 665 BY SIMILARITY.
FT DISULFID 475 550 BY SIMILARITY.
FT DISULFID 499 693 BY SIMILARITY.
FT DISULFID 509 523 BY SIMILARITY.
FT DISULFID 520 533 BY SIMILARITY.
FT DISULFID 591 605 BY SIMILARITY.
FT DISULFID 643 648 BY SIMILARITY.
FT METAL 78 78 IRON 1 (BY SIMILARITY).
FT METAL 110 110 IRON 1 (BY SIMILARITY).
FT METAL 210 210 IRON 1 (BY SIMILARITY).
FT METAL 271 271 IRON 1 (BY SIMILARITY).
FT METAL 413 413 IRON 2 (BY SIMILARITY).
FT METAL 451 451 IRON 2 (BY SIMILARITY).
FT METAL 544 544 IRON 2 (BY SIMILARITY).
FT METAL 613 613 IRON 2 (BY SIMILARITY).
FT BINDING 139 139 ANION (POTENTIAL).
FT BINDING 481 481 ANION (POTENTIAL).
FT CARBOHYD 118 118 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 494 494 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 1 2 MR -> IQG (IN REF. 1).
FT CONFLICT 25 25 R -> Q (IN REF. 2).
FT CONFLICT 82 82 M -> L (IN REF. 2).
FT CONFLICT 359 359 S -> T (IN REF. 2).
FT CONFLICT 382 382 A -> D (IN REF. 1).
FT CONFLICT 449 449 E -> G (IN REF. 2).
FT CONFLICT 629 629 L -> V (IN REF. 1).
SQ SEQUENCE 707 AA; 77865 MW; F26AE0340A4C19A8 CRC64;

Query Match 61.4%; Score 43; DB 1; Length 707;
Best Local Similarity 63.6%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWQNMKRV 11
DB 37 CLRQNMKRV 47

```

RESULT 6
BUB2_YEAST
ID BUB2_YEAST STANDARD; PRT; 306 AA.
AC F25448;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mitotic checkpoint protein BUB2 (Cell cycle arrest protein BUB2).
GN BUB2 OR YNR055C OR YMR926.08C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=91330299; PubMed=1651171;
RA Hoyt M.A., Totis L., Roberts B.T.;
RT "S. cerevisiae genes required for cell cycle arrest in response to
RT loss of microtubule function.";
RL Cell 66:507-517(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=21385309; PubMed=11493673;
RA Lee S.B., Jensen S., Frenz L.W., Johnson A.L., Pesquet D.,
RA Johnston L.H.;
RT "The Bub2-dependent mitotic pathway in yeast acts every cell cycle and
RT regulates cytokinesis.";
RL J. Cell Sci. 114:2345-2354(2001).
CC -!- FUNCTION: Part of a checkpoint which monitors spindle integrity
CC and prevents premature exit from mitosis. This cell-cycle arrest
CC depends upon inhibition of the G-protein tem1 by the BFA1/BUB2
CC complex.
CC -!- SUBUNIT: Interacts with BFA1.
CC -!- SUBCELLULAR LOCATION: Spindle poles.
CC -!- SIMILARITY: TO S.POMBE CDC16.
CC
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CC
DR EMBL; M64706; AAA16885.1; -.
DR EMBL; 249703; CAA89765.1; -.
DR PIR; A39654; A39654.
DR SGD; S0004659; BUB2.
DR InterPro; IPR000195; RabGAP_TBC.
DR Pfam; PF00566; TBC; 1.
DR SMART; SM00164; TBC; 1.
KW Cell cycle; Mitosis.
SQ SEQUENCE 306 AA; 35027 MW; A1DDBF548E81EA3 CRC64;

Query Match 58.6%; Score 41; DB 1; Length 306;
Best Local Similarity 60.0%; Pred. No. 2.7; Mismatches 0; Gaps 0;
Matches 6; Conservative 1; Indels 3;

QY 1 CFAWQGRNMRK 10
Db 108 CFAWQGRNMRK 117

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RESULT 7
IL2A_BOVIN

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IL2A_BOVIN STANDARD; PRT; 275 AA.
ID IL2A_BOVIN STANDARD; PRT; 275 AA.
AC P12342;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
DE subunit) (P55) (TAC antigen) (CD25).
GN IL2RA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88212503; PubMed=2835311;
RA Weinberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S.,
RA Reeves R., Magnusen J.A.;
RT "Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";
RL Immunology 63:603-610(1988).
RN [2]
RP SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=96116968; PubMed=8563178;
RA Yoo J., de Leon F.A., Stone R.T., Beattie C.W.;
RT "Cloning and chromosomal assignment of the bovine interleukin-2
RT receptor alpha (IL-2R alpha) gene.";
RL Mamm. Genome 6:751-753(1995).
CC -!- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
CC WITH A GAMMA CHAIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
CC
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CC
DR EMBL; M20818; AAA51414.1; -.
DR EMBL; U24226; AAC48487.1; -.
DR PIR; S07442; S07442.
DR HSP; P01589; IILM.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00084; sush1; 2.
DR SMART; SM00032; CCP; 2.
KW Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
RN SIGNAL 1 21
FT CHAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
FT DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 244 262 POTENTIAL.
FT DOMAIN 263 275 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 78 SUSHI 1.
FT DOMAIN 122 185 SUSHI 2.
FT DISULFID 24 64 BY SIMILARITY.
FT DISULFID 251 77 BY SIMILARITY.
FT DISULFID 123 168 BY SIMILARITY.
FT DISULFID 152 184 BY SIMILARITY.
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 275 AA; 31238 MW; 4901BBF9A4862390 CRC64;

Query Match 54.3%; Score 38; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. No. 8.5; Mismatches 0; Gaps 0;
Matches 6; Conservative 1; Indels 5;

QY 1 CFAWQGRNMRK 12

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Db 261 CLTWQRKWKQR 272

RESULT 8

IL2A_SHEEP STANDARD; PRT; 275 AA.

AC P26898;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (P55) (TAC antigen) (CD25).

GN IL2RA.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.

OC NCBI_TaxID=9940;

OX [1]

RP SEQUENCE FROM N.A.

RC TISSUE=T-cell;

RA Verhagen A.A.;

RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=92241682; PubMed=1572550;

RA Bujdosó R., Sargan D.R., Williamson M.L., McConnell I.,

RT "Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa protein, CD25.";

RL Gene 113:283-284 (1992).

CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.

CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE WITH A GAMMA CHAIN.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.

CC

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CC

EMBL; Z11560; CAA77652.1; -

DR EMBL; X60149; CAA42723.1; -

DR EMBL; A19167; CAA01447.1; -

DR PIR; S18910; S18910.

DR PIR; S18899; S18899.

DR PIR; JC1113; JC1113.

DR HSSP; P01589; I1LM.

DR InterPro; IPR000436; Sushi_SCR_CCP.

DR Pfam; PF00084; sushi.2.

DR SMART; SM00032; CCP; 2.

KW Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.

FT SIGNAL 1 21 BY SIMILARITY.

FT CHAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.

FT DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 244 262 POTENTIAL.

FT DOMAIN 263 275 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 23 78 SUSHI 1.

FT DOMAIN 122 185 SUSHI 2.

FT DISULFID 24 64 BY SIMILARITY.

FT DISULFID 751 77 BY SIMILARITY.

FT DISULFID 123 168 BY SIMILARITY.

FT DISULFID 152 184 BY SIMILARITY.

FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).

FT CONFLICT 166 166 S -> T (IN REF. 2).

SQ SEQUENCE 275 AA; 30904 MW; 1101A2DE5AC5A088 CRC64;

Query Match 54.3%; Score 38; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. No. 8.5;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 CFAMQRNKRKVR 12
DB 261 CLTWQRKWKQR 272

RESULT 9

VP4_ROTGA STANDARD; PRT; 749 AA.

AC Q04316;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).

GN S4.

OS Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).

OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.

OX NCBI_TaxID=12705;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93233240; PubMed=8386274;

RA Mackow E.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M.;

RT "Identification and baculovirus expression of the VP4 protein of the human group B rotavirus ADRV.";

RL J. Virol. 67:2730-2738 (1993).

CC -1- SUBCELLULAR LOCATION: Outer capsid.

CC -1- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.

CC

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CC

EMBL; M91434; AAA47338.1; -

DR InterPro; IPR000416; Cap_VP4.

DR Pfam; PF00426; VP4; 1.

KW Coat protein; Glycoprotein.

FT CARBOHYD 29 29 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 109 109 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 133 133 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 407 407 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 527 527 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 568 568 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 620 620 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 681 681 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 698 698 N-LINKED (GLCNAC...) (POTENTIAL).

SQ SEQUENCE 749 AA; 84362 MW; D123527DEAE0P21 CRC64;

Query Match 54.3%; Score 38; DB 1; Length 749;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 CFAMQRNKRKVR 12
DB 195 CFTWDMCANVR 206

RESULT 10

ABCR_HUMAN STANDARD; PRT; 2273 AA.

AC P78363; O60438; O60915; O15112;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Retinal-specific ATP-binding cassette transporter (RIM ABC transporter) (RIM protein) (RMP) (Stargardt disease protein).

GN ABCA4 OR ABCR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., VARIANTS STGD, AND VARIANTS HIS-846 AND GLN-943.
 RX MEDLINE=97207641; PubMed=9054934;
 RA Allikmets R., Singh N., Sun H., Shroyer N.F., Hutchinson A.,
 RA Chidambaram A., Gerrard B., Baird L., Stauffer D., Peiffer A.,
 RA Rattner A., Smallwood P.M., Li Y., Anderson K.L., Lewis R.A.,
 RA Nathans J., Leppert M., Dean M., Lupski J.R.;
 RA "A photoreceptor cell-specific ATP-binding transporter gene (ABCR) is
 RT mutated in recessive Stargardt macular dystrophy.";
 RL Nat. Genet. 15:236-246(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97345663; PubMed=9202155;
 RA Azarian S.M., Travis G.H.;
 RA "The photoreceptor rim protein is an ABC transporter encoded by the
 RT gene for recessive Stargardt's disease (ABCR).";
 RL FEBS Lett. 409:247-252(1997).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS STGD TRP-18 AND CYS-212.
 RX MEDLINE=98153759; PubMed=9503029;
 RA Gerber S., Rozet J.-M., van de Pol T.J.R., Hoyng C.B., Munnich A.,
 RA Blankenslag A., Kaplan J., Cremers F.P.M.;
 RA "Complete exon-intron structure of the retina-specific ATP binding
 RT transporter gene (ABCR) allows the identification of novel mutations
 RT underlying Stargardt disease.";
 RL Genomics 48:139-142(1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS STGD.
 RX MEDLINE=98141123; PubMed=9490294;
 RA Nasonkin I., Illing M., Koehler M.R., Schmid M., Molday R.S.,
 RA Weber B.H.F.;
 RA "Mapping of the rod photoreceptor ABC transporter (ABCR) to 1p21-p22.1
 RT and identification of novel mutations in Stargardt's disease.";
 RL Hum. Genet. 102:21-26(1998).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=99175213; PubMed=10075733;
 RA Sun H., Molday R.S., Nathans J.;
 RA "Retinal stimulates ATP hydrolysis by purified and reconstituted ABCR,
 RT the photoreceptor-specific ATP-binding cassette transporter
 RT responsible for Stargardt disease.";
 RL J. Biol. Chem. 274:8269-8281(1999).
 RN [6]
 RP DISEASE.
 RX MEDLINE=98133912; PubMed=9466990;
 RA Cremers F.P.M., van de Pol D.J.R., van Driel M.A., den Hollander A.I.,
 RA van Haren F.J.J., Knoers N.V.A.M., Tijmes N., Bergen A.A.B.,
 RA Rohrschneider K., Blankenslag A., Pinckers A.J.L.G., Deutman A.F.,
 RA Hoyng C.B.;
 RA "Autosomal recessive retinitis pigmentosa and cone-rod dystrophy
 RT caused by splice site mutations in the Stargardt's disease gene
 RT ABCR.";
 RL Hum. Mol. Genet. 7:355-362(1998).
 RN [7]
 RP VARIANTS ARMD2, AND VARIANTS.
 RX MEDLINE=97442530; PubMed=9295269;
 RA Allikmets R., Shroyer N.F., Singh N., Seddon J.M., Lewis R.A.,
 RA Bernstein P.S., Peiffer A., Zabarskie N.A., Li Y., Hutchinson A.,
 RA Dean M., Lupski J.R., Leppert M.;
 RA "Mutation of the Stargardt disease gene (ABCR) in age-related macular
 RT degeneration.";
 RL Science 277:1805-1807(1997).
 RN [8]
 RP VARIANTS STGD W-18; C-212; H-636; M-1019; V-1038; C-1108; W-1640;
 RP S-1977 AND H-2107, AND VARIANTS FFM P-11; P-541; V-1038; E-1091;
 RP C-1508; F-1970 AND R-1971.
 RX MEDLINE=98454319; PubMed=9781034;
 RA Rozet J.-M., Gerber S., Souied E., Perrault I., Chatelain S., Ghazi I.,
 RA Leowski C., Dufier J.-L., Munnich A., Kaplan J.;
 RT "Spectrum of ABCR gene mutations in autosomal recessive macular
 RT dystrophies.";
 RL Eur. J. Hum. Genet. 6:291-295(1998).
 RN [9]
 RP VARIANTS STGD.
 RX MEDLINE=99138655; PubMed=9973280;
 RA Lewis R.A., Shroyer N.F., Singh N., Allikmets R., Hutchinson A.,
 RA Li Y., Lupski J.R., Leppert M., Dean M.;
 RA "Genotype/phenotype analysis of a photoreceptor-specific ATP-binding
 RT cassette transporter gene, ABCR, in Stargardt disease.";
 RL Am. J. Hum. Genet. 64:422-434(1999).
 RN [10]
 RP VARIANTS STGD, AND VARIANTS.
 RX MEDLINE=99192348; PubMed=10090887;
 RA Maugeri A., van Driel M.A., van de Pol D.J.R., Klevering B.J.,
 RA van Haren F.J.J., Tijmes N., Bergen A.A.B., Rohrschneider K.,
 RA Blankenslag A., Pinckers A.J.L.G., Dahl N., Brunner H.G.,
 RA Deutman A.F., Hoyng C.B., Cremers F.P.M.;
 RA "The 2589G->C mutation in the ABCR gene is a mild frequent founder
 RT mutation in the western European population and allows the
 RT classification of ABCR Mutations in patients with Stargardt disease.";
 RL Am. J. Hum. Genet. 64:1024-1035(1999).
 RN [11]
 RP VARIANT STGD TYR-54, AND VARIANT ALA-863.
 RX MEDLINE=20077755; PubMed=10612508;
 RA Zhang K., Garibaldi D.C., Khazeva M., Albini T., Chiang M.F.,
 RA Kerrigan M., Sunness J.S., Han M., Allikmets R.;
 RA "A novel mutation in the ABCR gene in four patients with autosomal
 RT recessive Stargardt disease.";
 RL Am. J. Ophthalmol. 128:720-724(1999).
 RN [12]
 RP VARIANTS STGD V-60; R-206; P-300; P-541; A-849; P-974; V-1038; C-1108;
 RP L-1408; R-1488; D-1652; P-1729; E-1961; W-2038; W-2077; H-2107; R-2128
 RP AND Y-2150.
 RX MEDLINE=99221420; PubMed=10206579;
 RA Fishman G.A., Stone E.M., Grover S., Derlacki D.J., Haines H.L.,
 RA Hockey R.R.;
 RA "Variation of clinical expression in patients with Stargardt dystrophy
 RT and sequence variations in the ABCR gene.";
 RL Arch. Ophthalmol. 117:504-510(1999).
 RN [13]
 RP VARIANTS GLU-1961 AND ASN-2177.
 RX MEDLINE=20349288; PubMed=10880298;
 RA Allikmets R., Tammur J., Hutchinson A., Lewis R.A., Shroyer N.F.,
 RA Dalakishvili K., Lupski J.R., Steiner K., Pauleikhoff D., Holz F.G.,
 RA Weber B.H.F., Dean M., Atkinson A., Gail M.H., Bernstein P.S.,
 RA Singh N., Peiffer A., Zabarskie N.A., Leppert M., Seddon J.M.,
 RA Zhang K., Sunness J.S., Udar N.S., Velchits S., Silva-Garcia R.,
 RA Small K.W., Simonelli F., Testa F., D'Urso M., Brancato R.,
 RA Rinaldi E., Ingavast S., Taube A., Wadelius C., Souied E., Ducroq D.,
 RA Kaplan J., Assink J.J.M., ten Brink J.B., de Jong P.T.V.M.,
 RA Bergen A.A.B., Maugeri A., van Driel M.A., Hoyng C.B., Cremers F.P.M.,
 RA Paloma E., Coco R., Balcells S., Gonzalez-Duarte R., Kermani S.,
 RA Stanga P., Thattacharya S.S., Bird A.C.;
 RA "Further evidence for an association of ABCR alleles with age-related
 RT macular degeneration.";
 RL Am. J. Hum. Genet. 67:487-491(2000).
 RN [14]
 RP VARIANTS STGD E-60; T-60; E-65; L-68; R-72; C-212; S-230; S-247;
 RP V-288; K-471; P-541; Q-572; R-607; K-635; C-653; Y-764; R-765; A-901;
 RP I-959; K-1036; P-1038; P-1063; D-1087; C-1097; C-1108; L-1380; K-1399;
 RP P-1430; V-1440; H-1443; L-1486; M-1537; P-1689; L-1705;
 RP T-1733; R-1748; P-1763; K-1885; H-1898; R-1961; R-1975; G-2077
 RP W-2077 AND V-2241, AND VARIANTS Q-152; H-212; I-552; R-914;
 RP Q-943; T-1562; I-1868; M-1921; L-1948; P-1970; A-2059; N-2177 AND
 RP V-2216.
 RX MEDLINE=20442027; PubMed=10959763;
 RA Rivera A., White K., Stoehr H., Steiner K., Hemmrich N., Grimm T.,
 RA Jurklics B., Lorenz B., Scholl H.P.N., Apfelstedt-Sylla E.,
 RA Weber B.H.F.;
 RA "A comprehensive survey of sequence variation in the ABCA4 (ABCR) gene
 RT in Stargardt disease and age-related macular degeneration.";

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RL Am. J. Hum. Genet. 67:800-813(2000).
RN [15]
RP VARIANTS CORD3 GLU-65; CYS-212; PRO-541; ALA-863; GUY-863 DEL;
RP VAL-1038; LYS-1122; TYR-1490 AND ASP-1598.
RX MEDLINE=20442040; PubMed=10958761;
RA Maugeri A., Klevering B.J., Kohrschneider K., Blankenagel A.,
RA Brunner H.G., Deutman A.F., Hoyng C.B., Cremers P.P.M.,
RT "Mutations in the ABCA4 (ABCR) gene are the major cause of autosomal
RT recessive cone-rod dystrophy."
RL Am. J. Hum. Genet. 67:960-966(2000).
RN [16]
RP VARIANTS STGD ASP-340; GLN-572; ALA-863; SER-965; VAL-1038; ALA-1780
RP AND HIS-1898, AND VARIANT GLN-943.
RX MEDLINE=20208356; PubMed=10746567;
RA Shroyer N.F., Lewis R.A., Lupski J.R.,
RT "Complex inheritance of ABCR mutations in Stargardt disease: linkage
RT disequilibrium, complex alleles, and pseudodominance."
RL Hum. Genet. 106:244-248(2000).
RN [17]
RP VARIANTS STGD.
RX MEDLINE=20098082; PubMed=10634594;
RA Papaiannou M., Otsaka L., Bessant D., Lois N., Bird A.C., Payne A.,
RA Bhattacharya S.S.,
RT "An analysis of ABCR mutations in British patients with recessive
RT retinal dystrophies."
RL Invest. Ophthalmol. Vis. Sci. 41:16-19(2000).
RN [18]
RP VARIANTS STGD C-212; D-767; I-897; V-1038; K-1087; K-1399; Q-1640 AND
RP E-1961, AND VARIANT HIS-212.
RX MEDLINE=20174852; PubMed=10711710;
RA Simonelli F., Testa F., de Crechcio G., Rinaldi E., Hutchinson A.,
RA Atkinson A., Dean M., D'Urso M., Allikmets R.,
RT "New ABCR mutations and clinical phenotype in Italian patients with
RT Stargardt disease."
RL Invest. Ophthalmol. Vis. Sci. 41:892-897(2000).
RN [19]
RP CHARACTERIZATION OF VARIANTS, AND MUTAGENESIS OF GLY-966; LYS-969;
RP GLY-1975 AND LYS-1978.
RX MEDLINE=20472331; PubMed=11017087;
RA Sun H., Smallwood P.M., Nathans J.,
RT "Biochemical defects in ABCR protein variants associated with human
RT retinopathies."
RL Nat. Genet. 26:242-246(2000).
RN [20]
RP VARIANTS STGD ASN-972, AND VARIANTS GLN-943, ILE-1868 AND LEU-1948.
RX MEDLINE=21478761; PubMed=11594993;
RA Eksandh L., Ekstrom U., Abrahamson M., Bauer B., Andreasson S.,
Query Match 54.3%; Score 38; DB 1; Length 2273;
Best Local Similarity 75.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CFAWQRNM 8
Db 779 CFAWQDRM 786
RESULT 11
DYHB CHLRE
ID DYHB CHLRE STANDARD; PRT; 4568 AA.
AC Q39565;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Dynein beta chain, flagellar outer arm.
GN ODA4 OR ODA-4 OR SUP1.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
CC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RL STRAIN=2197;
Am. J. Hum. Genet. 67:800-813(2000).
RX MEDLINE=94274778; PubMed=8006077;
RA Mitchell D.R., Brown K.S.,
RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
chain genes."
RL J. Cell Sci. 107:635-644(1994).
CC -!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
CC FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC DYNEIN HAS ATPASE ACTIVITY.
CC -!- SURUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
CC GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
CC -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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CC -----
CC EMBL; U02963; AAA19956.1;
CC InterPro; IPR004273; Dynein heavy.
CC Pfam; PF03028; Dynein_heavy; 1.
CC Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
CC Coiled coil.
CC FT DOVAIN 1158 277 293 COILED COIL (POTENTIAL).
CC FT DOVAIN 1158 1175 COILED COIL (POTENTIAL).
CC FT DOVAIN 1372 1400 COILED COIL (POTENTIAL).
CC FT DOVAIN 1614 1650 COILED COIL (POTENTIAL).
CC FT DOVAIN 1778 1825 COILED COIL (POTENTIAL).
CC FT DOVAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
CC FT DOVAIN 2831 2848 COILED COIL (POTENTIAL).
CC FT DOVAIN 3106 3162 COILED COIL (POTENTIAL).
CC FT DOVAIN 3339 3425 COILED COIL (POTENTIAL).
CC FT DOVAIN 3648 3728 COILED COIL (POTENTIAL).
CC FT NP_BIND 1919 1926 ATP (POTENTIAL).
CC FT NP_BIND 2202 2209 ATP (POTENTIAL).
CC FT NP_BIND 2530 2537 ATP (POTENTIAL).
CC FT NP_BIND 2879 2886 ATP (POTENTIAL).
CC SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;
Query Match 54.3%; Score 38; DB 1; Length 4568;
Best Local Similarity 41.7%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 CFAWQRNMKVR 12
Db 1852 CFQWQSLRYIQ 1863
RESULT 12
RS3A DROME
ID RS3A DROME STANDARD; PRT; 267 AA.
AC P55830; O44389; Q9V4A9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S3a (C3 protein).
GN RPS3A OR C3 OR M(4)101 OR CG2168.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
RP SPECIFICITY.
RC STRAIN=Oregon-R; TISSUE=Embryo;
EX MEDLINE=98055162; PubMed=9393444;
RA Reynaud E., Bolshakov V.N., Barajas V.N., Kafatos F.C., Zurita M.,
RT "Antisense suppression of the putative ribosomal protein S3a gene
RT disrupts ovarian development in Drosophila melanogaster."
RL Mol. Gen. Genet. 256:462-467(1997).

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[2]
RN SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
RP TISSUE=Embryo;
RC MEDLINE=98416207; PubMed=9742251;
RX van Beest M., Morin M., Clevers H.;
RT "Drosophila Rp3a, a novel minute gene situated between the segment
RT polarity genes cubitus interruptus and dTcf.";
RL Nucleic Acids Res. 26:4471-4475(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley; PubMed=10731132;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Wan X.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fessler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moberg C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupeki M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: ESSENTIAL FOR OOOGENESIS; REQUIRED FOR LATE FOLLICLE CELL
CC -1- DEVELOPMENT. MAY BIND TO THE 40S RIBOSOMAL SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: UBICUOUSLY EXPRESSED IN STAGE 8 EMBRYOS.
CC DURING OOOGENESIS, EXPRESSION IS LOCATED BASALLY IN SOMATIC
CC FOLLICULAR EPITHELIUM AND IN THE OOCYTE AT THE LATER STAGES.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY
CC THROUGHOUT ALL DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE S3AE FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
CC EMBL: Y10115; CAA71201.1; -
CC DR EMBL: AF034971; AAC62117.1; -
CC DR EMBL: AF003845; AAF59372.1; -
CC DR FlyBase: FBgn0017545; RpS3A.
CC InterPro: IPR001593; Ribosomal_S3AE.

Pfam: PF01015; Ribosomal_S3AE; 1.
DR ProDom: PD003035; Ribosomal_S3AE; 1.
DR PROSITE: PS01191; RIBOSOMAL_S3AE; 1.
KW Ribosomal protein.
FT INIT MET 0 0 BY SIMILARITY.
FT CONFLICT 61 61 L -> F (IN REF. 1).
FT CONFLICT 71 71 A -> VP (IN REF. 1).
FT CONFLICT 81 81 R -> H (IN REF. 1).
FT CONFLICT 159 160 QQ -> HE (IN REF. 1).
FT CONFLICT 168 168 A -> SG (IN REF. 1).
FT CONFLICT 252 260 VIDRPGVE -> PKSTALKVK (IN REF. 1).
FT CONFLICT 266 266 S -> A (IN REF. 3).
SQ SEQUENCE 267 AA; 30225 MW; 3FF51141158455E7 CRC64;
Query Match 52.9%; Score 37; DB 1; Length 267;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CFQWRNRKVR 12
Db 156 CYAQSQSVRKIR 167
RESULT 13
1A34 HUMAN STANDARD; PRT; 365 AA.
ID 1A34 HUMAN STANDARD; PRT; 365 AA.
AC P30453; P30454;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, AW-34(A-10) alpha chain
DE precursor.
GN HLA-A OR HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A. (A*3401/A*3402).
RX MEDLINE=9305508; PubMed=1431115;
RA Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
RA Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
RA Martell R.W., du Toit E.D., Parham P.;
RT "Distinctive HLA-A,B antigens of black populations formed by
RT interallelic conversion.";
RL J. Immunol. 149:3411-3415(1992).
RN [2]
RX SEQUENCE FROM N.A. (A*3401/A*3402).
RX MEDLINE=93235211; PubMed=8475492;
RA Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,
RA Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
RA du Toit E.D., Parham P.;
RT "Structural diversity in the HLA-A10 family of alleles: correlations
RT with serology.";
RL Tissue Antigens 41:72-80(1993).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -1- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401
CC (AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
CC A*3401.
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CC EMBL: X61704; CAA43873.1; -
CC DR EMBL: X61705; CAA43874.1; -

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DR EMBL; AJ235273; CAA15167.1; -;
DR EMBL; Y11778; CAA72457.1; -;
DR InterPro; IPR004667; ADP_ATP_car.
DR Pfam; PF03219; TLC; 1.
DR TIGRFAMs; TIGR00769; AAA; 1.
KW Transmembrane, Transport; ATP-binding; Multigene family;
KW Complete proteome.
FT TRANSMEM 26 46 POTENTIAL.
FT TRANSMEM 62 82 POTENTIAL.
FT TRANSMEM 94 114 POTENTIAL.
FT TRANSMEM 149 169 POTENTIAL.
FT TRANSMEM 184 204 POTENTIAL.
FT TRANSMEM 224 244 POTENTIAL.
FT TRANSMEM 287 307 POTENTIAL.
FT TRANSMEM 328 348 POTENTIAL.
FT TRANSMEM 357 377 POTENTIAL.
FT TRANSMEM 381 401 POTENTIAL.
FT TRANSMEM 459 489 POTENTIAL.
SQ SEQUENCE 500 AA; 57073 MW; FE3DB48D08CF5F72 CRC64;

Query Match 52.9%; Score 37; DB 1; Length 500;
Best Local Similarity 54.5%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAMQRMVKV 11
Db 482 CFAMYYVRKI 492

Search completed: February 21, 2003, 07:27:42
Job time : 5.6 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds
(without alignments)
118.873 Million cell updates/sec

Title: US-09-743-107B-70
Perfect score: 70
Sequence: 1 CFQWRNMRKV 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	85.7	711	4 Q8TCD2	Q8TCD2 homo sapien
2	56	80.0	38	4 Q9UCY5	Q9UCY5 homo sapien
3	47	67.1	511	16 Q8Z462	Q8Z462 salmonella
4	45	64.3	33	6 Q9TR80	Q9TR80 ovis aries
5	43	61.4	121	16 Q8U6K3	Q8U6K3 agrobacteri
6	43	61.4	282	16 Q98Q19	Q98Q19 mycoplasma
7	40	57.1	114	11 Q63104	Q63104 rattus norv
8	40	57.1	234	11 Q63112	Q63112 rattus norv
9	40	57.1	298	16 Q8YP77	Q8YP77 anabaena sp
10	40	57.1	393	16 Q9ZK94	Q9ZK94 helicobacte
11	40	57.1	469	9 Q38115	Q38115 bacterioph
12	40	57.1	519	10 P33833	P33833 arabidopsis
13	40	57.1	584	17 Q9HPA3	Q9HPA3 halobacteri
14	40	57.1	720	10 Q9CA22	Q9CA22 arabidopsis
15	39	55.7	205	8 Q98RR2	Q98RR2 guillardia
16	39	55.7	341	11 Q8R2A4	Q8R2A4 mus musculu

17	39	55.7	393	16	Q25611	helicobacte
18	39	55.7	681	5	Q9XVD1	Q9XVD1 caenorhabdi
19	39	55.7	783	16	Q9FBV4	Q9FBV4 streptomyce
20	39	55.7	886	5	Q9VZV1	Q9VZV1 drosophila
21	38	54.3	196	4	O14557	O14557 homo sapien
22	38	54.3	232	4	Q96H38	Q96H38 homo sapien
23	38	54.3	246	4	Q96GY3	Q96GY3 homo sapien
24	38	54.3	273	2	O31090	O31090 rhizobium 1
25	38	54.3	289	10	Q9C6N2	Q9C6N2 arabidopsis
26	38	54.3	553	4	Q9NZL7	Q9NZL7 homo sapien
27	38	54.3	554	4	Q9NY67	Q9NY67 homo sapien
28	38	54.3	558	4	Q9U7K6	Q9U7K6 homo sapien
29	38	54.3	2310	11	O35600	O35600 mus musculu
30	37	52.9	217	5	Q8SZD2	Q8SZD2 drosophila
31	37	52.9	232	11	Q91W07	Q91W07 mus musculu
32	37	52.9	236	10	Q9SK05	Q9SK05 arabidopsis
33	37	52.9	246	11	Q9D8N6	Q9D8N6 mus musculu
34	37	52.9	294	11	Q9DCU6	Q9DCU6 mus musculu
35	37	52.9	482	10	Q9M5C0	Q9M5C0 volvox cart
36	37	52.9	500	10	Q41383	Q41383 spinacia ol
37	37	52.9	550	11	Q9JUZ5	Q9JUZ5 mus musculu
38	37	52.9	607	4	Q9H8A5	Q9H8A5 homo sapien
39	37	52.9	676	5	Q9K4T5	Q9K4T5 caenorhabdi
40	37	52.9	678	10	Q9FG26	Q9FG26 arabidopsis
41	37	52.9	679	2	Q9SLK8	Q9SLK8 streptover
42	37	52.9	737	5	Q95QJ8	Q95QJ8 caenorhabdi
43	37	52.9	2348	5	Q9V346	Q9V346 drosophila
44	37	52.9	2858	5	Q9GYP6	Q9GYP6 caenorhabdi
45	37	52.9	5636	4	Q96RW7	Q96RW7 homo sapien

ALIGNMENTS

RESULT 1

Q8TCD2 PRELIMINARY; PRT; 711 AA.
AC Q8TCD2; 01-JUN-2002 (TREMREL. 21, Created)
DT 01-JUN-2002 (TREMREL. 21, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Lactotransferrin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022347; AAH2347.1; -.
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7E097C45FAF CRC64;

Query Match 85.7%; Score 60; DB 4; Length 711;
Best Local Similarity 90.9%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRNMRKV 11
Db 39 CFQWRNMRKV 49

RESULT 2

Q9UCY5 PRELIMINARY; PRT; 38 AA.
AC Q9UCY5; 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE Lactoferrin homolog (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96081613; PubMed=8551695;
 RA Sato I.;
 RT "Characterization of the 84-kDa protein with ABH activity in human
 seminal plasma";
 RL Jpn. J. Legal Med. 49:281-293(1995).
 DR HSP; P02788; IBA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDEB CRC64;

Query Match 80.08; Score 56; DB 4; Length 38;
 Best Local Similarity 90.94; Pred. No. 0.0025;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FAWQNRNMRKV 12
 | | | | |
 Db 21 FQWQNRNMRKV 31

RESULT 3
 Q8Z462 PRELIMINARY; PRT; 511 AA.
 AC Q8Z462;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein STY3070.
 GN STY3070.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felwell T., Hanlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrall B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18";
 RL Nature 413:848-852(2001).
 DR EMBL; AL627276; CAD06049.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 511 AA; 58126 MW; E2DD124E10D178B CRC64;

Query Match 67.18; Score 47; DB 16; Length 51;
 Best Local Similarity 66.76; Pred. No. 1.9;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 FAWQNRNMRKV 12
 | | | | |
 Db 350 FQWQNRNMRKV 361

RESULT 4
 Q9TR80 PRELIMINARY; PRT; 33 AA.
 AC Q9TR80;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Lactoferrin (Fragment).
 OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95127729; PubMed=7827104;
 RA Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
 RL Biochim. Biophys. Acta 1243:25-32(1995).
 DR HSP; O77698; ICE2.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 64.34; Score 45; DB 6; Length 33;
 Best Local Similarity 54.54; Pred. No. 0.23;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAWQNRNMRKV 11
 | | | | |
 Db 19 CYQWQKQYKRL 29

RESULT 5
 Q8U6K3 PRELIMINARY; PRT; 121 AA.
 AC Q8U6K3;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein Atu4804.
 GN Atu4804.
 OS Agrobacterium tumefaciens (strain CS8 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood R., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyee D. Sr.,
 RA Chapman P., Deenening J., Deatherage G., Gillet W., Grant C.,
 RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tac Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT CS8";
 RL Science 294:2317-2323(2001).
 DR EMBL; AE009409; AAL45598.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 121 AA; 14085 MW; EBAP41617A3CEA53 CRC64;

Query Match 61.44; Score 43; DB 16; Length 121;
 Best Local Similarity 63.64; Pred. No. 2.2;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FAWQNRNMRKV 11
 | | | | |
 Db 14 CLAWQNRNMRV 24

RESULT 6
 Q98Q19 PRELIMINARY; PRT; 282 AA.
 AC Q98Q19;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE tRNA pseudouridine synthase B (TRNA pseudouridine 55 synthase) (PSI55

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DE synthase) (Pseudouridylylate synthase) (Uracil hydrolyase)
DE (EC 4.2.1.70).
GN MYP0 5500.
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmatadaceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAB CTIP;
RA MEDLINE=21267165; PubMed=11353084;
RX Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dydvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis.";
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL: AL445565; CAC13723.1; -.
DR MYPULIST; MYP0 5500; -.
DR InterPro; IPR004510; TruB.
DR InterPro; IPR002501; TruB_N.
DR Pfam; PF01509; TruB_N; 1.
DR TIGRPFAMs; TIGR00431; TruB; 1.
KW Lyase; Complete proteome.
SQ SEQUENCE 282 AA; 31961 MW; A598529F52B1EBEE CRC64;

Query Match 61.4%; Score 43; DB 16; Length 282;
Best Local Similarity 60.0%; Pred. No. 5.5;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FAWQNNMKV 11
Db |||:::
20 FAWQNNIKKI 29

RESULT 7
Q63104 PRELIMINARY; PRT; 114 AA.
AC Q63104
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Carcinoembryonic antigen (Fragment).
GN CE4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BD II; TISSUE=LIVER;
RX Medline=8924106; PubMed=2708349;
RA Kodellja V., Lucas K., Barnert S., von Kleist S., Thompson J.A.,
RA Zimmermann W.A.;
RT "Identification of a carcinoembryonic antigen gene family in the rat:
RT Analysis of the N-terminal domains reveals immunoglobulin-like,
RT hypervariable regions.";
RL J. Biol. Chem. 264:6906-6912(1989).
DR EMBL; M60026; AAA40911.1; -.
FT NON TER 1
SQ SEQUENCE 114 AA; 12832 MW; 3AE10869B061686 CRC64;

Query Match 57.1%; Score 40; DB 11; Length 114;
Best Local Similarity 60.0%; Pred. No. 7.4;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FAWQNNMKV 11
Db |||:::
42 FAWYGLRKI 51

RESULT 8
Q63112 PRELIMINARY; PRT; 234 AA.
AC Q63112
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Carcinoembryonic antigen-related protein (Fragment).
GN CGM4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RX Rebrostock S., Lucas K., Thompson J.A., Zimmermann W.A.;
RL Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RX MEDLINE=90243655; PubMed=2335509;
RA Rebrostock S., Lucas K., Thompson J.A., Zimmermann W.A.;
RT "cDNA and gene analyses imply a novel structure for a rat
RT carcinoembryonic antigen-related protein.";
RL J. Biol. Chem. 265:7872-7879(1990).
DR EMBL; M32475; AAA66038.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
FT NON TER 1
SQ SEQUENCE 234 AA; 26171 MW; 69BBC9EE0C773F2A CRC64;

Query Match 57.1%; Score 40; DB 11; Length 234;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FAWQNNMKV 11
Db |||:::
42 FAWYGLRKI 51

RESULT 9
Q8YP77 PRELIMINARY; PRT; 298 AA.
AC Q8YP77
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Alr4323.
GN ALR4323.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AF003596; BAB76022.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 298 AA; 34513 MW; 64036E6B52299A9F CRC64;

Query Match 57.1%; Score 40; DB 16; Length 298;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FAWQNNMKV 10

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Db 163 FHWQRYRX 171

RESULT 10

Q2KPK4 ID Q9ZKP4 PRELIMINARY; PRT; 393 AA.
 AC Q9ZKP4;
 DT 01-MAY-1999 (TREMELrel. 10, Created)
 DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
 DE 3-deoxy-D-manno-octulosonic-acid transferase.
 GN WAAA OR JHP0831.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=85963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.B., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 Smith D.R., Noonan B., Guild B.C., deJonghe B.L., Carmel G.,
 Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 Trust T.J.;
 RA "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori.";
 RL Nature 397:176-180(1999).
 DR EMBL; AB001519; AAD06459.1; -.
 KW Complete proteome.
 SQ SEQUENCE 393 AA; 45442 MW; ADDDA88C1EC0C18D CRC64;

Query Match

Best Local Similarity 57.1%; Score 40; DB 16; Length 393;
 Matches 4; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 2 FAWQNRKVR 12

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Db 110 FAWKULKRLK 120

RESULT 11

Q38115 ID Q38115 PRELIMINARY; PRT; 469 AA.
 AC Q38115;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMELrel. 08, Last annotation update)
 DE ORF29.
 OS Bacteriophage rlt.
 OC Viruses.
 OX NCBI_TaxID=43685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96332668; PubMed=8730874;
 RA Nauta A., Van Sinderen D., Karsens H., Smit E., Venema G., Kok J.;
 RT "Inducible gene expression mediated by a repressor-operator system
 RT isolated from Lactococcus lactis bacteriophage rlt.";
 RL Mol. Microbiol. 19:1331-1341(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96332669; PubMed=8730875;
 RA Van Sinderen D., Karsens H., Kok J., Terpstra P., Ruiters M.H.,
 RA Venema G., Nauta A.;
 RT "Sequence analysis and molecular characterization of the temperate
 RT lactococcal bacteriophage rlt.";
 RL Mol. Microbiol. 19:1343-1355(1996).
 DR EMBL; U38906; AAB18704.1; -.
 KW Complete proteome.
 SQ SEQUENCE 469 AA; 53160 MW; 1F8E02D4325C6BB9 CRC64;

Query Match

Best Local Similarity 57.1%; Score 40; DB 9; Length 469;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQNRMK 10

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Db 39 CYPWQKNLLK 48

RESULT 12

P93833 ID P93833 PRELIMINARY; PRT; 519 AA.
 AC P93833;
 DT 01-MAY-1997 (TREMELrel. 03, Created)
 DT 01-MAY-1997 (TREMELrel. 03, Last sequence update)
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
 DE Hypothetical 58.5 kDa protein.
 GN PPK1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsia.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kwart M., Bucherer T., Frommer W.B.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; Y11930; CAA72680.1; -.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TKG; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
 DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Hypothetical protein; Serine/threonine-protein kinase;
 KW Transferase.
 SQ SEQUENCE 519 AA; 58492 MW; 6252EE001B2BC035 CRC64;

Query Match

Best Local Similarity 57.1%; Score 40; DB 10; Length 519;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQNRMK 9

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Db 420 CLAWDRNQR 428

RESULT 13

Q9HPA3 ID Q9HPA3 PRELIMINARY; PRT; 584 AA.
 AC Q9HPA3;
 DT 01-MAR-2001 (TREMELrel. 16, Created)
 DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
 DE Vng1732c.
 GN VNG1732C.
 OS Halobacterium sp. (strain NRC-1).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20504483; PubMed=11016950;
 RA NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonaki P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Beck R.F., Pohlshroder M., Spudis J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dasarma S.;
 RT "Genome sequence of Halobacterium species NRC-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

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DR EMBL; AE005078; AAC19967.1; ..
DR InterPro; IPR001646; Speptide repeat..
DR InterPro; IPR001622; X-channel pore..
DR Pfam; PF00805; Pentapeptide; 2.
SQ COMPLETE PROTEOME.
KW Complete proteome.
SQ SEQUENCE 584 AA; 65151 MW; 21BF5DF0486CCC6 CRC64;

Query Match
Best Local Similarity 57.1%; Score 40; DB 17; Length 584;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQNRKVR 12
Db 445 CFTWRKDMERRK 456
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|||:::|

RESULT 14
Q9CA22 PRELIMINARY; PRT; 720 AA.
AC Q9CA22;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 80.0 kDa protein.
GN T32E8.5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egtu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana."
RL Nature 408:816-820(2000).
DR EMBL; AC012193; AAG51619.1; ..
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SMO0220; S TKC; 1.
DR SMART; SMO0219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
DR KW ATP-binding; Hypothetical protein; Transferase.
SQ SEQUENCE 720 AA; 80027 MW; F26A9A031C6D91DE CRC64;

Query Match
Best Local Similarity 57.1%; Score 40; DB 10; Length 720;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQNRMR 9
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Db 616 C1AWDRNQR 624

RESULT 15
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AC Q98RR2;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 26S proteasome SU BS.
GN PRS95.
OS Guillardia theta (Cryptomonas phi).
OC Nucleomorph.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2122349; PubMed=1133671;
RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,
RA Wu X., Reith M., Cavalier-Smith T., Maier U.G.;
RT "The highly reduced genome of an enslaved algal nucleus."
EL Nature 410:1091-1096(2001).
DR EMBL; AF165818; AAK39885.1; ..
DR InterPro; IPR000243; Proteasome_B.
DR InterPro; IPR001353; Proteasome; 1.
DR Pfam; PF00227; proteasome; 1.
DR PRINTS; PR00141; PROTEASOME.
KW Proteasome.
SQ SEQUENCE 205 AA; 22691 MW; D30F5289C8C85049 CRC64;

Query Match
Best Local Similarity 55.7%; Score 39; DB 8; Length 205;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQNRNM 8
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Db 63 CFFWERNL 70

Search completed: February 21, 2003, 07:44:20
Job time : 22.8 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds
(without alignments)
56.502 Million cell updates/sec

Title: US-09-743-107B-71
Perfect score: 64
Sequence: 1 CPOAQRNMRKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*

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5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
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20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	100.0	12	21	AAV78071 Human lactoferrin
2	59	92.2	12	21	AAV78080 Human lactoferrin
3	57	89.1	12	21	AAV78038 Human lactoferrin
4	57	89.1	12	21	AAV78046 Human lactoferrin
5	57	89.1	12	21	AAV78047 Human lactoferrin
6	57	89.1	13	21	AAV78037 Human lactoferrin
7	57	89.1	13	21	AAV78048 Human lactoferrin
8	57	89.1	13	21	AAV78049 Human lactoferrin
9	57	89.1	14	21	AAV78036 Human lactoferrin
10	57	89.1	14	21	AAV78050 Human lactoferrin

11	57	89.1	14	21	AAV78051 Human lactoferrin
12	57	89.1	15	17	AAV98554 Peptide for anti-u
13	57	89.1	15	21	AAV78035 Human lactoferrin
14	57	89.1	15	21	AAV78062 Human lactoferrin
15	57	89.1	15	21	AAV78063 Human lactoferrin
16	57	89.1	16	21	AAV78031 Human lactoferrin
17	57	89.1	16	21	AAV78064 Human lactoferrin
18	57	89.1	16	21	AAV78065 Human lactoferrin
19	57	89.1	17	21	AAV78034 Human lactoferrin
20	57	89.1	17	21	AAV78066 Human lactoferrin
21	57	89.1	17	21	AAV78067 Human lactoferrin
22	57	89.1	18	15	AAV69352 Human lactoferrin
23	57	89.1	18	17	AAV13397 Advanced glycosyla
24	57	89.1	18	21	AAV78033 Human lactoferrin
25	57	89.1	19	21	AAV68667 Amino acid sequenc
26	57	89.1	19	21	AAV78032 Human lactoferrin
27	57	89.1	20	13	AAV21810 Anti microbial pep
28	57	89.1	20	14	AAV44841 Lactoferrin-relate
29	57	89.1	20	15	AAV48530 Lactoferrin derive
30	57	89.1	20	15	AAV48531 Lactoferrin derive
31	57	89.1	20	15	AAV57461 Lactoferrin derive
32	57	89.1	20	15	AAV57462 Lactoferrin derive
33	57	89.1	20	16	AAV84698 Bovine lactoferrin
34	57	89.1	20	16	AAV84699 Bovine lactoferrin
35	57	89.1	20	16	AAV80263 Anti-parasitic lac
36	57	89.1	20	16	AAV80264 Anti-parasitic lac
37	57	89.1	20	17	AAV98553 Peptide for anti-u
38	57	89.1	20	17	AAV91852 Lactoferrin-derive
39	57	89.1	20	17	AAV03045 Lactoferrin-derive
40	57	89.1	20	17	AAV90507 Lactoferrin-derive
41	57	89.1	20	17	AAV87821 Lactoferrin-derive
42	57	89.1	20	17	AAV87822 Lactoferrin-derive
43	57	89.1	20	18	AAV26150 Lactoferrin deriva
44	57	89.1	20	18	AAV14036 Anti-parasitic pep
45	57	89.1	20	19	AAV70310 Thrombus formation

ALIGNMENTS

RESULT 1
AAV78071
ID AAV78071 standard; Peptide; 12 AA.
XX
AC AAV78071;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:71.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; candida infection; fungicidal;
KW bactericidal; preservative.

OS Homo sapiens.
OS Synthetic.

XX WO200001730-A1.

PD 13-JAN-2000.

PF 06-JUL-1999; 99WO-SE01230.

PR 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

PA (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX Claim 22; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX SQ Sequence 12 AA;
Query Match 100.0%; Score 64; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFOAQRNMRKVR 12
||| |||||
DB 1 CFOAQRNMRKVR 12

RESULT 2
AAY78080
ID AAY78080 standard; Peptide; 12 AA.
XX AAY78080;
AC AAY78080;
XX 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:80.
DE Human, lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX Homo sapiens.
OS Synthetic.
XX WO200001730-A1.
XX 13-JAN-2000.
XX 06-JUL-1999; 99WO-S001230.
XX 06-JUL-1998; 98SE-0002441.
XX 17-JUL-1998; 98SE-0002562.
XX 29-DEC-1998; 98SE-0004614.
XX (ASCI-) A+ SCI INVEST AB.
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX Claim 22; Page 36; 102pp; English.
XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX SQ Sequence 12 AA;
Query Match 92.2%; Score 59; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.00031;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFOAQRNMRKVR 12
||| |||||
DB 1 CFQLQRNMRKVR 12

RESULT 3
AAY78038
ID AAY78038 standard; Peptide; 12 AA.
XX AAY78038;
AC AAY78038;
XX 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:38.
DE Human, lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX Homo sapiens.
OS Synthetic.
XX WO200001730-A1.
XX 13-JAN-2000.
XX 06-JUL-1999; 99WO-S001230.
XX 06-JUL-1998; 98SE-0002441.
XX 17-JUL-1998; 98SE-0002562.
XX 29-DEC-1998; 98SE-0004614.
XX (ASCI-) A+ SCI INVEST AB.
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX Claim 12; Page 70; 102pp; English.
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also

QY 1 CFQQRNMRKVR 12
 DB 1 CFQQRNMRKVR 12

RESULT 6

AAAY78037
 ID AAAY78037 standard; Peptide; 13 AA.

XX AAAY78037;
 AC AAAY78037;

XX 25-APR-2000 (first entry)
 DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:37.
 DE Human lactoferrin derived peptide SEQ ID NO:37.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.
 PN WO200001730-A1.

XX 13-JAN-2000.
 PD 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.
 PF 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.
 PR 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.
 PR 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.
 PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.
 PA (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.
 DR WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PT inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 70; 102pp; English.
 PS Claim 12; Page 70; 102pp; English.

XX AAAY78001 to AAAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 13 AA;
 SQ Sequence 13 AA;

Query Match 89.1%; Score 57; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 0.00077;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNMRKVR 12
 DB 2 CFQQRNMRKVR 13

RESULT 7

AAAY78048

ID AAAY78048 standard; Peptide; 13 AA.

XX AAAY78048;
 AC AAAY78048;

XX 25-APR-2000 (first entry)
 DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:48.
 DE Human lactoferrin derived peptide SEQ ID NO:48.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.
 PN WO200001730-A1.

XX 13-JAN-2000.
 PD 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.
 PF 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.
 PR 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.
 PR 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.
 PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.
 PA (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.
 DR WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PT inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 74; 102pp; English.
 PS Claim 15; Page 74; 102pp; English.

XX AAAY78001 to AAAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 13 AA;
 SQ Sequence 13 AA;

Query Match 89.1%; Score 57; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 0.00077;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNMRKVR 12
 DB 2 CFQQRNMRKVR 13

RESULT 8

AAAY78049

ID AAAY78049 standard; Peptide; 13 AA.

XX AAAY78049;
 AC AAAY78049;

XX 25-APR-2000 (first entry)
 DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:49.
 DE Human lactoferrin derived peptide SEQ ID NO:49.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SE01230.
 XX
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 XX (ASCI-) A+ SCI INVEST AB.
 PA
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PT
 XX Claim 18; Page 74; 102pp; English.
 PS
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 13 AA;
 Query Match 89.1%; Score 57; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 0.00077;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQQRNNRKVR 12
 Db 2 CFQWRNNRKVR 13
 RESULT 9
 AAY78036
 ID AAY78036 standard; Peptide; 14 AA.
 AC AAY78036;
 XX
 XX 25-APR-2000 (first entry)
 DT
 XX Human lactoferrin derived peptide SEQ ID NO:36.
 DE
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.

OS Synthetic.
 XX WO200001730-A1.
 PN
 XX 13-JAN-2000.
 PD
 XX 06-JUL-1999; 99WO-SE01230.
 XX
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 XX (ASCI-) A+ SCI INVEST AB.
 PA
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PT
 XX Claim 12; Page 69; 102pp; English.
 PS
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 14 AA;
 Query Match 89.1%; Score 57; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00083;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQQRNNRKVR 12
 Db 3 CFQWRNNRKVR 14
 RESULT 10
 AAY78050
 ID AAY78050 standard; Peptide; 14 AA.
 AC AAY78050;
 XX
 XX 25-APR-2000 (first entry)
 DT
 XX Human lactoferrin derived peptide SEQ ID NO:50.
 DE
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 PN
 XX 13-JAN-2000.
 PD
 XX 06-JUL-1999; 99WO-SE01230.
 PF

XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food
 XX Claim 15; Page 75; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 14 AA;
 SQ Query Match 89.1%; Score 57; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00083;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQOQRNMRKVR 12
 DB ||| ||||| |||||
 3 CFQOQRNMRKVR 14
 RESULT 11
 AAY78051 ID AAY78051 standard; Peptide; 14 AA.
 XX AC AAY78051;
 XX DT 25-APR-2000 (first entry)
 XX DE Human lactoferrin derived peptide SEQ ID NO:51.
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX OS Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX PD 13-JAN-2000.
 XX PF 06-JUL-1999; 99WO-SE01230.
 XX PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food
 XX Claim 18; Page 75; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 14 AA;
 SQ Query Match 89.1%; Score 57; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00083;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQOQRNMRKVR 12
 DB ||| ||||| |||||
 3 CFQOQRNMRKVR 14
 RESULT 12
 AAR98554 ID AAR98554 standard; Peptide; 15 AA.
 XX AC AAR98554;
 XX DT 12-NOV-1996 (first entry)
 XX DE Peptide for anti-ulcer agent.
 XX KW anti-ulcer agent; low toxicity; stable; heat-resistant.
 XX OS Synthetic.
 XX PN JPC8143468-A.
 XX PD 04-JUN-1996.
 XX PF 17-NOV-1994; 94JP-0283869.
 XX PR 17-NOV-1994; 94JP-0283869.
 XX (MORG) MORINAGA MILK IND CO LTD.
 XX WPI; 1996-318857/32.
 XX Anti-ulcer agent contg. peptide - has low toxicity, is
 PT heat-resistant and water-soluble
 XX Claim 1; Page 11; 11pp; Japanese.
 XX AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
 CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be
 CC administered orally and be produced in large amounts.
 XX Sequence 15 AA;

Query Match 89.1%; Score 57; DB 17; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.00089;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12
 DB 2 CFQQRNRKVR 13

RESULT 13

AAV78035
 ID AAY78035 standard; Peptide; 15 AA.

XX AAY78035;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:35.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.

XX Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SB01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 69; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 15 AA;

Query Match 89.1%; Score 57; DB 21; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.00089;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12
 DB 4 CFQQRNRKVR 15

RESULT 14

AAV78062
 ID AAY78062 standard; Peptide; 15 AA.

XX AAY78062;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:62.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.

XX Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SB01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 81; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 15 AA;

Query Match 89.1%; Score 57; DB 21; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.00089;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12
 DB 4 CFQQRNRKVR 15

RESULT 15

AAV78063
 ID AAY78063 standard; Peptide; 15 AA.

XX AAY78063;

Tue Dec 9 06:51:27 2003

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XX 25-APR-2000 (first entry)
DT
XX
XX DE Human lactoferrin derived peptide SEQ ID NO:63.
XX
XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
PN
XX
XX 13-JAN-2000.
PD
XX
XX 06-JUL-1999; 99WO-SE01230.
PF
XX
XX 06-JUL-1998; 98SE-0002441.
PR
XX 17-JUL-1998; 98SE-0002562.
PR
XX 29-DEC-1998; 98SE-0004614.
PR
XX
XX (ASCI-) A+ SCI INVEST AB.
PA
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
PI
XX
XX WPI; 2000-147388/13.
DR
XX
XX New peptides used for treatment and prevention of infections,
PT inflammation and tumors and for use in infant formula food -
XX
XX Claim 18; Page 81; 102pp; English.
PS
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX SQ Sequence 15 AA;

Query Match 89.1%; Score 57; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.00089;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQAQRNRKVR 12
DB 4 CFQWRNRKVR 15

Search completed: February 21, 2003, 07:37:11
Job time : 28.35 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 Seconds
(without alignments)
40.818 Million cell updates/sec

Title: US-09-743-107B-71
Perfect score: 64
Sequence: 1 CFQQRNMEKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	89.1	18	1	US-08-204-487-3
2	57	89.1	18	2	US-08-485-948-8
3	57	89.1	18	2	US-08-628-380-8
4	57	89.1	18	2	US-08-475-055-8
5	57	89.1	20	1	US-07-755-161A-3
6	57	89.1	20	1	US-07-891-174-3
7	57	89.1	20	1	US-08-204-487-1
8	57	89.1	20	1	US-08-256-771-24
9	57	89.1	20	1	US-08-256-771-25
10	57	89.1	20	1	US-08-381-984-24
11	57	89.1	20	1	US-08-381-984-25
12	57	89.1	22	4	US-09-508-734-4
13	57	89.1	24	4	US-09-508-734-6
14	57	89.1	25	1	US-07-755-161A-10
15	57	89.1	25	1	US-07-891-174-10
16	57	89.1	25	1	US-08-204-487-7
17	57	89.1	29	4	US-09-508-734-8
18	57	89.1	36	1	US-07-755-161A-8
19	57	89.1	36	1	US-07-891-174-8
20	57	89.1	36	1	US-08-256-771-30
21	57	89.1	36	1	US-08-381-984-29
22	57	89.1	47	2	US-08-464-182A-6
23	57	89.1	47	2	US-08-406-271-6
24	57	89.1	50	2	US-08-693-274A-7
25	57	89.1	52	4	US-09-017-043A-3
26	57	89.1	53	2	US-08-464-182A-5
27	57	89.1	53	2	US-08-406-271-5

28	57	89.1	54	2	US-08-464-182A-2	Sequence 2, Appli
29	57	89.1	54	2	US-08-406-271-2	Sequence 2, Appli
30	57	89.1	694	3	US-08-724-586-2	Sequence 2, Appli
31	57	89.1	694	4	US-09-421-632-2	Sequence 2, Appli
32	57	89.1	694	4	US-09-332-190-2	Sequence 2, Appli
33	57	89.1	705	2	US-08-655-640-2	Sequence 2, Appli
34	57	89.1	708	2	US-08-655-640-4	Sequence 4, Appli
35	57	89.1	711	1	US-08-154-019-4	Sequence 4, Appli
36	57	89.1	711	1	US-08-461-333-4	Sequence 4, Appli
37	57	89.1	711	3	US-08-464-167-4	Sequence 4, Appli
38	57	89.1	711	3	US-09-158-313-4	Sequence 4, Appli
39	57	89.1	711	4	US-08-476-798-4	Sequence 4, Appli
40	54	84.4	711	1	US-08-145-681-2	Sequence 2, Appli
41	54	84.4	711	1	US-08-250-308-2	Sequence 2, Appli
42	54	84.4	711	1	US-08-453-703-2	Sequence 2, Appli
43	54	84.4	711	2	US-08-456-106-2	Sequence 2, Appli
44	54	84.4	711	3	US-08-456-108-2	Sequence 2, Appli
45	54	84.4	711	4	US-09-265-577-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN-ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIYAKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESS: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: R0N-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1-18
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"


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; OTHER INFORMATION: (20-37)"
US-08-204-487-3

Query Match      89.1%; Score 57; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.00019;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12
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Db 1 CFQQRNRKVR 12

RESULT 2
US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,948
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,217
; FILING DATE: JUNE 7, 1995
; APPLICATION NUMBER: 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-CL, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
;
US-08-485-948-8
Query Match      89.1%; Score 57; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.00019;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12
   |||||
Db 1 CFQQRNRKVR 12

RESULT 3
US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341
; GENERAL INFORMATION:
; APPLICANT: LI, YONG MING
; APPLICANT: VLASSARA, HELEN
; APPLICANT: CERAMI, ANTHONY
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,380
; FILING DATE: April 4, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-CL, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
;
US-08-628-380-8
Query Match      89.1%; Score 57; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.00019;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12
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Db 1 CFQQRNRKVR 12

RESULT 4
US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; NUMBER OF SEQUENCES: 9
```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LP-C1, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8

Query Match 89.1%; Score 57; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.00019;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQQRNMRKV 12
   ||| |||||
Db 1 CFQQRNMRKV 12

RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KB
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

Query Match 89.1%; Score 57; DB 1; Length 20;
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Best Local Similarity 91.7%; Pred. No. 0.00021;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQAOQNRKVR 12
DB 2 CFQAOQNRKVR 13

RESULT 6
US-07-891-174-3
; Sequence 3, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 89.1%; Score 57; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00021;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQAOQNRKVR 12
DB 2 CFQAOQNRKVR 13

RESULT 7
US-08-204-487-1
; Sequence 1, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIAKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FJN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
US-08-204-487-1

Query Match 89.1%; Score 57; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00021;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNMRKVR 12
||| |||||
Db 2 CFQQRNMRKVR 13

RESULT 8
US-08-256-771-24
Sequence 24, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"

US-08-256-771-24

Query Match 89.1%; Score 57; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00021;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNMRKVR 12
||| |||||
Db 2 CFQQRNMRKVR 13

RESULT 9
US-08-256-771-25
Sequence 25, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are protected to
OTHER INFORMATION: prevent disulfide bond"

Query Match 89.1%; Score 57; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00021;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNMRKVR 12
||| |||||
Db 2 CFQQRNMRKVR 13

RESULT 10
US-08-381-984-24

Sequence 24, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
US-08-381-984-24

Query Match 89.1%; Score 57; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00021;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQQRNRKVR 12
Db 2 CFQQRNRKVR 13

RESULT 11

US-08-381-984-25
Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
US-08-381-984-25

Query Match 89.1%; Score 57; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00021;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQQRNRKVR 12
Db 2 CFQQRNRKVR 13

RESULT 12

US-09-508-734-4
Sequence 4, Application US/09508734
Patent No. 6423509
GENERAL INFORMATION:
APPLICANT: Sanyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
FILE OF INVENTION: useful microorganism thereof
FILE REFERENCE: PA/SYG/00139
CURRENT FILING DATE: 2000-06-01
CURRENT APPLICATION NUMBER: US/09/508,734
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1998-07-13
PRIOR APPLICATION NUMBER: KR1998-29351
NUMBER OF SEQ ID NOS: 12
SOFTWARE: KopatentIn 1.71
SEQ ID NO 4

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; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4

Query Match      89.1%; Score 57; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 0.00023;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNNRKVR 12
   ||| |||||
Db 2 CFQWRNNRKVR 13

RESULT 13
US-09-508-734-6
; Sequence 6, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SVG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-6

Query Match      89.1%; Score 57; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 0.00025;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNNRKVR 12
   ||| |||||
Db 3 CFQWRNNRKVR 14

RESULT 14
US-07-755-161A-10
; Sequence 10, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755,161A
; FILING DATE: 19910905
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHEetical:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10

Query Match      89.1%; Score 57; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNNRKVR 12
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Db 4 CFQWRNNRKVR 15
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RESULT 15
US-07-891-174-10
Sequence 10, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,567
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
LOCATION: 21

IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
Query Match 89.1%; Score 57; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQAGRNRKVR 12
||| |||||
DB 4 CFQAGRNRKVR 15
Search completed: February 21, 2003, 07:50:33
Job time : 8.7 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds
(without alignments)

35.508 Million cell updates/sec

Title: US-09-743-107B-71
Perfect score: 64
Sequence: 1 CFQQRNMKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pap.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pap.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pap.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pap.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW PUB.pap.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pap.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW PUB.pap.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	89.1	15	9	US-09-798-869-2
2	57	89.1	25	9	US-09-798-869-20
3	57	89.1	694	9	US-10-023-096-2
4	49	76.6	15	9	US-09-798-869-6
5	40	62.5	15	9	US-09-798-869-3
6	40	62.5	25	9	US-09-798-869-23
7	37	57.8	97	9	US-09-738-626-5597
8	35	54.7	184	10	US-09-925-301-1248
9	34	53.1	596	9	US-10-093-766-29
10	34	53.1	700	9	US-10-013-310-5
11	34	53.1	882	9	US-10-174-590-574
12	34	53.1	882	9	US-10-176-758-574
13	34	53.1	882	9	US-10-173-737-574
14	34	53.1	882	9	US-10-173-706-574
15	34	53.1	882	9	US-10-175-738-574
16	34	53.1	882	9	US-10-175-752-574
17	34	53.1	882	9	US-10-176-482-574
18	34	53.1	882	9	US-10-176-757-574
19	34	53.1	882	9	US-10-176-913-574

20	34	53.1	882	9	US-10-180-552-574	Sequence 574, App
21	34	53.1	882	9	US-10-180-557-574	Sequence 574, App
22	34	53.1	882	9	US-10-173-700-574	Sequence 574, App
23	34	53.1	882	9	US-10-174-572-574	Sequence 574, App
24	34	53.1	882	9	US-10-174-579-574	Sequence 574, App
25	34	53.1	882	9	US-10-174-582-574	Sequence 574, App
26	34	53.1	882	9	US-10-174-588-574	Sequence 574, App
27	34	53.1	882	9	US-10-175-739-574	Sequence 574, App
28	34	53.1	882	9	US-10-175-740-574	Sequence 574, App
29	34	53.1	882	9	US-10-175-743-574	Sequence 574, App
30	34	53.1	882	9	US-10-176-488-574	Sequence 574, App
31	34	53.1	882	9	US-10-176-492-574	Sequence 574, App
32	34	53.1	882	9	US-10-176-747-574	Sequence 574, App
33	34	53.1	882	9	US-10-176-750-574	Sequence 574, App
34	34	53.1	882	9	US-10-176-985-574	Sequence 574, App
35	34	53.1	882	9	US-10-176-987-574	Sequence 574, App
36	34	53.1	882	9	US-10-176-991-574	Sequence 574, App
37	34	53.1	882	9	US-10-176-992-574	Sequence 574, App
38	34	53.1	882	9	US-10-176-993-574	Sequence 574, App
39	34	53.1	882	9	US-10-184-658-574	Sequence 574, App
40	34	53.1	882	9	US-10-173-695-574	Sequence 574, App
41	34	53.1	882	9	US-10-173-697-574	Sequence 574, App
42	34	53.1	882	9	US-10-173-705-574	Sequence 574, App
43	34	53.1	882	9	US-10-174-576-574	Sequence 574, App
44	34	53.1	882	9	US-10-174-585-574	Sequence 574, App
45	34	53.1	882	9	US-10-174-586-574	Sequence 574, App

ALIGNMENTS

RESULT 1
US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2

Query Match 89.1%; Score 57; DB 9; Length 15;
Best Local Similarity 91.7%; Pred. No. 4.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNMKVR 12
DB 3 CFQQRNMKVR 14

RESULT 2
US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON

APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match 89.1%; Score 57; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 7.4e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQAOQNRKVR 12
||| |||||
DB 3 CFQAOQNRKVR 14

RESULT 3

US-10-023-096-2
Sequence 2, Application US/10023096
Patent No. US20020160941A1
GENERAL INFORMATION:
APPLICANT: Kruzel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P59185C
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-023-096-2

Query Match 89.1%; Score 57; DB 9; Length 694;
Best Local Similarity 91.7%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQAOQNRKVR 12
||| |||||
DB 22 CFQAOQNRKVR 33

RESULT 4

US-09-798-869-6
Sequence 6, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
OTHER INFORMATION: sequence)
US-09-798-869-6

Query Match 76.6%; Score 49; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.0015;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQAOQNRKVR 12
||| |||||
DB 3 CFQAOQNRKVR 14

RESULT 5

US-09-798-869-3
Sequence 3, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15
TYPE: PRT
ORGANISM: CAPRINE
US-09-798-869-3

Query Match 62.5%; Score 40; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.084;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQAOQNRK 11
|:|:|:|:|:|:
Db 3 CYQWQRMRKL 13

RESULT 6

US-09-798-869-23
; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (VSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJARNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23

Query Match 62.5%; Score 40; DB 9; Length 25;
Best Local Similarity 63.6%; Pred. No. 0.15;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQAOQNRK 11
|:|:|:|:|:|:
Db 3 CYQWQRMRKL 13

RESULT 7

US-09-738-626-5597
; Sequence 5597, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SETKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5597
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5597

Query Match 57.8%; Score 37; DB 9; Length 97;
Best Local Similarity 70.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQAOQNRK 10
|:|:|:|:|:|:
Db 73 CFLVQRNRK 82

RESULT 8

US-09-925-301-1248
; Sequence 1248, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN ET AL.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1248
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1248

Query Match 54.7%; Score 35; DB 10; Length 184;
Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FOAQRNRKVR 12
|:|:|:|:|:|:
Db 61 FKXKRNPRKVR 71

RESULT 9

US-10-093-766-29
; Sequence 29, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: LASEX, AMY W.
; APPLICANT: JONES, DAVID A.
; APPLICANT: KARPI, ADAM R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: PA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093,766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
; SEQ ID NO 29
; LENGTH: 596
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030013099A1 476301CD1
US-10-093-766-29

Query Match 53.1%; Score 34; DB 9; Length 596;
Best Local Similarity 54.5%; Pred. No. 65;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQAOQNRK 11
|:|:|:|:|:|:
Db 336 CFMAEQNMVSV 346

RESULT 10

US-10-013-310-5
 ; Sequence 5, Application US/10013310
 ; Publication No. US20020192216A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lamb, Jonathon Robert
 ; APPLICANT: Hoyne, Gerard Francis
 ; APPLICANT: Dallman, Margaret Jane
 ; TITLE OF INVENTION: Therapeutic Use
 ; FILE REFERENCE: 674525-2003
 ; CURRENT APPLICATION NUMBER: US/10/013,310
 ; CURRENT FILING DATE: 2001-12-07
 ; PRIOR APPLICATION NUMBER: PCT/GB00/02191
 ; PRIOR FILING DATE: 2000-06-05
 ; PRIOR APPLICATION NUMBER: UK 9913350.6
 ; PRIOR FILING DATE: 1999-06-08
 ; PRIOR APPLICATION NUMBER: UK 9921953.7
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 700
 ; TYPE: PRT
 ; ORGANISM: House Mouse
 US-10-013-310-5

Query Match 53.1%; Score 34; DB 9; Length 700;
 Best Local Similarity 54.5%; Pred. No. 77;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAQARNRKV 11

Db 666 CEQVDRNRRV 676

RESULT 11

US-10-174-590-574
 ; Sequence 574, Application US/10174590
 ; Publication No. US20030008352A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C42
 ; CURRENT APPLICATION NUMBER: US/10/174,590
 ; CURRENT FILING DATE: 2002-06-18
 ; Prior application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 574
 ; LENGTH: 882
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-174-590-574

Query Match 53.1%; Score 34; DB 9; Length 882;
 Best Local Similarity 54.5%; Pred. No. 99;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAQARNRKV 11

Db 848 CEQVDRNRRV 858

RESULT 12

US-10-176-758-574
 ; Sequence 574, Application US/10176758
 ; Publication No. US20030008353A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C104
 ; CURRENT APPLICATION NUMBER: US/10/176,758
 ; CURRENT FILING DATE: 2002-06-21
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 574
 ; LENGTH: 882
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-176-758-574

Query Match 53.1%; Score 34; DB 9; Length 882;
 Best Local Similarity 54.5%; Pred. No. 99;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAQARNRKV 11

Db 848 CEQVDRNRRV 858

RESULT 13

US-10-175-737-574
 ; Sequence 574, Application US/10175737
 ; Publication No. US20030013153A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C50
 ; CURRENT APPLICATION NUMBER: US/10/175,737
 ; CURRENT FILING DATE: 2002-06-19
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 574
 ; LENGTH: 882
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-175-737-574

Query Match 53.1%; Score 34; DB 9; Length 882;
 Best Local Similarity 54.5%; Pred. No. 99;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAQARNRKV 11

Db 848 CEQVDRNRRV 858

Db 848 CEQVDRNIRRV 858

RESULT 14

US-10-173-706-574

; Sequence 574, Application US/10173706

; Publication No. US2003002293A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430RIC7

; CURRENT APPLICATION NUMBER: US/10/173,706

; CURRENT FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 574

; LENGTH: 882

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-173-706-574

Query Match

53.1%; Score 34; DB 9; Length 882;

Best Local Similarity 54.5%; Pred. No. 99;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFOAQRNMRKV 11

Db 848 CEQVDRNIRRV 858

RESULT 15

US-10-175-738-574

; Sequence 574, Application US/10175738

; Publication No. US2003002294A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430RIC45

; CURRENT APPLICATION NUMBER: US/10/175,738

; CURRENT FILING DATE: 2002-06-19

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 574

; LENGTH: 882

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-175-738-574

Query Match

53.1%; Score 34; DB 9; Length 882;

Best Local Similarity 54.5%; Pred. No. 99;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 seconds
(without alignments)
120.168 Million cell updates/sec

Title: US-09-743-107B-71

Perfect score: 64

Sequence: 1 CFQQRNKKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:**

1: Pirl:**

2: Pirl:**

3: Pirl:**

4: Pirl:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	89.1	711	1	TFHUL
2	40	62.5	47	2	T29370
3	40	62.5	708	2	JC2323
4	38	59.4	57	2	D81949
5	37	57.8	33	2	S52107
6	37	57.8	664	2	T28952
7	37	57.8	887	2	H96315
8	37	57.8	990	1	G46335
9	36	56.2	223	2	T37974
10	36	56.2	238	2	T40568
11	36	56.2	267	2	S77802
12	36	56.2	658	2	E69228
13	35	54.7	325	2	C96784
14	35	54.7	335	2	T33211
15	35	54.7	431	2	S50977
16	35	54.7	545	2	E97728
17	35	54.7	622	2	T86309
18	35	54.7	743	2	T00634
19	35	54.7	993	2	D96512
20	34	53.1	81	2	E95172
21	34	53.1	81	2	E98038
22	34	53.1	104	2	D95003
23	34	53.1	114	2	JQ0149
24	34	53.1	126	2	AB0119
25	34	53.1	151	2	G86760
26	34	53.1	225	2	A90260
27	34	53.1	510	2	S62545
28	34	53.1	527	2	C87375
29	34	53.1	887	2	A96516

30 34 53.1 994 2 T21356
31 34 53.1 1145 2 A59251
32 33 51.6 125 2 C71669
33 33 51.6 125 2 H97822
34 33 51.6 130 2 C72602
35 33 51.6 133 2 A97324
36 33 51.6 178 2 AB2743
37 33 51.6 185 2 S50094
38 33 51.6 227 2 I64016
39 33 51.6 249 2 A13401
40 33 51.6 351 2 S20078
41 33 51.6 375 2 C71286
42 33 51.6 433 2 T37605
43 33 51.6 516 2 T00974
44 33 51.6 624 2 T01585
45 33 51.6 862 2 T38996

ALIGNMENTS

RESULT 1

TFHUL

Lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 08-Dec-2000

C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74;

R:Cho, Y.

submitted to the EMBL Data Library, March 1994

A:Reference number: G06820

A:Accession: G01394

A>Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-711 <CHO>

A:CROSS-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237

R:REV, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A:Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A:Reference number: S11228; MUID:90384839; PMID:2402455

A:Accession: S11228

A:Molecule type: mRNA

A:Residues: 1-148, 'T', 150-422, 'C', 424-711 <REV>

A:CROSS-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R:Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A:Title: Differential molecular mechanism of the estrogen action that regulates lactoferrin

A:Reference number: A45401; MUID:93125571; PMID:1450183

A:Accession: A45401

A:Molecule type: DNA

A:Residues: 1-15 <TEN>

A:CROSS-references: GB:S52659; NID:G263311; PIDN:AAB24877.1; PID:G263312

A:Experimental source: placenta

A>Note: sequence extracted from NCBI backbone (NCBIP:122202)

R:Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A:Title: Nucleotide sequence of human lactoferrin cDNA.

A:Reference number: S10324; MUID:90326549; PMID:2374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <POM>

A:CROSS-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A:Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A:Reference number: S15853; MUID:91264786; PMID:2049066

A:Accession: S15853

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 20-31 <ST1>

A:Accession: S20841

A:Molecule type: protein

A:Residues: 20-28, 'X', 30-31 <ST2>

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 389-393, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
A;Reference number: S07160; MUID:88001031; PMID:3477300
A;Accession: S07160
A;Molecule type: mRNA
A;Residues: 436-487, 'A', 489-711 <RAD>
A;Cross-references: EMBL:M18642; NID:9186815; PIDN:AAA86665.1; PID:g386855
R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
A;Reference number: A61169; MUID:91235214; PMID:1674448
A;Accession: A61169
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 3-701, 'SWKPVN' <PAN>
R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, P.; Legerand, D.; Spik, G.; Eur. J. Biochem. 145, 659-666, 1984
A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with other
A;Reference number: A31000; MUID:85076667; PMID:6510420
A;Accession: A31000
A;Molecule type: protein
A;Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4
A;Note: this is the final paper in a series
R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
Eur. J. Biochem. 241, 303-308, 1996
A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity
A;Reference number: S74119; MUID:97054624; PMID:8898921
A;Accession: S74119
A;Molecule type: protein
A;Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>
A;Experimental source: neutrophil granulocytes
C;Genetics:
A;Gene: GDB:17F
A;Cross-references: GDB:119368; OMIM:150210
A;Map position: 3q21-3q23
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein; iron binding; milk
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-71/Product: lactotransferrin #status experimental <MAT>
F;21-356/Domain: transferrin repeat homology <TRH1>
F;360-699/Domain: transferrin repeat homology <TRH2>
F;29-65, 99-55, 135-218, 177-193, 190-201, 251-265, 503-637, 595-609/Disulfide bonds: #status e
F;157, 498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400, 378-391, 425-706, 447-665, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #stat

Query Match 89.1%; Score 57; DB 1; Length 711;
Best Local Similarity 91.7%; Pred. No. 0.0059;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQAQRNMRKV 12
||| |||||
DB 39 CFQWRNMRKV 50

RESULT 2
T29970
hypothetical protein ZK682.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29970
R;Du, Z.; Le, T.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid ZK682.
A;Reference number: Z20714
A;Accession: T29970
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-47 <DUZ>
A;Cross-references: EMBL:U41110; PIDN:AAA82417.1; CESP:ZK682.1
C;Genetics:
A;Gene: CESP:ZK682.1

Query Match 59.4%; Score 38; DB 2; Length 57;
Best Local Similarity 58.3%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQAQRNMRKV 12
||| |||||
DB 21 CFPSRREMGKVR 32

RESULT 5
S52107
lactoferrin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107

A;Introns: 33/2
Query Match 62.5%; Score 40; DB 2; Length 47;
Best Local Similarity 63.6%; Pred. No. 0.77;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQAQRNMRKV 11
||| |||||
DB 26 CNEARRNMRV 36

RESULT 3
JC2323
lactoferrin - goat
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: JC2323
R;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
A;Reference number: JC2323; MUID:94380047; PMID:8093048
A;Accession: JC2323
A;Molecule type: mRNA
A;Residues: 1-708 <LEP>
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
F;359-696/Domain: transferrin repeat homology <TRH2>
F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.5%; Score 40; DB 2; Length 708;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQAQRNMRKV 11
||| |||||
DB 38 CYQWRNMRKL 48

RESULT 4
D81949
hypothetical protein NMA1014 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: D81949
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jorgels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: D81949
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-57 <PAR>
A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84283.1; PID:g737971
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA1014

Query Match 59.4%; Score 38; DB 2; Length 57;
Best Local Similarity 58.3%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQAQRNMRKV 12
||| |||||
DB 21 CFPSRREMGKVR 32

RESULT 5
S52107
lactoferrin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107

```

A;Gene: FltN3.18
A;Map position: 1

Query Match          57.8%; Score 37; DB 2; Length 887;
Best Local Similarity 58.3%; Pred. NO. 53;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQAQRNMRKVR 12
    |||:|:|:|:|
Db 659 CQIERNRNV 670

RESULT 8
G46335
env polyprotein precursor - Maedi/Visna virus (strain SA-OMVW)
N;Alternate names: coat polyprotein
N;Contains: exterior membrane glycoprotein; transmembrane glycoprotein
C;Species: Maedi/Visna virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C;Accession: G46335
R;Querat, G.; Audoly, G.; Sonigo, P.; Vigne, R.
Virology 175; 434-447, 1990
A;Title: Nucleotide sequence analysis of SA-OMVW, a visna-related ovine lentivirus: phyl-
A;Reference number: A46335; MUID:90223989; PMID:2158181
A;Accession: G46335
A;Molecule type: DNA
A;Residues: 1-990 <QUE>
A;Cross-references: GB:M31646; NID:g808756; PIDN:AAA66817.1; PID:g332551
C;Genetics:

C;Superfamily: visna lentivirus type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
F;1-101/Domain: signal sequence #status predicted <SIG>
F;102-662/Product: exterior membrane glycoprotein #status predicted <EXT>
F;663-990/Product: transmembrane glycoprotein #status predicted <TM>
F;663-689/Region: hydrophobic
F;842-863/Domain: transmembrane #status predicted <TMN>
F;141,162,207,259,299,363,386,402,413,434,438,469,474,480,490,500,514,526,536,542,550,56

Query Match          57.8%; Score 37; DB 1; Length 990;
Best Local Similarity 50.0%; Pred. NO. 60;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQAQRNMRKVR 12
    |||:|:|:|:|
Db 862 CQAYRQVREIR 873

RESULT 9
T37974
Probable peroxisomal membrane protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accession: T37974
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z21759
A;Accession: T37974
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-223 <MUR>
A;Cross-references: EMBL:Z69909; PIDN:CAA93785.1; GSPDB:GN00066; SPDB:SPAC19G10.03c
A;Experimental source: strain 972h; cosmid c19G10
C;Genetics:

A;Gene: SPDB:SPAC19G10.03c
A;Map position: 1
A;Introns: 10/3; 170/2
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC582.09
C;Keywords: peroxisome

Query Match          56.2%; Score 36; DB 2; Length 223;
Best Local Similarity 33.3%; Pred. NO. 21;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 CFQOQRNRKVR 12
|:|:|:|:|:
Db 140 CYELQNSKKIK 151

RESULT 10

T40568
hypothetical protein SPBC582.09 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C:Accession: T40568
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Davis, P.; Churcher, C.M.
submitted to the EMBL Data Library, July 1999
A:Reference number: Z41937
A:Accession: T40568
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-238 <WOO>
A:Cross-references: EMBL:AL096788; PIDN:CAB46672.1; GSPDB:GN00067; SPDB:SPBC582.09
A:Experimental source: strain 972h; cosmid c582
C:Genetics:
A:Gene: SPBC:SPBC582.09
A:Map position: 2
A:Introns: 15/3; 25/3; 185/2
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC582.09

Query Match 56.2%; Score 36; DB 2; Length 238;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQOQRNRKVR 12
|:|:|:|:|:
Db 155 CYELQNSKKIK 166

RESULT 11

S77802
hypothetical protein MC003 - Mycoplasma capricolum (fragment)
C:Species: Mycoplasma capricolum
C>Date: 09-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-Dec-1999
C:Accession: S77802
R:Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.;
Mol. Microbiol. 16, 955-967, 1995
A:Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology
A:Reference number: S77739; MUID:96059641; PMID:7476192
A:Accession: S77802
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-267 <BOR>
A:Cross-references: EMBL:233006
A:Experimental source: ATCC 27343
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C:Genetics:
A:Genetic code: SGC3

Query Match 56.2%; Score 36; DB 2; Length 267;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQOQRNRKVR 12
|:|:|:|:|:
Db 158 CFGKKNRQWR 169

RESULT 12

E69228
ATP synthase, subunit I - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: E69228
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: E69228
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-658 <MTH>
A:Cross-references: GB:AE000869; GB:AE000666; NID:G2622042; PIDN:AAB85456.1; PID:G26220;
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH960
A:Start codon: GTG

Query Match 56.2%; Score 36; DB 2; Length 658;
Best Local Similarity 54.5%; Pred. No. 62;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 FOAQRNRKVR 12
|:|:|:|:|:
Db 647 FRAERNFKIR 657

RESULT 13

C96784
hypothetical protein F1B16.9 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C96784
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurus, J.S.; Maity, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C96784
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <STO>
A:Cross-references: GB:AE005173; NID:G10120446; PIDN:AAG13071.1; GSPDB:GN00141
C:Genetics:
A:Gene: F1B16.9
A:Map position: 1

Query Match 54.7%; Score 35; DB 2; Length 325;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 FOAQRNRK 10
|:|:|:|:|:
Db 315 FRAKRNLRK 323

RESULT 14

T33211
hypothetical protein K10C9.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 08-Dec-2000
C:Accession: T33211
R:Du, Z.; Maggi, L.
submitted to the EMBL Data Library, May 1998
A:Description: The sequence of C. elegans cosmid K10C9.
A:Reference number: Z21302
A:Accession: T33211
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-335 <DUZ>
A:Cross-references: EMBL:AF067944; PIDN:AAC17673.1; GSPDB:GN00023; CESP:K10C9.6

A;Experimental source: strain Bristol N2; clone K10C9

C;Genetics:

A;Gene: CESP.K10C9.6

A;Map position: 5

C;Introns: 163/2; 313/1

C;Superfamily: Caenorhabditis elegans hypothetical protein C45H4.12

Query Match 54.7%; Score 35; DB 2; Length 335;

Best Local Similarity 60.0%; Pred. No. 50;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPOAQRNRK 10

DB 217 CVQMRNRK 226

RESULT 15:

S50977

Hypothetical protein YDL005c - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein D2930; hypothetical protein YD8119.02c

C;Species: Saccharomyces cerevisiae

C;Date: 11-Feb-1995 #sequence revision 12-May-1995 #text_change 19-Apr-2002

C;Accession: S50977; S52514; S67537

R;Murphy, L.; Richards, C.; Gentles, S.; Harris, D.

submitted to the EMBL Data Library, January 1995

A;Reference number: S50976

A;Accession: S50977

A;Molecule type: DNA

A;Residues: 1-431 <MUR>

A;Cross-references: EMBL:Z48008; NID:G642799; PIDN:CAA98056.1; PID:G642801

R;Andrie, B.; Visers, S.; Urrestarazu, L.

submitted to the EMBL Data Library, February 1995

A;Description: The sequence of a 42 kb segment located on the left arm of chromosome IV

A;Reference number: S52492

A;Accession: S52514

A;Molecule type: DNA

A;Residues: 1-431 <AND>

A;Cross-references: EMBL:Z48432; NID:G683669; PIDN:CAA88354.1; PID:G683692

R;Urrestarazu, L.A.; Andre, B.; Visers, S.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S67535

A;Accession: S67537

A;Molecule type: DNA

A;Residues: 1-431 <URR>

A;Cross-references: EMBL:Z74053; NID:G1430962; PIDN:CAA98561.1; PID:E252970; PID:G143096

A;Experimental source: strain S288C

C;Genetics:

A;Gene: SGD:MED2

A;Cross-references: SGD:S0002163

A;Map position: 4L

Query Match

54.7%; Score 35; DB 2; Length 431;

Best Local Similarity 87.5%; Pred. No. 64;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 QRNRKVR 12

DB 122 QRNRKVR 129

Search completed: February 21, 2003, 07:47:41

Job time : 11.65 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds
(without alignments)
108.199 Million cell updates/sec

Title: US-09-743-107b-71

Perfect score: 64

Sequence: 1 CFOAQRNMRKV 12

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	57	89.1	711	1	TRFL_HUMAN	P02788 homo sapien
2	43	67.2	695	1	TRFL_HORSE	O77811 equus caball
3	40	62.5	708	1	TRFL_CAMD	Q97um0 camelus dro
4	40	62.5	708	1	TRFL_CAPHI	Q29477 capra hircu
5	37	57.8	990	1	ENV_OVVIS	P16899 ovine lenti
6	36	56.2	238	1	YBN9_SCHPO	Q10333 schizosacch
7	36	56.2	267	1	Y125_MYCCA	P53661 mycoplasma
8	36	56.2	658	1	VATI_METH	O27041 methanobact
9	35	54.7	545	1	RECN_RICCN	Q92J40 rickettsia
10	34	53.1	510	1	YAGF_SCHPO	Q09877 schizosacch
11	34	53.1	557	1	TKT2_HUMAN	P51854 homo sapien
12	33	51.6	125	1	RS13_RICCN	Q32978 rickettsia
13	33	51.6	125	1	RS13_RICPR	Q32c87 rickettsia
14	33	51.6	227	1	Y940_HAEIN	P44081 haemophilus
15	33	51.6	267	1	RS3A_DROME	P55830 drosophila
16	33	51.6	351	1	NOV_CHICK	P28686 gallus gall
17	33	51.6	564	1	ARAB_BACST	Q98468 bacillus et
18	33	51.6	573	1	URE1_LACFE	P26929 lactobacill
19	32	50.0	226	1	NUKM_NEUCR	O47950 neurospora
20	32	50.0	238	1	AGRA_STRAH	P13131 staphylococ
21	32	50.0	252	1	YGRH_ECOLI	Q46842 escherichia
22	32	50.0	272	1	UL24_HSVB1	P09314 equine herp
23	32	50.0	272	1	UL24_HSVB4	P24432 equine herp
24	32	50.0	272	1	UL24_HSVB8	P28937 equine herp
25	32	50.0	399	1	YGV7_SCHPO	O43021 schizosacch
26	32	50.0	618	1	DNAK_CYACA	Q97l11 cyanidium c
27	32	50.0	770	1	MAOI_RHIME	O30807 rhizobium m
28	32	50.0	795	1	DEGY_CABEL	O01635 caenorhabd
29	32	50.0	985	1	LOM1_MAIZE	P93647 zea mays (m
30	32	50.0	992	1	FRQ_LEPAU	Q01115 leptosphaer
31	32	50.0	1040	1	RAG1_MOUSE	P15919 mus musculu
32	32	50.0	1132	1	TRFT_HUMAN	Q14746 homo sapien
33	31	48.4	137	1	KDGL_STRMU	Q05888 streptococc

RESULT 1

ID	TRFL_HUMAN	STANDARD;	PRT:	711 AA.
AC	P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96KZ4;			
AC	Q96KZ5;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin A;			
DE	Lactoferrin B; Lactoferrin C].			
GN	LTF OR LTF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RX	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;			
RT	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RL	Nucleic Acids Res. 19:5288-5288(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cho Y.Y.;			
RL	Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Conneely O.M.;			
RL	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RT	"Molecular cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Rado T.A.;			
RT	"Human neutrophil lactoferrin coding and 5' flanking region DNA			
RL	sequences.";			
RN	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cheng H., Chen X., Huan L.;			
RT	"cDNA cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN	[8]			

ALIGNMENTS

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE=Mammary Gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ogden J.E.;
RT "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
[9]
RP SEQUENCE OF 20-711.
RX MEDLINE=95076667; PubMed=5510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
RG Legrand D., Spik G., Montreuil J., Jolles P.;
RT "Human lactotransferrin: amino acid sequence and structural
RL comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1984).
[10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RJ Jolles P.;
RT "The present state of the human lactotransferrin sequence. Study and
RL alignment of the cyanogen bromide fragments and characterization of
RT N- and C-terminal domains.";
RL Biochim. Biophys. Acta 670:243-254(1981).
[11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J.,
RJ Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
RL lactotransferrin.";
RL FEBS Lett. 142:107-110(1982).
[12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
[13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Dragan Y., Giacalone J., Fae A., Powell E., Solinsky K.A., Desilva U.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sagripanti J.I.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
[14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2589506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
[15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human diferric lactoferrin refined at 2.2-A
RT resolution.";
RL Acta Crystallogr. D 51:629-646(1995).
[16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97158796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
RA Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RT 253--methionine mutant.";
RL Biochemistry 36:341-346(1997).
[17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in Aspergillus
RT awamori.";
RL Acta Crystallogr. D 55:403-407(1999).
[18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
RT and analysis of ligand-induced conformational change.";
RL Acta Crystallogr. D 54:1319-1335(1998).
[19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of opioid antagonist peptides derived
RT from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810(1990).
[20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
RA Sugar J., Kumarananickavel G., Munier F., Schorderet D.F.,
RA El Matiri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
RA Hejtmancik J.P., Teng C.T.;
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RL Mol. Vision 4:31-32(1998).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; X53961; CAA37914.1; -
CC EMBL; U07643; AAB60324.1; -
CC EMBL; M93150; AAA36159.1; -
CC EMBL; M83202; AAA59511.1; -
CC EMBL; M83205; AAA58656.1; -
CC EMBL; M18642; AAA86655.1; -
CC EMBL; AF332168; AAG48753.1; -
CC EMBL; BC015822; AAH15822.1; -
CC EMBL; BC015823; AAH15823.1; -
CC EMBL; M73700; AAA59479.1; -
CC EMBL; X52941; CAA37116.1; -
CC EMBL; U95626; AAB57795.1; -
CC PIR; S11228; TFHUL.
CC PDB; 1LFC; 31-AUG-94.
CC PDB; 1LCT; 31-OCT-93.
CC PDB; 1LEF; 31-JUL-94.
CC PDB; 1LEH; 31-OCT-93.
CC PDB; 1LFI; 31-OCT-93.
CC PDB; 1LGB; 31-AUG-94.
CC PDB; 1LGC; 31-AUG-94.
CC PDB; 1BKA; 08-NOV-96.
CC PDB; 1DSN; 08-MAR-96.
CC PDB; 1HSE; 12-MAR-97.
CC PDB; 1VPD; 21-APR-97.

Query Match 89.1%; Score 57; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.0011;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNMKVR 12
 ||| |||||
 DB 39 CFQQRNMKVR 50

RESULT 2

TRFL_HORSE STANDARD; PRT; 695 AA.
 AC O77811;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin) (Fragment).
 GN LTF.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "cDNA sequence of mare lactoferrin";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]

RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RC TISSUE=Milk;
 RC MEDLINE=92296633; PubMed=10366507;
 RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "Three-dimensional structure of mare diferric lactoferrin at 2.6-A resolution.";
 RL J. Mol. Biol. 289:303-317(1999).

CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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 CC -----

DR EMBL; AJ010930; CAA09407.1; -.
 DR FDB; 1B1X; 02-DEC-98.
 DR PDB; 1B7U; 02-FEB-99.
 DR PDB; 1B7Z; 02-FEB-99.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN 1; 2.
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.
 DR PROSITE; PS00207; TRANSFERRIN 3; 1.
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal; 3D-structure.
 FT NON_TER 1
 FT SIGNAL <1 6
 FT CHAIN 7 695 LACTOTRANSFERRIN.
 FT REPEAT 7 350 1.
 FT REPEAT 351 695 2.
 FT DISULFID 15 51
 FT DISULFID 25 42
 FT DISULFID 121 204

FT DISULFID 163 179
 FT DISULFID 166 189
 FT DISULFID 176 187
 FT DISULFID 237 251
 FT DISULFID 254 286
 FT DISULFID 364 377
 FT DISULFID 411 690
 FT DISULFID 431 653
 FT DISULFID 463 538
 FT DISULFID 487 681
 FT DISULFID 497 511
 FT DISULFID 508 521
 FT DISULFID 579 593
 FT DISULFID 631 636
 FT METAL 66 66
 FT METAL 98 98
 FT METAL 198 198
 FT METAL 259 259
 FT METAL 401 401
 FT METAL 439 439
 FT METAL 532 532
 FT METAL 601 601
 FT BINDING 127 127
 FT BINDING 469 469
 FT CARBOHYD 143 143
 FT CARBOHYD 287 287
 FT CARBOHYD 482 482
 SQ SEQUENCE 695 AA; 75991 MW; 07BB84D50E1B165D CRC64;

Query Match 67.2%; Score 43; DB 1; Length 695;
 Best Local Similarity 66.7%; Pred. No. 0.7;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQQRNMKVR 12
 | : |||: |||
 DB 25 CAFQQRNMKVR 36

RESULT 3

TRFL_CAMDR STANDARD; PRT; 708 AA.
 AC Q9TUM0; Q9MZS5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;
 RA Kappeler S.R., Ackermann M., Farah Z., Fuhan Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
 RL Int. Dairy J. 9:481-486(1999).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M., Srinivasan A., Singh R., Sehani M.S., Singh T.P.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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CC EMBL; AJ131674; CAB53387.1; -.
CC EMBL; AF165879; AAF82241.1; -.
CC HSSP; O77811; 1B1X.
CC InterPro; IPR001156; Transferrin.
CC Pfam; PF00405; transferrin; 2.
CC PRINTS; PR00422; TRANSFERRIN.
CC SMART; SM00094; TR_FER; 2.
CC PROSITE; PS00205; TRANSFERRIN_1; 2.
CC PROSITE; PS00206; TRANSFERRIN_2; 2.
CC PROSITE; PS00207; TRANSFERRIN_3; 2.
CC Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal.
FT SIGNAL. 1 19 BY SIMILARITY.
FT CHAIN 20 708 LACTOTRANSFERRIN.
FT REPEAT 20 363 1.
FT REPEAT 364 708 2.
FT DISULFID 28 64 BY SIMILARITY.
FT DISULFID 38 55 BY SIMILARITY.
FT DISULFID 134 217 BY SIMILARITY.
FT DISULFID 176 192 BY SIMILARITY.
FT DISULFID 189 200 BY SIMILARITY.
FT DISULFID 250 264 BY SIMILARITY.
FT DISULFID 367 399 BY SIMILARITY.
FT DISULFID 377 390 BY SIMILARITY.
FT DISULFID 424 703 BY SIMILARITY.
FT DISULFID 444 666 BY SIMILARITY.
FT DISULFID 476 551 BY SIMILARITY.
FT DISULFID 500 694 BY SIMILARITY.
FT DISULFID 510 524 BY SIMILARITY.
FT DISULFID 521 534 BY SIMILARITY.
FT DISULFID 592 606 BY SIMILARITY.
FT DISULFID 644 649 BY SIMILARITY.
FT METAL 79 79 IRON 1 (BY SIMILARITY).
FT METAL 111 111 IRON 1 (BY SIMILARITY).
FT METAL 211 211 IRON 1 (BY SIMILARITY).
FT METAL 272 272 IRON 1 (BY SIMILARITY).
FT METAL 414 414 IRON 2 (BY SIMILARITY).
FT METAL 452 452 IRON 2 (BY SIMILARITY).
FT METAL 545 545 IRON 2 (BY SIMILARITY).
FT METAL 614 614 IRON 2 (BY SIMILARITY).
FT METAL 140 140 ANION (BY SIMILARITY).
FT BINDING 482 482 ANION (BY SIMILARITY).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 594 594 F -> S (IN REF. 2).
FT CONFLICT 261 261 G -> A (IN REF. 2).
FT CONFLICT 304 304 S -> P (IN REF. 2).
FT CONFLICT 330 330 LLS -> PLF (IN REF. 2).
FT CONFLICT 492 494 L -> P (IN REF. 2).
FT CONFLICT 506 506 A -> P (IN REF. 2).
FT CONFLICT 609 609 R -> Q (IN REF. 2).
FT CONFLICT 642 642
SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match 62.5%; Score 40; DB 1; Length 708;
Best Local Similarity 66.7%; Pred. No. 2.8;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQQRNRKVR 12
Db 38 CAQWRMRKVR 49

RESULT 4
TRFL_CAPHI STANDARD; PRT; 708 AA.
AC Q29477; Q29479;

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DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (lactoferrin).
GN LTF.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Lee T., Yu S., Kim S., Lee K., Yu D.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=94380047; PubMed=8093048;
RA le Provost F., Nocard M., Guerin G., Martin P.;
RT "Characterization of the goat lactoferrin cDNA. Assignment of the
RT relevant locus to bovine U2 synteny group.";
RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC
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CC EMBL; U53957; AAA97958.1; -.
CC EMBL; X78902; CAA55517.1; -.
CC HSSP; O77698; 1CE2.
CC InterPro; IPR001156; Transferrin.
CC Pfam; PF00405; transferrin; 2.
CC PRINTS; PR00422; TRANSFERRIN.
CC SMART; SM00094; TR_FER; 2.
CC PROSITE; PS00205; TRANSFERRIN_1; 2.
CC PROSITE; PS00206; TRANSFERRIN_2; 2.
CC PROSITE; PS00207; TRANSFERRIN_3; 2.
CC Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal.
FT SIGNAL. 1 19 BY SIMILARITY.
FT CHAIN 20 708 LACTOTRANSFERRIN.
FT REPEAT 20 363 1.
FT REPEAT 364 708 2.
FT DISULFID 28 64 BY SIMILARITY.
FT DISULFID 38 55 BY SIMILARITY.
FT DISULFID 134 217 BY SIMILARITY.
FT DISULFID 176 192 BY SIMILARITY.
FT DISULFID 189 200 BY SIMILARITY.
FT DISULFID 250 264 BY SIMILARITY.
FT DISULFID 367 399 BY SIMILARITY.
FT DISULFID 377 390 BY SIMILARITY.
FT DISULFID 424 703 BY SIMILARITY.
FT DISULFID 444 666 BY SIMILARITY.
FT DISULFID 476 551 BY SIMILARITY.
FT DISULFID 500 694 BY SIMILARITY.
FT DISULFID 510 524 BY SIMILARITY.
FT DISULFID 521 534 BY SIMILARITY.
FT DISULFID 592 606 BY SIMILARITY.
FT DISULFID 644 649 BY SIMILARITY.
FT METAL 79 79 IRON 1 (BY SIMILARITY).
FT METAL 111 111 IRON 1 (BY SIMILARITY).

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FT METAL 211 211 IRON 1 (BY SIMILARITY).
 FT METAL 272 272 IRON 2 (BY SIMILARITY).
 FT METAL 414 414 IRON 2 (BY SIMILARITY).
 FT METAL 452 452 IRON 2 (BY SIMILARITY).
 FT METAL 545 545 IRON 2 (BY SIMILARITY).
 FT METAL 614 614 IRON 2 (BY SIMILARITY).
 FT BINDING 140 140 ANION (BY SIMILARITY).
 FT BINDING 482 482 ANION (BY SIMILARITY).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .)
 FT CONFLICT 56 56 I -> V (IN REF. 2).
 FT CONFLICT 88 88 L -> R (IN REF. 2).
 FT CONFLICT 124 124 Q -> K (IN REF. 2).
 FT CONFLICT 154 154 F -> P (IN REF. 2).
 FT CONFLICT 304 304 S -> R (IN REF. 2).
 FT CONFLICT 414 414 D -> G (IN REF. 2).
 SQ SEQUENCE 708 AA; 77358 MW; F2EDA3C83539960D CRC64;

Query Match 62.5%; Score 40; DB 1; Length 708;
 Best Local Similarity 63.6%; Pred. No. 2.8;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQQRNRKV 11
 Db 38 CYQWRMRKL 48

RESULT 5

ENV_OMVVS STANDARD; PRT; 990 AA.
 AC P16899;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE ENV polypeptide precursor (Coat polypeptide).
 GN ENV.
 OS Ovine lentivirus (strain SA-OMV).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90223989; PubMed=2158181;
 RA Querat G., Audoly G., Sonigo P., Vigne R.;
 RT "Nucleotide sequence analysis of SA-OMV, a visna-related ovine
 lentivirus: phylogenetic history of lentiviruses.";
 RL Virology 175:434-447(1990).
 CC -----
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 CC -----
 DR EMBL; M34193; AAA6783.1; -;
 DR EMBL; M31646; AAA66817.1; -;
 DR PIR; G46335; G46335.
 DR HIV; M34193; ENV5OMVSACG.
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KW Glycoprotein; Coat protein; Polyprotein; Transmembrane.
 FT PEPTIDE 1 101
 FT CHAIN 102 662
 FT TRANSMEM 842 863
 FT CHAIN 663 990
 FT TRANSMEM 842 863
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .)

FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 469 469 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 474 474 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 480 480 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 490 490 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 500 500 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 526 526 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 536 536 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 550 550 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 560 560 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 567 567 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 703 703 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 771 771 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 778 778 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 794 794 N-LINKED (GLCNAC. . .)
 SQ SEQUENCE 990 AA; 114498 MW; 279B816BE55614F3 CRC64;

Query Match 57.8%; Score 37; DB 1; Length 990;
 Best Local Similarity 50.0%; Pred. No. 16;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQQRNRKV 12
 Db 862 CLQAYRQVREIR 873

RESULT 6

YBM9 SCHPO STANDARD; PRT; 238 AA.
 AC Q10333;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein C582.09 in chromosome II.
 GN SPBC582.09.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

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RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutini L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
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CC -----
DR EMBL; AL096788; CAB46672.1; -
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26479 MW; 58095AA8CD708180 CRC64;

Query Match 56.2%; Score 36; DB 1; Length 238;
Best Local Similarity 33.3%; Pred. No. 5.7;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAOQNMKVR 12
   |||:|:|:|
DB 155 CVELQNSKKIK 166

RESULT 7
Y125_MYCCA STANDARD; PRT; 267 AA.
ID Y125_MYCCA
AC F53661;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mycoplasma capricolum.
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Entomoplasmataceae.
OX NCBI_TaxID=2095;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27343 / KID;
RX MEDLINE=96059641; PubMed=7476192;
RA Bork P., Ouzounis C., Casari G., Schneider R., Sander C.,
RA Dolan M., Gilbert W., Gillevet P.M.;
RA "Exploring the Mycoplasma capricolum genome: a minimal cell reveals
RA its physiology.";
RT Mol. Microbiol. 16:985-987(1995).
CC -1- SIMILARITY: BELONGS TO THE COF/YEHA/YIDA/YIGL (E.COLI) / YCSE/YXEH
CC (B.SUBTILIS) FAMILY.
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CC -----
DR EMBL; Z33006; CAAB3689.1; -
DR InterPro; IPR001454; HlgHase/hydrilase.
DR InterPro; IPR000150; HypoHase_hf.
DR Pfam; PF00702; Hydrolase_1.
DR PROSITE; PS01228; COF_1; 1.
DR PROSITE; PS01229; COF_2; 1.
KW Hypothetical protein.
FT NON_TER 267
SQ SEQUENCE 267 AA; 30425 MW; D5912DD5B39A8451 CRC64;

Query Match 56.2%; Score 36; DB 1; Length 267;
Best Local Similarity 50.8%; Pred. No. 6.4;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CFAOQNMKVR 12
   |||:|:|:|
DB 158 CPGKKNRQMR 169

RESULT 8
VATI_METH STANDARD; PRT; 658 AA.
ID VATI_METH
AC Q27041;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE V-type ATP synthase subunit I (EC 3.6.3.14) (V-type ATPase subunit I).
GN ATP1 OR MTH960.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwanji N., Caruso A., Bush D., Sauer H., Fatwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
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CC -----
DR EMBL; AE000869; AAB85456.1; -
DR InterPro; IPR002490; V_ATPase_sub116.
DR Pfam; PF01496; V_ATPase_sub_a; 1.
KW Hydrolase; Hydrogen ion transport; Transmembrane; Complete proteome.
SQ SEQUENCE 658 AA; 74475 MW; 98E48D62EB43BE81 CRC64;

Query Match 56.2%; Score 36; DB 1; Length 658;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 FOAQRNMRKVR 12
   |||:|:|:|
DB 647 FRAENFTKIR 657

RESULT 9
REC_N R1CNC STANDARD; PRT; 545 AA.
ID REC_N R1CNC
AC Q92J40;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA repair protein recN (Recombination protein N).
GN REC_N OR RC0229.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsia; Rickettsia.
```

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NCBI_TaxID=781;
[1]
SEQUENCE FROM N.A.
RA STRAIN=Valish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
CC -1- FUNCTION: MAY BE INVOLVED IN RECOMBINATIONAL REPAIR OF DAMAGED
CC DNA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE REC N FAMILY.
CC -----
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CC -----
DR EMBL; AE008590; AL02767.1; -.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR04604; RecN; 1.
DR TIGRFAMs; TIGR00634; recN; 1.
KW DNA repair; ATP-binding; Complete proteome.
FT NP BIND 29 36
FT ATP (POTENTIAL).
SQ SEQUENCE 545 AA; 61729 MW; 59E02AEC8628E283 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 545;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAQRNMRK 10
DB 160 CYQAWQNRK 169
|:|:|:|:|
|:|:|:|:|

RESULT 10
YAGF SCHPO STANDARD; PRT; 510 AA.
AC Q09877; O94555;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C12G12.15 in chromosome I.
GN SPAC12G12.15.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Scouras J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moutle S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Gymnopoulos B.,
RA Waltjens J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
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RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu B., Dreano S., Gloux S., Jelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hunt S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: SOME, TO YEAST YF048W.
CC -----
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CC -----
DR EMBL; Z66568; CA91510.2; -.
DR InterPro; IPR003734; DUF155.
DR Pfam; PF02582; DUF155; 1.
KW Hypothetical protein: Transmembrane.
FT TRANSMEM 238 258
FT POTENTIAL.
SQ SEQUENCE 510 AA; 58445 MW; 232C7729233861C CRC64;

Query Match 53.1%; Score 34; DB 1; Length 510;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQAQRNMRKV 11
DB 58 FORRENARKI 67
|:|:|:|:|
|:|:|:|:|

RESULT 11
TKT2_HUMAN STANDARD; PRT; 557 AA.
AC P51854;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transketolase-like 1 (EC 2.2.1.1) (Transketolase 2) (TK 2)
DE (Transketolase related protein).
GN TKT1 OR TKT2 OR TKR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Fetal brain;
RX MEDLINE=96435907; PubMed=8838793;
RA Coy J.P., Duebel S., Kioschis P., Thomas K., Micklem G., Delius H.,
RA Pouetka A.;
RT "Molecular cloning of tissue-specific transcripts of a transketolase-
RT related gene: implications for the evolution of new vertebrate
RT genes.";
RL Genomics 32:309-316(1996).
RN [2]
SEQUENCE OF 436-498 FROM N.A.
RA Hochgeschwender U.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
CC 3-phosphate = D-ribose 5-phosphate + D-xylulose 5-phosphate.
CC -1- COPACITOR: THIAMINE PYROPHOSPHATE (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS ARE DERIVED BY
CC ALTERNATIVE SPLICING; THE HEART-SPECIFIC FORM LACKS THE N-
CC TERMINAL COMPARED TO THE BRAIN-SPECIFIC FORM WHICH IS SHOWN HERE.
CC -1- TISSUE SPECIFICITY: FETAL AND ADULT HEART, BRAIN, LUNG, LIVER,
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CC KIDNEY, ADULT PLACENTA, SKELETAL MUSCLE, PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.
CC -----
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CC -----
DR EMBL; X91817; CAA62925.1; -
DR EMBL; X91818; CAA62925.1; JOINED.
DR EMBL; U14622; AAA21557.1; -
DR Genew; HGNC:11835; TXLL1.
DR MIM; 300044; -
DR InterPro; IPR000360; Transketolase.
DR Pfam; PF00456; transketolase; 2.
DR Pfam; PF02779; transket_pyr; 1.
DR Pfam; PF02780; transketolase C; 1.
DR PROSITE; PS00801; TRANSKETOLASE 1; FALSE_NEG.
DR PROSITE; PS00802; TRANSKETOLASE 2; 1.
DR Transferase; Thiamine Pyrophosphate; Alternative splicing.
KW CONFLICT 480 480 I -> N (IN REF. 2).
FT CONFLICT 493 493 T -> S (IN REF. 2).
SQ SEQUENCE 557 AA; 61199 MW; 3F773DB8469447F7 CRC64;

Query Match 53.1%; Score 34; DB 1; Length 557;
Best Local Similarity 54.5%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQQRNMRKV 11
|||:|:|
Db 280 CFNAEQNWVS 290

RESULT 12
RS13_RICCN STANDARD; PRT; 125 AA.
AC Q92G8;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 308 ribosomal protein S13.
DS RSM OR RC0984.
GN Rickettsia conorii.
OS Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Sanson D., Roux V., Cossart P., Weissbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
CC -1- FUNCTION: INVOLVED IN THE BINDING OF FMET-TRNA AND, HENCE, IN THE
CC INITIATION OF TRANSLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL; A008651; AAL03522.1; -
DR InterPro; IPR001892; Ribosomal_S13.
DR Pfam; PF00416; Ribosomal_S13; 1.
DR PROSITE; PS00646; RIBOSOMAL_S13; 1.
DR PROSITE; PS00646; RIBOSOMAL_S13; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 125 AA; 14145 MW; 76923FD23E77B2F1 CRC64;

Query Match 51.6%; Score 33; DB 1; Length 125;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQQRNMRKV 11
|||:|:|
Db 86 CYQGLRHIRKL 96

RESULT 14
Y940_HAEIN STANDARD; PRT; 227 AA.
ID Y940_HAEIN
AC P44081;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
```

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DR ProDom; PD001363; Ribosomal_S13; 1.
DR PROSITE; PS00646; RIBOSOMAL_S13; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 125 AA; 14096 MW; 38C712DF3A51E95D CRC64;

Query Match 51.6%; Score 33; DB 1; Length 125;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQQRNMRKV 11
|||:|:|
Db 86 CYQGLRHIRKL 96

RESULT 13
RS13_RICPR STANDARD; PRT; 125 AA.
AC Q92GS;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 308 ribosomal protein S13.
DS RSM OR RP637.
GN Rickettsia prowazekii.
OS Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomrodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alismark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -1- FUNCTION: INVOLVED IN THE BINDING OF FMET-TRNA AND, HENCE, IN THE
CC INITIATION OF TRANSLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL; AJ235272; CAA15077.1; -
DR InterPro; IPR001892; Ribosomal_S13.
DR Pfam; PF00416; Ribosomal_S13; 1.
DR ProDom; PD001363; Ribosomal_S13; 1.
DR PROSITE; PS00646; RIBOSOMAL_S13; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 125 AA; 14145 MW; 76923FD23E77B2F1 CRC64;

Query Match 51.6%; Score 33; DB 1; Length 125;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQQRNMRKV 11
|||:|:|
Db 86 CYQGLRHIRKL 96

RESULT 14
Y940_HAEIN STANDARD; PRT; 227 AA.
ID Y940_HAEIN
AC P44081;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
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DE Hypothetical protein HI0940.
 GN HI0940.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Karlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Frichman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT RD.";
 RL Science 269:496-512(1995).
 CC -----
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 CC -----
 CC EMBL; U32775; AAC22604.1; -;
 DR IGR; HI0940; -;
 DR TRANSMEM 7 26 POTENTIAL.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT SEQUENCE 227 AA; 25484 MW; 576A870A3160A275 CRC64;
 SQ
 Query Match 51.6%; Score 33; DB 1; Length 227;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 FQAQNRK 10
 :|||:
 Db 34 FQAQNRK 42
 RESULT 15
 RS3A DROME
 ID RS3A DROME STANDARD; PRT; 267 AA.
 AC P5830; O4389; Q9V4A9;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 13-JUN-2002 (Rel. 41, Last annotation update)
 DE 40S ribosomal protein S3a (C3 protein).
 GN RP3A OR C3 OR M(4)101 OR CG2168.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
 RP SPECIFICITY.
 RC STRAIN=Oregon-R; TISSUE=Embryo;
 RX MEDLINE=96055152; PubMed=9393444;
 RA Reynaud E., Bolshakov V.N., Barajas V.N., Kafatos F.C., Zurita M.;
 RT "Antisense suppression of the putative ribosomal protein S3a gene
 RT disrupts ovarian development in Drosophila melanogaster.";
 RL Mol. Gen. Genet. 256:462-467(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
 RC TISSUE=Embryo;
 RX MEDLINE=98416207; PubMed=9742251;

van Beest M., Mortin M., Clevers H.;
 "Drosophila Rp3a, a novel minute gene situated between the segment
 polarity genes cubitus interruptus and dTCF.";
 Nucleic Acids Res. 26:4471-4475(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.C., Wortman J.R., Yeung M.D., Zhang Q., Chen L.Y.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 BAILEY R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Fowler C., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laso P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matti B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclik J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.C.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasman D.A., Weinstein G.M., Weissbach J., Yao Q.A.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: ESSENTIAL FOR Oogenesis; REQUIRED FOR LATE FOLLICLE CELL
 CC DEVELOPMENT. MAY BIND TO THE 40S RIBOSOMAL SUBUNIT.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED IN STAGE 8 EMBRYOS.
 CC DURING Oogenesis. EXPRESSION IS LOCATED BASALLY IN SOMATIC
 CC FOLLICULAR EPITHELIUM AND IN THE OOCYTE AT THE LATER STAGES.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY
 CC THROUGHOUT ALL DEVELOPMENT.
 CC -!- SIMILARITY: BELONGS TO THE S3AE FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 CC EMBL; Y10115; CAA71201.1; -;
 DR EMBL; AF034971; AAC62117.1; -;
 DR EMBL; AF034971; AAC62117.1; -;
 DR EMBL; AF034971; AAC62117.1; -;
 DR Flybase; FBgn0017545; Rps3A.
 DR InterPro; IPR001593; Ribosomal_S3AE.
 DR Pfam; PF01015; Ribosomal_S3AE; 1.
 DR ProDom; PD003035; Ribosomal_S3AE; 1.
 DR PROSITE; PS01191; RIBOSOMAL_S3AE; 1.
 KW Ribosomal protein.

FT INIT MET 0 0 BY SIMILARITY.
 FT CONFLICT 61 61 L -> F (IN REF. 1).
 FT CONFLICT 71 71 A -> VP (IN REF. 1).
 FT CONFLICT 81 81 R -> H (IN REF. 1).
 FT CONFLICT 139 180 QQ -> HE (IN REF. 1).
 FT CONFLICT 188 188 A -> SG (IN REF. 1).
 FT CONFLICT 252 260 VIDRPEGVE -> PKSTALKVK (IN REF. 1).
 FT CONFLICT 266 266 S -> A (IN REF. 3).
 SQ SEQUENCE 267 AA; 30225 NW; 3FF51141158455E7 CRC64;

Query Match 51.6%; Score 33; DB 1; Length 267;
 Best Local Similarity 41.7%; Pred. No. 26;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFOAQENMRKVR 12
 Db 156 CYAQSQVRKIR 167

Search completed: February 21, 2003, 07:27:44
 Job time : 6.6 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 seconds
(without alignments)

118.873 Million cell updates/sec

Title: US-09-743-107b-71

Perfect score: 64

Sequence: 1 CFAQNRKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHA:*

2: SP_BACTERIA:*

3: SP_FUNGI:*

4: SP_HUMAN:*

5: SP_INVERTEBRATE:*

6: SP_MAMMAL:*

7: SP_NBC:*

8: SP_ORGANELLE:*

9: SP_PHAGE:*

10: SP_PLANT:*

11: SP_RODENT:*

12: SP_VIRUS:*

13: SP_VERTEBRATE:*

14: SP_UNCLASSIFIED:*

15: SP_VIRUS:*

16: SP_BACTERIAP:*

17: SP_ARCHA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	81.2	711	4 Q8TCD2	Q8tcd2 homo sapien
2	48	75.0	38	4 Q9UCY5	Q9ucy5 homo sapien
3	40	62.5	47	5 Q23578	Q23578 caenorhabdi
4	39	60.9	729	12 Q91TW1	Q91tw1 tupaia herp
5	38	59.4	57	16 Q9JV34	Q9jv34 neisseria m
6	37	57.8	33	6 Q9TR80	Q9tr80 ovis aries
7	37	57.8	675	5 Q9GYM8	Q9gym8 caenorhabdi
8	37	57.8	887	10 Q9SX85	Q9sx85 arabidopsis
9	35	54.7	150	4 Q9BS42	Q9bs42 homo sapien
10	35	54.7	163	4 Q96HJ1	Q96hj1 homo sapien
11	35	54.7	163	4 Q96C76	Q96c76 homo sapien
12	35	54.7	163	4 Q96B04	Q96b04 homo sapien
13	35	54.7	163	4 Q9JHA3	Q9jha3 homo sapien
14	35	54.7	163	11 Q99L28	Q99l28 mus musculu
15	35	54.7	170	16 Q98M11	Q98m11 rhizobium 1
16	35	54.7	238	2 Q68L58	Q68l58 staphylococ

17	35	54.7	238	2 Q86862	Q86862 staphylococ
18	35	54.7	239	8 Q9TL13	Q9tl13 nephroselmi
19	35	54.7	253	5 Q9VZ06	Q9vz06 drosophila
20	35	54.7	274	11 Q9CQ47	Q9cq47 mus musculu
21	35	54.7	298	10 Q9AY53	Q9ay53 oryza sativ
22	35	54.7	315	5 Q9SSH7	Q9ssh7 drosophila
23	35	54.7	325	10 Q9FWS6	Q9fws6 arabidopsis
24	35	54.7	335	5 Q61888	Q61888 caenorhabdi
25	35	54.7	431	3 Q12124	Q12124 saccharomyc
26	35	54.7	461	2 Q9AK10	Q9ak10 rickettsia
27	35	54.7	536	5 Q8SUS1	Q8sus1 encephalito
28	35	54.7	622	10 Q9SH16	Q9sh16 arabidopsis
29	35	54.7	740	10 Q9S887	Q9s887 arabidopsis
30	35	54.7	993	10 Q9M9F3	Q9m9f3 arabidopsis
31	35	54.7	5147	4 Q9Y6V0	Q9y6v0 homo sapien
32	34	53.9	735	10 Q9LG17	Q9lg17 arabidopsis
33	34	53.1	81	16 Q97FW0	Q97fw0 streptococ
34	34	53.1	104	16 Q97TB1	Q97tb1 streptococ
35	34	53.1	121	10 Q9LTN4	Q9ltn4 arabidopsis
36	34	53.1	126	16 Q8ZHD0	Q8zhd0 yersinia pe
37	34	53.1	129	3 Q59956	Q59956 candida alb
38	34	53.1	130	4 Q9H7E7	Q9h7e7 homo sapien
39	34	53.1	151	16 Q9CGK9	Q9cgk9 lactococcus
40	34	53.1	225	17 Q97Z59	Q97z59 sulfobus
41	34	53.1	306	12 Q55587	Q55587 avian rotav
42	34	53.1	527	2 Q9AGK0	Q9agk0 caulobacter
43	34	53.1	527	2 Q9RQV0	Q9rqv0 caulobacter
44	34	53.1	527	16 Q9A9H2	Q9a9h2 caulobacter
45	34	53.1	536	4 Q9NVN3	Q9nvn3 homo sapien

ALIGNMENTS

RESULT 1

Q8TCD2 PRELIMINARY; PRT; 711 AA.

ID Q8TCD2; (TRENBLrel. 21, Created)

AC Q8TCD2; (TRENBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE Lactotransferrin.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=PROSTATE;

RA Strausberg R.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL, BC022347; AAH22347.1; -- 1B9CTEE097C45PAF CRC64;

SQ SEQUENCE 711 AA; 78327 MW; 1B9CTEE097C45PAF CRC64;

Query Match 81.2%; Score 52; DB 4; Length 711;
Best Local Similarity 90.9%; Pred. NO. 0.054;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAQNRKRV 11
DB 39 CFAQNRKRV 49

RESULT 2

Q9UCY5 PRELIMINARY; PRT; 38 AA.

ID Q9UCY5; (TRENBLrel. 13, Created)

AC Q9UCY5; (TRENBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)

DE Lactoferrin homolog (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Query Match	62.5%;	Score 40;	DB 5;	Length 47;
Best Local Similarity	53.6%;	Pred. No. 0.86;		
Matches	7; Conservative	3; Mismatches	1; Indels	0; Gaps
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DR	EMBL; AL162754; CAB84283.1; -.			
KW	Hypotheical protein; Complete proteome.			
SQ	SEQUENCE 57 AA; 6491 MW; A6D8781C29E212C5 CRC64;			
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Qy	1 CFQAQRNMRKV 11	Query Match	59.4%;	Score 38; DB 16; Length 57;
	: : : :	Best Local Similarity	58.3%;	Pred. No. 2.7;
		Matches	7; Conservative	Mismatches 3; Indels 0; Gaps 0;

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Db      21 CFSRREMGKVR 32
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Query Match      57.8%; Score 37; DB 5; Length 675;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
Q9TR80
ID Q9TR80 PRELIMINARY; PRT; 33 AA.
AC Q9TR80;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE Lactoferrin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RN SEQUENCE.
RX MEDLINE=95127729; PubMed=7827104;
RA Qian Z.Y., Jollies P., Migliore-Samour D., Fiat A.M.;
RL Biochim. Biophys. Acta 1243:25-32(1995).
DR HSSP: O77698; ICE2
DR InterPro; IPR011156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A71961 CRC64;

Query Match      57.8%; Score 37; DB 6; Length 33;
Best Local Similarity 54.5%; Pred. No. 2.4;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CFAQQRNMKVR 11
Db      19 CYQWKKMKRL 29
      |||::|||
Query Match      57.8%; Score 37; DB 6; Length 887;
Best Local Similarity 58.3%; Pred. No. 72;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT 7
Q9GYM8
ID Q9GYM8 PRELIMINARY; PRT; 675 AA.
AC Q9GYM8;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Hypothetical 78.0 kDa protein.
GN M60.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Stellyes L.;
RT "The sequence of C. elegans cosmid M60.";
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Waterston R.;
RT "Direct Submission.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U39995; AAF99993.2; -
KW Hypothetical protein.
SQ SEQUENCE 675 AA; 77981 MW; 3A5E193769BD1FA2 CRC64;

Query Match      54.7%; Score 35; DB 4; Length 150;
Best Local Similarity 54.7%; Score 35; DB 4; Length 150;

Qy      3 QAQRNMKVR 12
Db      69 QQRNLRIR 78
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Query Match      57.8%; Score 37; DB 5; Length 675;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 8
Q9SX85
ID Q9SX85 PRELIMINARY; PRT; 887 AA.
AC Q9SX85;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE F16N3.18 protein.
GN F16N3.18
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Vyotskaya V.S., Schwartz J.R., Yu G., Tortumi M., Lenz C., Liu S.,
RA Lee J., Liu A., Li J., Kremenetskaia I., Gonzalez A., Altafi H.,
RA Araujo R., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
RA Dunn P., Hansen N., Huizar L., Khan S., Kim C., Palm C., Rowley D.,
RA Shinn P., Walker M., Davis R.W., Ecker J.R., Federspiel N.A.,
RA Theologis A.;
RT "Arabidopsis thaliana chromosome 1 BAC F16N3 sequence.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007519; AAD46032.1; -
DR InterPro; IPR02048; EF-hand.
DR PROSITE; PS00018; EF HAND; UNKNOWN 1.
SQ SEQUENCE 887 AA; 100064 MW; 533510830A4A5099 CRC64;

Query Match      57.8%; Score 37; DB 10; Length 887;
Best Local Similarity 58.3%; Pred. No. 72;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CFAQQRNMKVR 12
Db      659 CQQRNLRIR 670
      |||::|||
Query Match      57.8%; Score 37; DB 10; Length 887;
Best Local Similarity 58.3%; Pred. No. 72;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT 9
Q9BS42
ID Q9BS42 PRELIMINARY; PRT; 150 AA.
AC Q9BS42;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (T-EMBLrel. 18, Last annotation update)
DE 60S ribosomal protein L30 isolog.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005344; AAH05344.1; -
DR InterPro; IPR000988; Ribosomal_L24E.
DR Pfam; PF01246; Ribosomal_L24e; 1.
DR PROSITE; PS01073; RIBOSOMAL_L24E; 1.
KW Ribosomal protein.
SQ SEQUENCE 150 AA; 18121 MW; 764482EBD4F53159 CRC64;

Query Match      54.7%; Score 35; DB 4; Length 150;
Best Local Similarity 54.7%; Score 35; DB 4; Length 150;

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Best Local Similarity 63.6%; Pred. No. 29;
Matches 7; Conservative 2; Mismatches 0; Gaps 0;

QY 2 FOAQRNMKVR 12
Db 40 FKXRNPKVR 50
|: :|||
|: :|||

RESULT 10
ID Q96HJ1 PRELIMINARY; PRT; 163 AA.
AC Q96HJ1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 60S ribosomal protein L30 isolog.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008499; AA08499.1; -
DR InterPro; IPR000988; Ribosomal_L24E.
DR Pfam; PF01246; Ribosomal_L24e; 1.
DR PROSITE; PS01073; RIBOSOMAL_L24E; UNKNOWN_1.
KW Ribosomal protein.
SQ SEQUENCE 163 AA; 19587 MW; 12AE9ECFF0057DB2 CRC64;

Query Match 54.7%; Score 35; DB 4; Length 163;
Best Local Similarity 63.6%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 0; Gaps 0;

QY 2 FOAQRNMKVR 12
Db 40 FKXRNPKVR 50
|: :|||
|: :|||

RESULT 11
ID Q96C76 PRELIMINARY; PRT; 163 AA.
AC Q96C76;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 60S ribosomal protein L30 isolog.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC014576; AA014576.1; -
DR InterPro; IPR000988; Ribosomal_L24E.
DR Pfam; PF01246; Ribosomal_L24e; 1.
DR PROSITE; PS01073; RIBOSOMAL_L24E; UNKNOWN_1.
KW Ribosomal protein.
SQ SEQUENCE 163 AA; 19522 MW; 5F5D9EDFFDFA09CD CRC64;

Query Match 54.7%; Score 35; DB 4; Length 163;
Best Local Similarity 63.6%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 0; Gaps 0;

QY 2 FOAQRNMKVR 12
Db 40 FKXRNPKVR 50
|: :|||
|: :|||

RESULT 12
ID Q96B04 PRELIMINARY; PRT; 163 AA.
AC Q96B04;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 60S ribosomal protein L30 isolog.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016312; AA016312.1; -
DR InterPro; IPR000988; Ribosomal_L24E.
DR Pfam; PF01246; Ribosomal_L24e; 1.
DR PROSITE; PS01073; RIBOSOMAL_L24E; UNKNOWN_1.
KW Ribosomal protein.
SQ SEQUENCE 163 AA; 19591 MW; 18ED987FFCF22D80 CRC64;

Query Match 54.7%; Score 35; DB 4; Length 163;
Best Local Similarity 63.6%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 0; Gaps 0;

QY 2 FOAQRNMKVR 12
Db 40 FKXRNPKVR 50
|: :|||
|: :|||

RESULT 13
ID Q9UHA3 PRELIMINARY; PRT; 163 AA.
AC Q9UHA3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 60S ribosomal protein L30 isolog (MY024 protein) (RPL24).
GN L30.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li Y., Peng Y., Li N., Gu W., Han Z., Fu G., Chen Z.;
RT "Novel genes expressed in human dendritic cells.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Gu J., Huang Q., Yu Y., Xu S., Wang Y., Han Z., Chen Z., Zhou J.,
RA Tu Y., Gu W., Fu G., Huang C.;
RT "Novel genes expressed in hematopoietic stem/progenitor cells from
RT Myelodysplastic Syndromes patient.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Mao Y.M., Xie Y., Lin Q., Mu Z.M., Yuan Y.Z.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Peng Y., Li Y., Tu Y., Xu S., Han Z., Fu G., Chen Z.;
RT "A novel gene expressed in human liver.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;

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RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BONE MARROW;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLADDER WART;
 RA Strausberg R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BONE MARROW;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF201949; AAF17241.1; -
 DR EMBL; AF165521; AAF86651.1; -
 DR EMBL; AF060926; AAG43138.1; -
 DR EMBL; AP212226; AAK26249.1; -
 DR EMBL; BC016777; AAH16777.1; -
 DR EMBL; BC008409; AAH08409.1; -
 DR EMBL; BC008422; AAH08422.1; -
 DR EMBL; BC008449; AAH08449.1; -
 DR EMBL; BC009593; AAH09593.1; -
 DR EMBL; BC009604; AAH09604.1; -
 DR EMBL; BC012913; AAH12913.1; -
 DR EMBL; BC016331; AAH16331.1; -
 DR EMBL; BC016725; AAH16725.1; -
 DR EMBL; BC026266; AAH26266.1; -
 DR EMBL; BC026267; AAH26267.1; -
 DR InterPro; IPR000988; Ribosomal L24E.
 DR Pfam; PF01246; Ribosomal L24E; 1.
 DR PROSITE; PS01073; RIBOSOMAL_L24E; 1.
 KW Ribosomal protein.
 SQ SEQUENCE 163 AA; 19621 MW; 1E5D9ECPFCF678D1 CRC64;

Query Match 54.7%; Score 35; DB 4; Length 163;
 Best Local Similarity 63.6%; Pred. No. 32;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FQAQNNMKVR 12
 | : : : : :
 Db 40 FKXKNPKVR 50

RESULT 14

Q99L28
 ID Q99L28 PRELIMINARY; PRT; 163 AA.
 AC Q99L28;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Similar to 60S ribosomal protein L30 isolog.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC003885; AAH03885.1; -.

DR InterPro; IPR000988; Ribosomal L24E.
 DR Pfam; PF01246; Ribosomal L24E; 1.
 DR PROSITE; PS01073; RIBOSOMAL_L24E; 1.
 KW Ribosomal protein.
 SQ SEQUENCE 163 AA; 19611 MW; 5393707FEA8CC417 CRC64;

Query Match 54.7%; Score 35; DB 11; Length 163;
 Best Local Similarity 63.6%; Pred. No. 32;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FQAQNNMKVR 12
 | : : : : :
 Db 40 FKXKNPKVR 50

RESULT 15

Q98M11
 ID Q98M11 PRELIMINARY; PRT; 170 AA.
 AC Q98M11;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 2-amino-4-hydroxy-6-hydroxymethylidihydropteridin e
 DE D-tyrophosphokinase.
 GN ML00786.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 CX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Ideawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohza M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP002995; BAB48302.1; -
 DR InterPro; IPR000550; Hppk.
 DR Pfam; PF01288; HPPK; 1.
 DR PROSITE; PS00794; HPPK; 1.
 KW Complete proteome.
 SQ SEQUENCE 170 AA; 18551 MW; 5F6C64AALD1668A7 CRC64;

Query Match 54.7%; Score 35; DB 16; Length 170;
 Best Local Similarity 41.7%; Pred. No. 33;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFAQNNMKVR 12
 | : : : : :
 Db 78 CLDAERKLRVR 89

Search completed: February 21, 2003, 07:44:23
 Job time : 23.8 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds
(without alignments)
56.502 Million cell updates/sec

Title: US-09-743-107B-72

Perfect score: 70

Sequence: 1 CFQWAEENMRKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SID27/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	12	AAV78072	Human lactoferrin
2	66	94.3	12	AAV78087	Human lactoferrin
3	66	94.3	12	AAV78088	Human lactoferrin
4	65	92.9	12	AAV78038	Human lactoferrin
5	65	92.9	12	AAV78046	Human lactoferrin
6	65	92.9	12	AAV78047	Human lactoferrin
7	65	92.9	12	AAV78084	Human lactoferrin
8	65	92.9	12	AAV78091	Human lactoferrin
9	65	92.9	12	AAV78092	Human lactoferrin
10	65	92.9	13	AAV78037	Human lactoferrin

11	65	92.9	13	21	AAV78048	Human lactoferrin
12	65	92.9	13	21	AAV78049	Human lactoferrin
13	65	92.9	14	21	AAV78036	Human lactoferrin
14	65	92.9	14	21	AAV78050	Human lactoferrin
15	65	92.9	14	21	AAV78051	Human lactoferrin
16	65	92.9	15	17	AAV78054	Peptide for anti-u
17	65	92.9	15	21	AAV78035	Human lactoferrin
18	65	92.9	15	21	AAV78062	Human lactoferrin
19	65	92.9	15	21	AAV78063	Human lactoferrin
20	65	92.9	16	21	AAV78031	Human lactoferrin
21	65	92.9	16	21	AAV78064	Human lactoferrin
22	65	92.9	16	21	AAV78055	Human lactoferrin
23	65	92.9	17	21	AAV78034	Human lactoferrin
24	65	92.9	17	21	AAV78066	Human lactoferrin
25	65	92.9	17	21	AAV78067	Human lactoferrin
26	65	92.9	18	15	AAV69352	Human lactoferrin
27	65	92.9	18	17	AAV13397	Advanced glycosyla
28	65	92.9	18	21	AAV78033	Human lactoferrin
29	65	92.9	19	21	AAV68867	Amino acid sequenc
30	65	92.9	19	21	AAV78032	Human lactoferrin
31	65	92.9	20	13	AAV21810	Anti microbial pep
32	65	92.9	20	14	AAV44841	Lactoferrin-relate
33	65	92.9	20	15	AAV48530	Lactoferrin derive
34	65	92.9	20	15	AAV48531	Lactoferrin derive
35	65	92.9	20	15	AAV57461	Lactoferrin derive
36	65	92.9	20	15	AAV57462	Lactoferrin derive
37	65	92.9	20	16	AAV4698	Bovine lactoferrin
38	65	92.9	20	16	AAV4699	Bovine lactoferrin
39	65	92.9	20	16	AAV80263	Anti-parasitic lac
40	65	92.9	20	16	AAV80264	Anti-parasitic lac
41	65	92.9	20	17	AAV98553	Peptide for anti-u
42	65	92.9	20	17	AAV91852	Lactoferrin-derive
43	65	92.9	20	17	AAV03045	Lactoferrin-derive
44	65	92.9	20	17	AAV06067	Lactoferrin derive
45	65	92.9	20	17	AAV87621	Lactoferrin-derive

ALIGNMENTS

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RESULT 1
AAV78072
ID AAV78072 standard; Peptide; 12 AA.
XX
AC AAV78072;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:72.
XX
DE Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 93WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
XX WPI; 2000-147388/13.

```

XX New peptides used for treatment and prevention of infections, -
PT inflammations and tumors and for use in infant formula food -
XX
PS Claim 22; Page 35; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 70; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFQWARRNRKVR 12
DB 1 CFQWARRNRKVR 12
RESULT 2
AAY78087
ID AAY78087 standard; Peptide; 12 AA.
XX
AC AAY78087;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:87.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
XX
PR 17-JUL-1998; 98SE-0002562.
XX
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattesby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 22; Page 37; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 12 AA;
Query Match 94.3%; Score 66; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 5.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWARRNRKVR 12
DB 1 CFQWARRNRKVR 12
RESULT 3
AAY78088
ID AAY78088 standard; Peptide; 12 AA.
XX
AC AAY78088;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:88.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
XX
PR 17-JUL-1998; 98SE-0002562.
XX
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattesby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 22; Page 37; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX XX
 SQ Sequence 12 AA;

Query Match 94.3%; Score 66; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 5.3e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWAZNNMKVR 12
 ||||| |||||
 DB 1 CFQWAZNNMKVR 12

RESULT 4
 AAY78038
 ID AAY78038 standard; Peptide; 12 AA.

XX XX

AC AAY78038;

XX 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:38.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCII-) A+ SCI INVEST AB.

XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

XX inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;
 Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 7.9e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 CFQWAZNNMKVR 12
 ||||| |||||
 DB 1 CFQWAZNNMKVR 12

RESULT 5
 AAY78046

ID AAY78046 standard; Peptide; 12 AA.

XX XX

AC AAY78046;

XX 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:46.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCII-) A+ SCI INVEST AB.

XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

XX inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 7.9e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARRNRKVR 12
DB 1 CFQWARRNRKVR 12

RESULT 6
AAV78047
ID AAV78047 standard; Peptide; 12 AA.
AC AAV78047;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:47.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
XX
PR 17-JUL-1998; 98SE-0002562.
XX
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
PS Claim 22; Page 36; 102pp; English.
XX
CC AAV78001 to AAV78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 12 AA;
Query Match 92.9%; Score 65; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARRNRKVR 12
DB 1 CFQWARRNRKVR 12

RESULT 8
AAV78091
ID AAV78091 standard; Peptide; 12 AA.
XX
AC AAV78091;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:91.

QY 1 CFQWARRNRKVR 12
DB 1 CFQWARRNRKVR 12

RESULT 6
AAV78047
ID AAV78047 standard; Peptide; 12 AA.
AC AAV78047;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:47.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
XX
PR 17-JUL-1998; 98SE-0002562.
XX
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
PS Claim 18; Page 73; 102pp; English.
XX
CC AAV78001 to AAV78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 12 AA;
Query Match 92.9%; Score 65; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARRNRKVR 12
DB 1 CFQWARRNRKVR 12

RESULT 7
AAV78084

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SE01230.
 XX
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 XX (ASCI-) A+ SCI INVEST AB.
 PA
 XX
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PT
 PS Claim 22; Page 38; 102pp; English.
 XX
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 7.9e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWARRNKKVR 12
 DB 1 CFQWARRNKKVR 12
 RESULT 9
 ID AAY78092 standard; Peptide; 12 AA.
 AC AAY78092;
 XX
 XX 25-APR-2000 (first entry)
 DT
 DE Human lactoferrin derived peptide SEQ ID NO:92.
 XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 XX Homo sapiens.
 OS

OS Synthetic.
 XX WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SE01230.
 XX
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 XX (ASCI-) A+ SCI INVEST AB.
 PA
 XX
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PT
 PS Claim 22; Page 38; 102pp; English.
 XX
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 7.9e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWARRNKKVR 12
 DB 1 CFQWARRNKKVR 12
 RESULT 10
 ID AAY78037 standard; Peptide; 13 AA.
 AC AAY78037;
 XX
 XX 25-APR-2000 (first entry)
 DT
 DE Human lactoferrin derived peptide SEQ ID NO:37.
 XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SE01230.
 PF

XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 12; Page 70; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
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 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX SQ Sequence 13 AA;
 Query Match 92.9%; Score 65; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 8.5e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWARNRKVR 12
 DB 2 CFQWQNNRKVR 13
 RESULT 11
 ID AAY78048 standard; Peptide; 13 AA.
 AC AAY78048;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:48.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 PN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 12; Page 70; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX SQ Sequence 13 AA;
 Query Match 92.9%; Score 65; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 8.5e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWARNRKVR 12
 DB 2 CFQWQNNRKVR 13
 RESULT 11
 ID AAY78048 standard; Peptide; 13 AA.
 AC AAY78048;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:48.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 PN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 12; Page 70; 102pp; English.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 74; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
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 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX SQ Sequence 13 AA;
 Query Match 92.9%; Score 65; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 8.5e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWARNRKVR 12
 DB 2 CFQWQNNRKVR 13
 RESULT 12
 ID AAY78049 standard; Peptide; 13 AA.
 AC AAY78049;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:49.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 PN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 74; 102pp; English.

PS Claim 18; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX SQ Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. No. 8.5e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARNRKVR 12

DB 2 CFQWQNRKVR 13

RESULT 13

AAY78036

ID AAY78036 standard; Peptide; 14 AA.

AC AAY78036;

XX 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:36.

DE Human; lactoferrin; modification; infection; inflammation; tumour;

XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

KW urinary tract infection; colitis; Candida infection; fungicidal;

KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

OS WO200001730-A1.

PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

PF 06-JUL-1998; 98SE-0002441.

FR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

DR New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food -

PS Claim 12; Page 69; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX SQ Sequence 14 AA;

Query Match 92.9%; Score 65; DB 21; Length 14;

Best Local Similarity 91.7%; Pred. No. 9.2e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARNRKVR 12

DB 3 CFQWQNRKVR 14

RESULT 14

AAY78050

ID AAY78050 standard; Peptide; 14 AA.

AC AAY78050;

XX 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:50.

DE Human; lactoferrin; modification; infection; inflammation; tumour;

XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

KW urinary tract infection; colitis; Candida infection; fungicidal;

KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

OS WO200001730-A1.

PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

PF 06-JUL-1998; 98SE-0002441.

FR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

DR New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food -

PS Claim 15; Page 75; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX
SQ Sequence 14 AA;
Query Match 92.9%; Score 65; DB 21; Length 14;
Best Local Similarity 91.7%; Pred. No. 9.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWARNMKVR 12
Db 3 CFQWQRMNKVR 14

RESULT 15
AAV78051.
ID AAV78051 standard; Peptide; 14 AA.
XX
AC AAV78051;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:51.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WC200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
PS Claim 18; Page 75; 102pp; English.
XX

AAV78001 to AAV78100 represent peptides having sequences based on human
lactoferrin. The peptides are taken up in the intestine through
binding to specific lactoferrin receptors and are then transported
through the circulation. A medicinal product of the peptide or fragment
can be used for treating and/or prevention of infections (such as
urinary tract infections, colitis, and Candida infection on a mucosal
membrane), inflammations and/or tumours. The peptides can also be used
in food stuffs such as infant formula food. The peptides are also
fungicidal and bactericidal and may also be used as preservatives.
Even though native human lactoferrin have been shown to have desired
anti-inflammatory anti-infectious and anti-tumoural properties they
cannot be used clinically on a broad basis because of high production
costs. Therefore, provision of peptides based on lactoferrin would
enable them to be used for the same purposes as lactoferrin at lower
cost.
XX
SQ Sequence 14 AA;

Query Match 92.9%; Score 65; DB 21; Length 14;

Best Local Similarity 91.7%; Pred. No. 9.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWARNMKVR 12
Db 3 CFQWQRMNKVR 14
Search completed: February 21, 2003, 07:37:11
Job time : 28.35 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 seconds
(without alignments)
40.818 Million cell updates/sec

Title: US-09-743-107B-72
Perfect score: 70
Sequence: 1 CFQWARMKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCUTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfilese1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	18	1	US-08-204-487-3
2	65	92.9	18	2	US-08-485-948-8
3	65	92.9	18	2	US-08-628-380-8
4	65	92.9	18	2	US-08-475-055-8
5	65	92.9	20	1	US-07-755-161A-3
6	65	92.9	20	1	US-07-891-174-3
7	65	92.9	20	1	US-08-204-487-1
8	65	92.9	20	1	US-08-256-771-24
9	65	92.9	20	1	US-08-256-771-25
10	65	92.9	20	1	US-08-381-984-24
11	65	92.9	20	1	US-08-381-984-25
12	65	92.9	22	4	US-09-508-734-4
13	65	92.9	24	4	US-09-508-734-6
14	65	92.9	25	1	US-07-755-161A-10
15	65	92.9	25	1	US-07-891-174-10
16	65	92.9	25	1	US-08-204-487-7
17	65	92.9	29	4	US-09-508-734-8
18	65	92.9	36	1	US-07-755-161A-8
19	65	92.9	36	1	US-07-891-174-8
20	65	92.9	36	1	US-08-256-771-30
21	65	92.9	36	1	US-08-381-984-29
22	65	92.9	47	2	US-08-464-182A-6
23	65	92.9	47	2	US-08-406-271-6
24	65	92.9	50	2	US-08-633-274A-7
25	65	92.9	52	4	US-09-017-043A-3
26	65	92.9	53	2	US-08-464-182A-5
27	65	92.9	53	2	US-08-406-271-5

28	65	92.9	54	2	US-08-464-182A-2	Sequence 2, Appli
29	65	92.9	54	2	US-08-406-271-2	Sequence 2, Appli
30	65	92.9	694	3	US-08-724-586-2	Sequence 2, Appli
31	65	92.9	694	4	US-09-421-632-2	Sequence 2, Appli
32	65	92.9	694	4	US-09-932-190-2	Sequence 2, Appli
33	65	92.9	705	2	US-08-655-640-2	Sequence 2, Appli
34	65	92.9	708	2	US-08-655-640-4	Sequence 4, Appli
35	65	92.9	711	1	US-08-154-019-4	Sequence 4, Appli
36	65	92.9	711	1	US-08-461-333-4	Sequence 4, Appli
37	65	92.9	711	3	US-08-464-167-4	Sequence 4, Appli
38	65	92.9	711	3	US-08-158-313-4	Sequence 4, Appli
39	65	92.9	711	4	US-08-476-798-4	Sequence 2, Appli
40	62	88.6	711	1	US-08-145-681-2	Sequence 2, Appli
41	62	88.6	711	1	US-08-250-308-2	Sequence 2, Appli
42	62	88.6	711	1	US-08-453-703-2	Sequence 2, Appli
43	62	88.6	711	2	US-08-456-106-2	Sequence 2, Appli
44	62	88.6	711	3	US-08-456-108-2	Sequence 2, Appli
45	62	88.6	711	4	US-09-285-577-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/082044487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN/ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FUN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37) "
US-08-204-487-3

Query Match 92.9%; Score 65; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 6.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMNRKVR 12
| | | | | | | | | | | | | | | | | |
DB 1 CFQWQNRNRKVR 12

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882

GENERAL INFORMATION:

APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
FILING DATE:

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

US-08-485-948-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 6.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMNRKVR 12
| | | | | | | | | | | | | | | | | |
DB 1 CFQWQNRNRKVR 12

RESULT 3

US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341

GENERAL INFORMATION:

APPLICANT: LI, YONG MING
APPLICANT: HELEN VLASSARA, HELEN
APPLICANT: CERAMI, ANTHONY
TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,380
FILING DATE: April 4, 1996
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

US-08-628-380-8

Query Match 92.9%; Score 65; DB 2; Length 18;

Best Local Similarity 91.7%; Pred. No. 6.6e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMNRKVR 12
| | | | | | | | | | | | | | | | | |

DB 1 CFQWQNRNRKVR 12

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245

GENERAL INFORMATION:

APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Klauber & Jackson
;; STREET: 411 Hackensack Avenue
;; CITY: Hackensack
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07601
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patent Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/475,055
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/485,948
;; FILING DATE:
;; APPLICATION NUMBER: 08/488,217
;; FILING DATE: JUNE 7, 1995
;; APPLICATION NUMBER: 08/418,642
;; FILING DATE: APRIL 7, 1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 947-1-008A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1694
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; DESCRIPTION: LF-C1, 8-25
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
;; US-08-475-055-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 6.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CFQWRNNRKVR 12
||| |||||
Db 1 CFQWRNNRKVR 12

RESULT 5
US-07-755-161A-3
; Sequence 3, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: DisplayWrite
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/755,161A
;; FILING DATE: 19910905
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX: 202-371-8856
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE:
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; CELL LINE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY: modified site
;; LOCATION: 2
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 19"
;; FEATURE:
;; NAME/KEY: modified site
;; LOCATION: 19
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 2"
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
;; US-07-755-161A-3

Query Match 92.9%; Score 65; DB 1; Length 20;

Best Local Similarity 91.7%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMRKVR 12
||| |||||
Db 2 CFQWQNRMRKVR 13

RESULT 6
US-07-891-174-3
; Sequence 3, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMRKVR 12
||| |||||
Db 2 CFQWQNRMRKVR 13

RESULT 7
US-08-204-487-1
; Sequence 1, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIAKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FJN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000

```

; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..20
; OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
; OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
; US-08-204-487-1
;
; Query Match 92.9%; Score 65; DB 1; Length 20;
; Best Local Similarity 91.7%; Pred. No. 7.3e-05;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 CFQWARRNRKVR 12
; DB 2 CFQWQRRNRKVR 13
;
; RESULT 8
; US-08-256-771-24
; Sequence 24, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,771
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are linked by
; OTHER INFORMATION: disulfide bond"
;
; Query Match 92.9%; Score 65; DB 1; Length 20;
; Best Local Similarity 91.7%; Pred. No. 7.3e-05;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 CFQWARRNRKVR 12
; DB 2 CFQWQRRNRKVR 13
;
; RESULT 9
; US-08-256-771-25
; Sequence 25, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,771
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are protected to
; OTHER INFORMATION: prevent disulfide bond"
;
; Query Match 92.9%; Score 65; DB 1; Length 20;
; Best Local Similarity 91.7%; Pred. No. 7.3e-05;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 CFQWARRNRKVR 12
; DB 2 CFQWQRRNRKVR 13
;
; RESULT 10
; US-08-381-984-24
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; US-08-256-771-24
;
; Query Match 92.9%; Score 65; DB 1; Length 20;
; Best Local Similarity 91.7%; Pred. No. 7.3e-05;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 CFQWARRNRKVR 12
; DB 2 CFQWQRRNRKVR 13
;
; RESULT 9
; US-08-256-771-25
; Sequence 25, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,771
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are protected to
; OTHER INFORMATION: prevent disulfide bond"
;
; Query Match 92.9%; Score 65; DB 1; Length 20;
; Best Local Similarity 91.7%; Pred. No. 7.3e-05;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 CFQWARRNRKVR 12
; DB 2 CFQWQRRNRKVR 13
;
; RESULT 10
; US-08-381-984-24
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; Sequence 24, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:

INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at positions 2
; OTHER INFORMATION: and 19 are bonded by disulfide linkage"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"

US-08-381-984-24

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMNRKVR 12

Db 2 CFQWQRMNRKVR 13

RESULT 11

US-08-381-984-25
; Sequence 25, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:

INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"

US-08-381-984-25

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMNRKVR 12

Db 2 CFQWQRMNRKVR 13

RESULT 12

US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 4

QY 1 CFQWARMNRKVR 12

Db 2 CFQWQRMNRKVR 13

RESULT 12

US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 4

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; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4
Query Match          92.9%; Score 65; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRNNRKVR 12
Db 2 CFQWRNNRKVR 13

RESULT 13
US-09-508-734-6
; Sequence 6, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-6
Query Match          92.9%; Score 65; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 8.7e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRNNRKVR 12
Db 3 CFQWRNNRKVR 14

RESULT 14
US-07-755-161A-10
; Sequence 10, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500KB
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755,161A
; FILING DATE: 19910905
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
Query Match          92.9%; Score 65; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 9.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRNNRKVR 12
Db 4 CFQWRNNRKVR 15
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RESULT 15
US-07-891-174-10
Sequence 10, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
Cys residue at location 4 connected by disulfide bond with
thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
LOCATION: 21

IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
Cys residue at location 21 connected by disulfide bond with
thiol group of Cys residue at location 4"
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
Query Match 92.9%; Score 65; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 9.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWARRNRKVR 12
DB 4 CFQWARRNRKVR 15
Search completed: February 21, 2003, 07:50:33
Job time : 8.7 secs

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OM protein - protein search, using sw model

Run On: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds
(without alignments)

35.508 Million cell updates/sec

Title: US-09-743-107B-72

Perfect score: 70

Sequence: 1 CFQWARRNRKVR 12

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	65	92.9	25	9	US-09-798-869-20
3	65	92.9	694	9	US-10-023-096-2
4	57	81.4	15	9	US-09-798-869-6
5	48	68.6	15	9	US-09-798-869-3
6	48	68.6	25	9	US-09-798-869-23
7	40	57.1	15	9	US-09-798-869-7
8	39	55.7	15	9	US-09-798-869-4
9	39	55.7	25	9	US-09-798-869-22
10	38	54.3	489	9	US-09-888-320-2
11	36	51.4	15	9	US-09-798-869-8
12	36	51.4	15	9	US-09-798-869-29
13	36	51.4	15	9	US-09-798-869-30
14	35	50.0	21	10	US-09-864-761-47985
15	35	50.0	62	10	US-09-764-877-1690
16	35	50.0	292	9	US-10-117-824-1
17	34	48.6	77	10	US-09-764-847-613
18	34	48.6	86	9	US-09-738-626-5715
19	34	48.6	312	10	US-09-935-428A-4

20	34	48.6	338	9	US-09-978-295A-119	Sequence 119, App
21	34	48.6	338	9	US-09-978-697-119	Sequence 119, App
22	34	48.6	338	9	US-09-978-132A-119	Sequence 119, App
23	34	48.6	338	9	US-09-999-832A-119	Sequence 119, App
24	34	48.6	338	9	US-09-978-189-119	Sequence 119, App
25	34	48.6	553	9	US-09-796-753-14	Sequence 14, Appli
26	34	48.6	553	10	US-09-981-649A-6	Sequence 6, Appli
27	34	48.6	553	10	US-09-981-649A-24	Sequence 24, Appli
28	34	48.6	554	10	US-09-981-649A-30	Sequence 30, Appli
29	34	48.6	554	10	US-09-981-649A-32	Sequence 32, Appli
30	34	48.6	556	10	US-09-795-691-2	Sequence 2, Appli
31	34	48.6	559	10	US-09-981-649A-28	Sequence 28, Appli
32	34	48.6	1212	9	US-10-219-248-3	Sequence 3, Appli
33	34	48.6	1212	9	US-10-219-247-3	Sequence 3, Appli
34	34	48.6	1212	10	US-09-855-722-3	Sequence 3, Appli
35	34	48.6	1238	9	US-10-219-248-5	Sequence 5, Appli
36	34	48.6	1238	9	US-10-219-247-5	Sequence 5, Appli
37	34	48.6	1238	10	US-09-855-722-5	Sequence 5, Appli
38	34	48.6	1238	10	US-09-944-849-4	Sequence 4, Appli
39	34	48.6	1258	10	US-09-867-852-107	Sequence 107, App
40	33	47.1	31	9	US-09-956-206A-13	Sequence 13, Appli
41	33	47.1	33	10	US-09-864-761-44211	Sequence 44211, A
42	33	47.1	95	10	US-09-764-864-1031	Sequence 1031, Ap
43	33	47.1	287	10	US-09-925-301-1386	Sequence 1386, Ap
44	33	47.1	309	9	US-09-510-332-93	Sequence 93, Appli
45	33	47.1	333	9	US-09-796-753-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1
US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2

Query Match 92.9%; Score 65; DB 9; Length 15;
Best Local Similarity 91.7%; Pred. No. 2.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARRNRKVR 12
DB 3 CFQWARRNRKVR 14

RESULT 2
US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON

```
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-798-869-20

Query Match      92.9%; Score 65; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMNRKVR 12
   |||||
Db 3 CFQWARMNRKVR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-023-096-2

Query Match      92.9%; Score 65; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMNRKVR 12
   |||||
Db 3 CFQWARMNRKVR 14

RESULT 4
US-09-798-869-6
; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
; OTHER INFORMATION: sequence)
; US-09-798-869-6

Query Match      81.4%; Score 57; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.00067;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWARMNRKVR 12
   |||||
Db 3 CFQWARMNRKVR 14

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
; US-09-798-869-3

Query Match      68.6%; Score 48; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.023;
```

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWARRMKV 11
|:|:|:|:|:|:
Db 3 CYQWQRRMKL 13

RESULT 6
US-09-798-869-23
; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23

Query Match 68.6%; Score 48; DB 9; Length 25;
Best Local Similarity 63.6%; Pred. No. 0.039;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWARRMKV 11
|:|:|:|:|:|:
Db 3 CYQWQRRMKL 13

RESULT 7
US-09-798-869-7
; Sequence 7, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-7

Query Match 57.1%; Score 40; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.55;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWARRMKV 11
|:|:|:|:|:|:
Db 3 CYQWQRRMKL 13

RESULT 8
US-09-798-869-4
; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4

Query Match 55.7%; Score 39; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWARRMKV 11
|:|:|:|:|:|:
Db 3 CLRWQNRMKV 13

RESULT 9
US-09-798-869-22
; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-22

Query Match 55.7%; Score 39; DB 9; Length 25;
Best Local Similarity 54.5%; Pred. No. 1.3;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWARRMKV 11
|:|:|:|:|:|:
Db 3 CLRWQNRMKV 13

```

RESULT 12
US-09-798-869-29
; Sequence 29, Application US/09798869
; Publication No. US2003002821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (VSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29

Query Match 51.4%; Score 36; DB 9; Length 15;
Best Local Similarity 45.5%; Pred. No. 2,7;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWARRNRKV 11
Db 3 CFQWRRMKKL 13

```

```

RESULT 13
US-09-798-869-30
; Sequence 30, Application US/09798859
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (VSTEIN REKDAL
; APPLICANT: BALDUR SVEINEBJ(RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-30

Query Match 51.4%; Score 36; DB 9; Length 15;
Best Local Similarity 45.5%; Pred. No. 2.7;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWARRNRKV 11
Db 3 CFQWQRRMKKL 13

```

RESULT 14
US-09-864-761-47985
; Sequence 47985, Application US/09864761
; Patent No. US20C20048763A1
; GENERAL INFORMATION:

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 seconds
(without alignments)
120.168 Million cell updates/sec

Title: US-09-743-107B-72

Perfect score: 70

Sequence: 1 CFQWARMKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	711	1 TFHUL	lactotransferrin p
2	48	68.6	708	2 JC2323	lactoferrin - goat
3	45	64.3	33	2 S52107	histidyl-tRNA synth
4	40	57.1	428	2 F81650	hypothetical prote
5	40	57.1	511	2 AB0858	hypothetical prote
6	39	55.7	275	2 T22597	hypothetical prote
7	39	55.7	536	2 T24218	hypothetical prote
8	39	55.7	707	1 A28438	lactoferrin precu
9	39	55.7	1213	2 T41378	probable helicase
10	38	54.3	428	2 H71508	histidine-tRNA lig
11	38	54.3	489	2 C70855	probable monooxyge
12	38	54.3	501	2 T39601	hypothetical sh3-c
13	38	54.3	743	2 T00634	hypothetical prote
14	38	54.3	1051	2 T48933	WD repeat domain p
15	38	54.3	4568	2 T08030	dynamin beta heavy
16	37	52.9	124	2 C96582	F1511.22 (imported
17	37	52.9	172	2 D64388	hypothetical prote
18	37	52.9	211	1 S40836	formate dehydrogen
19	37	52.9	211	2 A86078	formate dehydrogen
20	37	52.9	211	2 B91231	formate dehydrogen
21	37	52.9	211	2 AD0946	formate dehydrogen
22	37	52.9	531	2 A84471	En/Spm-like transp
23	37	52.9	594	2 C84325	hypothetical prote
24	37	52.9	742	2 T25415	hypothetical prote
25	37	52.9	2150	2 T08165	RNA1 polypeptid -
26	36	51.4	224	2 D89836	hypothetical prote
27	36	51.4	274	2 B60950	apolipoprotein B-1
28	36	51.4	298	2 AD2346	hypothetical prote
29	36	51.4	361	2 A24470	probable proteinase

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N/Alternate names: lactoferrin

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74:

R/Cho. Y.

submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:U07643; NID:9467236; PIDN:AAB60324.1; PID:9467237

R/Rev. M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 16, 5288, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; MUID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>

A/Cross-references: EMBL:X53961; NID:934415; PIDN:CAA37914.1; PID:934416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Fanelia, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactoferrin

A/Reference number: A45401; MUID:93125571; PMID:1480183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <REN>

A/Cross-references: GB:S52659; NID:9263311; PIDN:AAB24877.1; PID:9263312

A/Experimental source: placenta

A/Note: sequence extracted from NCBI backbone (NCBIP:122202)

R/Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; MUID:90328549; PMID:2374734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POW>

A/Cross-references: EMBL:X52941; NID:934411; PIDN:CAA37116.1; PID:934412

R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A/Reference number: S15853; MUID:91264786; PMID:2049066

A/Accession: S15853

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 20-31 <ST1>

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-28, 'X', 30-31 <ST2>

R:Rado, T.A.; Wei, X.; Benz Jr., E.J.
 Blood 70, 989-993, 1987
 A:Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
 A:Reference number: S07160; MUID:88001031; PMID:3477300
 A:Accession: S07160
 A:Molecule type: mRNA
 A:Residues: 436-487, 'A', 489-711 <RAD>
 A:Cross-references: EMBL:M18642; NID:G196815; PIDN:AAA8665.1; PID:G386855
 R:Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
 Cancer Res. 51, 3037-3043, 1991
 A:Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
 A:Reference number: A61169; MUID:91235214; PMID:1674448
 A:Accession: A61169
 A:Molecule type: mRNA
 A>Status: not compared with conceptual translation
 A:Keywords: conceptual translation
 A:Residues: 3-701, 'SMKPVN' <PAN>
 A:Experimental source: normal breast tissue
 R:Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.; Eur. J. Biochem. 145, 659-666, 1984
 A:Title: Human lactotransferrin: amino acid sequence and structural comparisons with other
 A:Reference number: A31000; MUID:85076667; PMID:6510420
 A:Accession: A31000
 A:Molecule type: protein
 A:Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-400
 A:Note: this is the final paper in a series
 R:Houen, G.; Hoegdall, E.V.; Barkholt, V.; Nørskov, L. Eur. J. Biochem. 241, 303-308, 1996
 A:Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity chromatography
 A:Reference number: S74119; MUID:97054624; PMID:8898921
 A:Accession: S74119
 A:Molecule type: protein
 A:Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>
 A:Experimental source: neutrophil granulocytes
 C:Genetics:
 A:Gene: GDB:LTF
 A:Cross-references: GDB:119368; OMIM:150210
 A:Map position: 3q21-3q23
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron binding; milk
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-711/Product: lactotransferrin #status experimental <MAT>
 F:21-356/Domain: transferrin repeat homology <TRH1>
 F:360-699/Domain: transferrin repeat homology <TRH2>
 F:23-65, 39-56, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status experimental
 F:157, 498/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #status experimental
 Query Match 92.9%; Score 65; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.0011;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWARMNRKV 12
 DB 39 CFQWQRMNRKV 50
 RESULT 2
 JC2323
 lactoferrin - goat
 C:Species: Capra aegagrus hircus (domestic goat)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 C:Accession: JC2323
 R:Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P. Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A:Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
 A:Reference number: JC2323; MUID:94380047; PMID:8093048
 A:Accession: JC2323
 A:Molecule type: mRNA
 A:Residues: 1-708 <LEP>
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:359-696/Domain: transferrin repeat homology <TRH2>
 F:252, 300, 387, 495, 564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.6%; Score 48; DB 2; Length 708;
 Best Local Similarity 63.6%; Pred. No. 1.2;
 Matches 7; Conservative 2; Mismatches 0; Gaps 0;

QY 1 CFQWARMNRKV 11
 DB 38 CYQWQRMNRKL 48

RESULT 3

S52107

lactoferrin - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997

C:Accession: S52107

R:Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M. Biochim. Biophys. Acta 1243, 25-32, 1995

A:Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet aggregation

A:Reference number: S52107; MUID:95127729; PMID:7827104

A:Accession: S52107

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-33 <QIA>

C:Superfamily: transferrin; transferrin repeat homology

C:Keywords: duplication

Query Match 64.3%; Score 45; DB 2; Length 33;
 Best Local Similarity 54.5%; Pred. No. 0.2;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWARMNRKV 11
 DB 19 CYQWQRMNRKL 29

RESULT 4

P81660

histidyl-tRNA synthetase TC0830 [imported] - Chlamydia muridarum (strain Nigg)

C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 28-Jul-2000

C:Accession: P81660

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: P81660

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-428 <TET>

A:Cross-references: GB:AE002349; GB:AE002160; NID:G7190851; PIDN:AAF39630.1; PID:G71908

A:Experimental source: strain Nigg (MoPn)

C:Genetics:

A:Gene: TC0830

C:Superfamily: histidine-tRNA ligase; histidine-tRNA ligase homology

Query Match 57.1%; Score 40; DB 2; Length 428;
 Best Local Similarity 55.6%; Pred. No. 19;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMNR 9
 DB 348 CFSWAKHLR 356

RESULT 5

AB0858

hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium

C:Species: Salmonella enterica subsp. enterica serovar Typhimurium

A:Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C:Accession: AB0858

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Th. T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulle, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov

A;Reference number: AB0502; PMID:11677608

A;Accession: AB0858

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-511 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:ig16504016; GSPDB:GN00176

C;Genetics:

A;Gene: STY3070

Query Match 57.1%; Score 40; DB 2; Length 511;

Best Local Similarity 58.3%; Pred. No. 23;

Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWARRNRKVR 12

||| :|||

Db 350 CFQWDMNKAKVR 361

RESULT 6

T22597

hypothetical protein F53H4.4 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

A;Accession: T22597

R;Dobson, R.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19587

A;Accession: T22597

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-275 <WLL>

A;Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4

A;Experimental source: clone F53H4

C;Genetics:

A;Gene: CESP:F53H4.4

A;Map position: X

A;Introns: 67/1; 153/1

C;Superfamily: *Caenorhabditis elegans* hypothetical protein F53H4.4

Query Match 55.7%; Score 39; DB 2; Length 275;

Best Local Similarity 63.6%; Pred. No. 19;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FQWARRNRKVR 12

||| :|||

Db 262 FQWKSMRKTR 272

RESULT 7

T24218

hypothetical protein R13G10.2 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

A;Accession: T24218

R;Gardner, A.

submitted to the EMBL Data Library, August 1994

A;Reference number: Z19857

A;Accession: T24218

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-536 <WLL>

A;Cross-references: EMBL:Z35602; PIDN:CAA84671.1; GSPDB:GN00021; CESP:R13G10.2

A;Experimental source: clone R13G10

C;Genetics:

A;Gene: CESP:R13G10.2

A;Map position: 3

A;Introns: 64/3; 194/1; 404/3

Query Match 55.7%; Score 39; DB 2; Length 536;

Best Local Similarity 50.0%; Pred. No. 36;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWARRNRKVR 12

||| :|||

Db 293 CIDWGRDGRKVK 304

RESULT 8

A28438

lactoferrin precursor - mouse

N;Alternate names: lactotransferrin

C;Species: *Mus musculus* (house mouse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

A;Accession: A28438; A41205

R;Pentecost, B.T.; Teng, C.T.

J. Biol. Chem. 262, 10134-10139, 1987

A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre

A;Reference number: A92596; MUID:87280033; PMID:3611056

A;Accession: A28438

A;Molecule type: mRNA

A;Residues: 3-707 <PEN>

A;Cross-references: EMBL:J03298

R;Liu, Y.; Teng, C.T.

J. Biol. Chem. 266, 21880-21885, 1991

A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.

A;Reference number: A41205; MUID:92042099; PMID:1939212

A;Accession: A41205

A;Molecule type: DNA

A;Residues: 1-15 <LIU>

A;Cross-references: GB:M74778

C;Superfamily: transferrin; transferrin repeat homology

C;Keywords: duplication; glycoprotein

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-707/Product: lactotransferrin #status predicted <MAT>

F;358-695/Domain: transferrin repeat homology <TRH2>

F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.7%; Score 39; DB 1; Length 707;

Best Local Similarity 54.5%; Pred. No. 48;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWARRNRKVR 11

||| :|||

Db 37 CLRQWQNRKVR 47

RESULT 9

T41378

probable helicase - fission yeast (*Schizosaccharomyces pombe*)

C;Species: *Schizosaccharomyces pombe*

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Feb-2001

A;Accession: T41378

R;Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, May 1998

A;Reference number: Z21990

A;Accession: T41378

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-1213 <MUR>

A;Cross-references: EMBL:AL023592; PIDN:CAA19107.1; GSPDB:GN00068; SPDB:SPCC550.03c

A;Experimental source: strain 972h; cosmid c550

C;Genetics:

A;Gene: SPDB:SPCC550.03c

A;Map position: 3

C;Superfamily: yeast probable SKI2 protein YJL050w

Query Match 55.7%; Score 39; DB 2; Length 1213;

Best Local Similarity 62.5%; Pred. No. 81;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;


```

QY 1 CFQWARMNKV 8
DB 1141 CYEWARGM 1149

RESULT 10
H71500
Histidine-tRNA ligase (EC 6.1.1.21) - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 03-Jun-2002
C:Accession: H71500
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: H71500
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-428 <ARN>
A:Cross-references: GB:AE001325; GB:AE001273; NID:G3328980; PIDN:AAC68145.1; PID:G332898
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: hns
C:Superfamily: histidine-tRNA ligase; histidine-tRNA ligase homology
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 54.3%; Score 38; DB 2; Length 428;
Best Local Similarity 45.5%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWARMNKV 11
DB 348 CFSWANRLRL 358

RESULT 11
C70655
probable monooxygenase - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: C70655
R:Coale, S.T.; Brosch, R.; Parkhill, J.; Garnier, C.; Churcher, C.; Harris, D.; Gordon, S.
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: C70655
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-489 <COL>
A:Cross-references: GB:283864; GB:AL123456; NID:G3261687; PIDN:CAB06212.1; PID:e301250;
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv3854c

Query Match 54.3%; Score 38; DB 2; Length 489;
Best Local Similarity 54.5%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWARMNKV 11
DB 253 CQKWRMNRKM 263

RESULT 12
T39801
hypothetical sh3-containing protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T39801
R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.

```

submitted to the EMBL Data Library, July 1999

A:Reference number: Z21880
 A:Accession: T39801
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-501 <MCD>
 A:Cross-references: EMBL:AL109731; PIDN:CAB52037.1; GSPDB:GN00067; SPDB:SPBCL9C2.10
 A:Experimental source: strain 972h-; cosmid c19C2
 C:Genetics:
 A:Gene: SPDB:SPBCL9C2.10
 A:Map position: 2
 A:Introns: 196/3

Query Match 54.3%; Score 38; DB 2; Length 501;
 Best Local Similarity 60.0%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWARMNRK 10
 DB 50 CTRVVRNMDK 59

RESULT 13

T00634
 hypothetical protein H_DJ0897G10.1 - human
 C:Species: Homo sapiens (man)
 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 05-Nov-1999
 C:Accession: T00634
 R:Kalicki, J.; Elliott, G.
 submitted to the EMBL Data Library, January 1998
 A:Description: The sequence of Homo sapiens PAC clone DJ0897G10.
 A:Reference number: Z14194
 A:Accession: T00634
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-743 <KAL>
 A:Cross-references: EMBL:AC004082; NID:G2822160; PIDN:AAB97937.1; PID:G2822161

C:Genetics:
 A:Map position: 7q11.23-q21.1
 A:Introns: 36/2; 59/1; 130/3; 172/2; 203/3; 227/3; 288/1; 353/1; 414/1; 461/2; 486/1; 54
 A:Note: H_DJ0897G10.1
 C:Superfamily: protein kinase C C2 region homology
 P:119-233/Domain: protein kinase C2 region homology <KC2>

Query Match 54.3%; Score 38; DB 2; Length 743;
 Best Local Similarity 50.0%; Pred. No. 76;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWARMNRKVR 12
 DB 498 CFLGRNMRKEIQ 509

RESULT 14

T48933
 WD repeat domain protein - Arabidopsis thaliana
 N:Alternate names: protein F14L2.80
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
 C:Accession: T48933
 R:Jordan, N.; Bangert, S.; Wiedemann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S.;
 submitted to the Protein Sequence Database, April 2000

A:Reference number: Z25008
 A:Accession: T48933
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1051 <JOR>
 A:Cross-references: EMBL:AL353818; GSPDB:GN00061; ATSP:F14L2.80
 A:Experimental source: cultivar Columbia; BAC clone F14L2
 C:Genetics:
 A:Gene: ATSP:F14L2.80
 A:Map position: 3
 A:Introns: 36/3; 121/3; 205/3; 336/2; 668/3; 739/1; 773/1; 853/2; 894/2; 932/3

Search completed: February 21, 2003, 07:47:42
Job time : 10.65 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds
(without alignments)
108.199 Million cell updates/sec

Title: US-09-743-107B-72
Perfect score: 70
Sequence: 1 CFQWARMKRV 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	65	92.9	711	1	TRFL_HUMAN
2	48	68.6	708	1	TRFL_CAMDR
3	48	68.6	708	1	TRFL_CAPHI
4	40	57.1	292	1	NLA_DROME
5	40	57.1	428	1	SYH_CHLMU
6	40	57.1	695	1	TRFL_HORSE
7	39	55.7	146	1	RPOB_LIBAF
8	39	55.7	707	1	TRFL_MOUSE
9	39	55.7	783	1	YNR2_CAEEL
10	38	54.3	422	1	PAFA_CHICK
11	38	54.3	428	1	SYH_CHLTR
12	38	54.3	989	1	T100_HUMAN
13	38	54.3	4568	1	DYHB_CHLRE
14	37	52.9	172	1	Y708_METJA
15	37	52.9	211	1	PD01_ECOLI
16	37	52.9	573	1	UREI_LACPE
17	36	51.4	369	1	SP11_MXVL
18	36	51.4	435	1	SNXP_HUMAN
19	36	51.4	451	1	GAGD_DROME
20	36	51.4	585	1	YHD9_YEAST
21	35	50.0	62	1	RL28_THETN
22	35	50.0	292	1	CNT8_HUMAN
23	35	50.0	355	1	MURG_NEIMA
24	35	50.0	355	1	MURG_NEIMB
25	35	50.0	365	1	1A34_HUMAN
26	35	50.0	372	1	AR1B_MOUSE
27	35	50.0	430	1	SYH_CHLPN
28	35	50.0	480	1	YQSI_CAEEL
29	35	50.0	749	1	VP4_ROTGA
30	35	50.0	851	1	EF2_CAEEL
31	35	50.0	857	1	EF2_CHICK
32	35	50.0	857	1	EF2_CHICK
33	35	50.0	857	1	EF2_HUMAN

34 35 50.0 857 1 EF2_MESAU
35 35 50.0 857 1 EF2_MOUSE
36 35 50.0 857 1 EF2_RAT
37 35 50.0 966 1 VJA_BBMV
38 35 50.0 4568 1 DYHC_CAEEL
39 34.5 49.3 727 1 KOGA_RAT
40 34.5 49.3 730 1 KOGA_MOUSE
41 34 48.6 198 1 PGD2_HUMAN
42 34 48.6 214 1 VIF_SIVS4
43 34 48.6 224 1 GTXA_ARATH
44 34 48.6 238 1 CCDA_BACHD
45 34 48.6 246 1 Y495_SINY3

P05086 mesocricetu
P38252 mus musculus
P05197 rattus norv
Q00020 broad bean
Q19020 caenorhabdi
P15556 rattus norv
O88673 mus musculus
O60760 homo sapien
P12505 simian immu
P46421 arabidopsis
Q9kdl8 bacillus ha
Q55185 synechocyst

ALIGNMENTS

RESULT 1
TRFL_HUMAN
ID TRFL_HUMAN STANDARD; PRT; 711 AA.
AC P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96K24;
AC Q96K25;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactoferrin precursor (lactoferrin) [Contains: Lactoferrin A;
DE Lactoferrin B; Lactoferrin C].
GN LTF OR LF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90384839; PubMed=2402455;
RA Rev M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";
RL Nucleic Acids Res. 18:5288-5288(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cho Y.Y.;
RL Thesis (1994), Genetic Engineering Research Institute / Taejeon, Korea.
RN [3]
RP SEQUENCE FROM N.A.
RA Connely O.M.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Liang Q., Jimenez-Flores R., Richardson T.;
RL "Molecular cloning and sequence analysis of human lactoferrin.";
RN Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Wei X., Han J., Rado T.A.;
RL "Human neutrophil lactoferrin coding and 5' flanking region DNA
sequences.";
RN Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cheng H., Chen X., Huan L.;
RL "cDNA cloning and sequence analysis of human lactoferrin.";
RN Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [8]

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE-Mammary Gland.
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ogden J.E.;
RL "Nucleotide sequence of human lactoferrin cDNA.";
RN Nucleic Acids Res. 18:4013-4013(1990).
[9]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
RL "Human lactotransferrin: amino acid sequence and structural
RT comparisons with other transferrins.";
RN Eur. J. Biochem. 145:659-666(1984).
[10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
Jolles P.;
RL "The present state of the human lactotransferrin sequence. Study and
RT alignment of the cyanogen bromide fragments and characterization of
RN N- and C-terminal domains.";
RX Biochim. Biophys. Acta 670:243-254(1981).
[11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
Jolles P.;
RL "An 88 amino acid long C-terminal sequence of human
RT lactotransferrin";
RN FEBS Lett. 142:107-110(1982).
[12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RL "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis.";
RN Blood 70:989-993(1987).
[13]
RP SEQUENCE OF 237-711 FROM N.A.
RX McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
Rao L., La Bastie M., Kaplan N., Greco T., Touchman J., Muzny D.,
Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
Sagripanti J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
[14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RL "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution.";
RN J. Mol. Biol. 209:711-734(1989).
[15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX Haridas M., Anderson B.F., Baker E.N.;
RL "Structure of human diferric lactoferrin refined at 2.2-A
RT resolution.";
RN Acta Crystallogr. D 51:629-646(1995).
[16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
Baker E.N.;
RL "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RN 253-->methionine mutant.";
RX Biochemistry 36:341-346(1997).
[17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RL "Structure of recombinant human lactoferrin expressed in Aspergillus
RT awamori.";
RX Acta Crystallogr. D 55:403-407(1999).
[18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RL "Structure of human apolactoferrin at 2.0-A resolution. Refinement
RT and analysis of ligand-induced conformational change.";
RN Acta Crystallogr. D 54:1319-1335(1998).
[19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.;
RL "Isolation and characterization of opioid antagonist peptides derived
RT from human lactoferrin.";
RN Agric. Biol. Chem. 54:1803-1810(1990).
[20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
Sugur J., Kumaramanickavel G., Munier F., Schorderet D.F.,
El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
Hejtmancik J.F., Teng C.T.;
RL "Familial subepithelial corneal amyloidosis (gelatinous drop-like
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RN Mol. Vision 4:31-32(1998).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC
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CC
CC EMBL; X53961; CAA37914.1; -
CC EMBL; U07643; AAB60124.1; -
CC EMBL; M93150; AAA36159.1; -
CC EMBL; M83202; AAA59511.1; -
CC EMBL; M83205; AAA58656.1; -
CC EMBL; M18642; AAA86665.1; -
CC EMBL; AF332168; AAG48753.1; -
CC EMBL; BC015822; AAH15822.1; -
CC EMBL; BC015823; AAH15823.1; -
CC EMBL; M73700; AAA59479.1; -
CC EMBL; X52941; CAA37116.1; -
CC EMBL; U95626; AAB57795.1; -
CC PIR; S11228; TPFUL.
CC PDB; 1LCF; 31-AUG-94.
CC PDB; 1LCT; 31-OCT-93.
CC PDB; 1LFG; 31-JUL-94.
CC PDB; 1LFH; 31-OCT-93.
CC PDB; 1LFI; 31-OCT-94.
CC PDB; 1LGB; 31-AUG-94.
CC PDB; 1LKA; 08-NOV-96.
CC PDB; 1DSN; 08-MAR-96.
CC PDB; 1HSE; 12-MAR-97.
CC PDB; 1VFD; 21-APR-97.

Query Match 92.9%; Score 65; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.00033;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARRMKVR 12
 |||||
 DB 39 CFQWARRMKVR 50

RESULT 2

TRFL_CAMDR STANDARD; PRT; 708 AA.
 AC Q9TUM0; Q9MZS5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;
 RA Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
 RL Int. Dairy J. 9:481-486(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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DR EMBL; AJ31674; CAB53387.1; -
 DR EMBL; AF165879; AAF82241.1; -
 DR HSSP; O77811; 1B1X.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PR00422; TRANSFERIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 708 BY SIMILARITY.
 FT REPEAT 20 363 LACTOTRANSFERRIN.
 FT REPEAT 364 708 1.
 FT REPEAT 64 64 BY SIMILARITY.
 FT DISULFID 28 55
 FT DISULFID 38 55 BY SIMILARITY.
 FT DISULFID 134 217 BY SIMILARITY.
 FT DISULFID 176 192 BY SIMILARITY.
 FT DISULFID 189 200 BY SIMILARITY.
 FT DISULFID 250 264 BY SIMILARITY.
 FT DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.
 FT DISULFID 424 703 BY SIMILARITY.
 FT DISULFID 444 666 BY SIMILARITY.
 FT DISULFID 476 551 BY SIMILARITY.
 FT DISULFID 500 694 BY SIMILARITY.
 FT DISULFID 510 524 BY SIMILARITY.
 FT DISULFID 521 534 BY SIMILARITY.
 FT DISULFID 592 606 BY SIMILARITY.
 FT DISULFID 644 649 BY SIMILARITY.
 FT METAL 79 79 IRON 1 (BY SIMILARITY).
 FT METAL 111 111 IRON 1 (BY SIMILARITY).
 FT METAL 211 211 IRON 1 (BY SIMILARITY).
 FT METAL 272 272 IRON 1 (BY SIMILARITY).
 FT METAL 414 414 IRON 2 (BY SIMILARITY).
 FT METAL 452 452 IRON 2 (BY SIMILARITY).
 FT METAL 545 545 IRON 2 (BY SIMILARITY).
 FT METAL 614 614 IRON 2 (BY SIMILARITY).
 FT BINDING 140 140 ANION (BY SIMILARITY).
 FT BINDING 482 482 ANION (BY SIMILARITY).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .)
 FT CONFLICT 261 261 F -> S (IN REF. 2).
 FT CONFLICT 304 304 G -> A (IN REF. 2).
 FT CONFLICT 330 330 S -> P (IN REF. 2).
 FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).
 FT CONFLICT 506 506 L -> F (IN REF. 2).
 FT CONFLICT 609 609 A -> P (IN REF. 2).
 FT CONFLICT 642 642 R -> Q (IN REF. 2).
 SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match 68.6%; Score 48; DB 1; Length 708;
 Best Local Similarity 66.7%; Pred. No. 0.39;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWARRMKVR 12
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 DB 38 CAQWARRMKVR 49

RESULT 3

TRFL_CAPHI STANDARD; PRT; 708 AA.
 ID TRFL_CAPHI
 AC Q29477; Q29479;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary Gland;
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=94380047; PubMed=8093048;
 RA Le Provost F., Nocart M., Guerin G., Martin P.;
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the relevant locus to bovine U12 syntenic group."
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; U53857; AAA97958.1; -;
 CC EMBL; X78902; CAA55517.1; -;
 CC HSP; O77698; 1CE2.
 CC Inter-Pro; IPR001156; Transferrin.
 CC Pfam; PF00405; transferrin; 2.
 CC PRINTS; PR00422; TRANSFERRIN.
 CC SMART; SM00094; TR_FER; 2.
 CC PROSITE; PS00205; TRANSFERRIN_1; 2.
 CC PROSITE; PS00206; TRANSFERRIN_2; 2.
 CC PROSITE; PS00207; TRANSFERRIN_3; 2.
 CC Transprot; Iron transport; Glycoprotein; Metal-binding; Repeat;
 CC Signal.
 CC -----
 CC FT CHAIN 1 19 BY SIMILARITY.
 CC FT REPEAT 20 708 LACTOTRANSFERRIN.
 CC FT REPEAT 364 708 1.
 CC FT DISULFID 28 64 BY SIMILARITY.
 CC FT DISULFID 38 55 BY SIMILARITY.
 CC FT DISULFID 134 217 BY SIMILARITY.
 CC FT DISULFID 176 192 BY SIMILARITY.
 CC FT DISULFID 189 200 BY SIMILARITY.
 CC FT DISULFID 250 264 BY SIMILARITY.
 CC FT DISULFID 367 399 BY SIMILARITY.
 CC FT DISULFID 377 390 BY SIMILARITY.
 CC FT DISULFID 424 703 BY SIMILARITY.
 CC FT DISULFID 444 666 BY SIMILARITY.
 CC FT DISULFID 476 551 BY SIMILARITY.
 CC FT DISULFID 500 694 BY SIMILARITY.
 CC FT DISULFID 510 524 BY SIMILARITY.
 CC FT DISULFID 521 534 BY SIMILARITY.
 CC FT DISULFID 592 606 BY SIMILARITY.
 CC FT DISULFID 644 649 BY SIMILARITY.
 CC FT METAL 79 IRON 1 (BY SIMILARITY).
 CC FT METAL 111 IRON 1 (BY SIMILARITY).
 CC FT METAL 211 IRON 1 (BY SIMILARITY).
 CC FT METAL 272 IRON 1 (BY SIMILARITY).
 CC FT METAL 414 IRON 2 (BY SIMILARITY).
 CC FT METAL 452 IRON 2 (BY SIMILARITY).
 CC FT METAL 545 IRON 2 (BY SIMILARITY).
 CC FT METAL 614 IRON 2 (BY SIMILARITY).
 CC FT BINDING 140 ANION (BY SIMILARITY).
 CC FT BINDING 482 ANION (BY SIMILARITY).
 CC FT CARBOHYD 252 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 300 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 387 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 495 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 564 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC FT CONFLICT 56 I -> V (IN REF. 2).
 CC FT CONFLICT 88 L -> R (IN REF. 2).
 CC FT CONFLICT 124 Q -> K (IN REF. 2).
 CC FT CONFLICT 154 F -> P (IN REF. 2).
 CC FT CONFLICT 304 S -> R (IN REF. 2).
 CC FT CONFLICT 414 D -> G (IN REF. 2).
 CC FT SEQUENCE 708 AA; 77358 MW; F2ED3C83539960D CRC64;

Query Match 68.6%; Score 48; DB 1; Length 708;
 Best Local Similarity 63.6%; Pred. No. 0.39;
 Matches 7; Conservative 2; Mismatches 0; Gaps 0;

QY 1 CFQWARRNRKV 11
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 Db 38 CYQWRMRKRL 48

RESULT 4
 NLA_DROME
 ID NLA_DROME STANDARD; PRT; 292 AA.
 AC OXZLG; Q9V391;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Nebula protein.
 GN NLA OR CG6072.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McCormick A.V., Goldberg M.L.;
 RT "Gene required for elongation of meiosis I spindle in Drosophila
 females.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiot E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Fertaz C., Ferreira S., Fleischmann W.,
 RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Liang P., Li Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhou L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
 CC -!- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.
 CC -----
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CC -----
CC EMBL; AF147700; AAD33987.1; -.
CC DR EMBL; AE003712; AAF55285.1; -.
CC DR FLYBase; FBGN0026629; nla.
CC SQ SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;

Query Match
Best Local Similarity 57.1%; Score 40; DB 1; Length 292;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 FOWARNMKVR 12
DB 150 FQMLRSFRLR 160

RESULT 5
SYN CHLMU
ID SYH CHLMU STANDARD; PRT; 428 AA.
AC Q9FJ09;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
DE (HIS)
DE (HIS)
GN HISS OR TC0830.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MOPN / Nig9;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Bruham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson M., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.
RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -1- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
CC di-phosphate + L-histidyl-tRNA(His).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; AE002349; AAF39630.1; -.
CC DR HSSP; Q32422; 1QE0.
CC DR TIGR; TC0830; -.
CC InterPro; IPR002106; AaRNA_ligaseII.
CC InterPro; IPR004154; HGTP_anticodon.
CC InterPro; IPR004516; Hiss.
CC InterPro; IPR002314; tRNA-synt 2b.
CC Pfam; PF00587; tRNA-synt 2b; 1.
CC DR TIGRFAMs; TIGR00442; Hiss; 1.
CC DR PROSITE; PS00862; AA tRNA_LIGASE II; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
SQ SEQUENCE 428 AA; 48939 MW; 9CF859ED05689DDF CRC64;

Query Match
Best Local Similarity 57.1%; Score 40; DB 1; Length 428;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

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OY 1 CPOARNMVR 9
DB 348 CFSWAKHLR 356

RESULT 6
TRFL HORSE
ID TRFL HORSE STANDARD; PRT; 695 AA.
AC O778L1;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin) (Fragment).
GN LTF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
RT "cDNA sequence of mare lactoferrin";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RC TISSUE=Milk;
RX MEDLINE=99296631; PubMed=10366507;
RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
RT "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
RT resolution."
RL J. Mol. Biol. 289:303-317(1999).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ010930; CAA09407.1; -.
CC DR PDB; 1B1X; 02-DEC-98.
CC DR PDB; 1B7U; 02-FEB-99.
CC DR PDB; 1B7Z; 02-FEB-99.
CC DR InterPro; IPR001156; Transferrin.
CC Pfam; PF00405; transferrin; 2.
CC DR PRINTS; PR00422; TRANSFERRIN.
CC SMART; SM00094; TR_FER; 2.
CC DR PROSITE; PS00205; TRANSFERRIN 1; 2.
CC DR PROSITE; PS00206; TRANSFERRIN 2; 2.
CC DR PROSITE; PS00207; TRANSFERRIN 3; 1.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal; 3D-structure.
FT NON TER 1 1
FT SIGNAL <1 6
FT CHAIN 7 695 LACTOTRANSFERRIN.
FT REPEAT 7 350 1.
FT REPEAT 351 695 2.
FT DISULFID 15 51
FT DISULFID 25 42
FT DISULFID 121 204
FT DISULFID 163 179
FT DISULFID 166 189
FT DISULFID 176 187
FT DISULFID 237 251
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CC EMBL; U09675; AAA19557.1; -
DR InterPro; IPR001572; RNA_POL_B.
DR Pfam; PF00562; RNA_POL_B; 1.
DR PROSITE; PS01166; RNA_POL_BETA; PARTIAL.
DR Transferrin; Transcription; DNA-directed RNA polymerase.
KW NON TPR 146
PT 146
SQ SEQUENCE 146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;

Query Match 55.7%; Score 39; DB 1; Length 146;
Best Local Similarity 60.0%; Pred. NO. 3.3;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CFQARNWRK 10
Db 10 CVQNSRGARK 19

RESULT 8
TRFL_MOUSE STANDARD; PRT; 707 AA.
AC P08071; P70690; Q61799; Q922P2;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
DE LTP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
OX [1]
RN RNP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=87280033; PubMed=3611056;
RA Pentecost B.T., Teng C.T.;
RT "Lactotransferrin is the major estrogen inducible protein of mouse
RL J. Biol. Chem. 262:10134-10139(1987).
RN [2]
RN RNP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX Moriishi K.;
RA Strausberg R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RN RNP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RN RNP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=92042099; PubMed=1999212;
RA Liu Y., Teng C.T.;
RT "Characterization of estrogen-responsive mouse lactoferrin promoter.";
RN J. Biol. Chem. 266:21880-21885(1991).
CC -|- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -|- SUBUNIT: MONOMER.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -|- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC
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CC
CC EMBL; J03298; AAA40525.1; -
CC EMBL; D88510; BAA13633.1; -
CC EMBL; BC006904; AAH06904.1; -

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DR EMBL; M74778; AAA39427.1; -.
DR PIR; A28438; A28438.
DR HSP; P02788; 1CB6.
DR MGD; MGI:96837; Lcf.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
FT SIGNAL.
FT CHAIN 1 19 BY SIMILARITY.
FT REPEAT 20 707 LACTOTRANSFERRIN.
FT REPEAT 20 357 1.
FT REPEAT 358 707 2.
FT DISULFID 27 63 BY SIMILARITY.
FT DISULFID 37 54 BY SIMILARITY.
FT DISULFID 133 216 BY SIMILARITY.
FT DISULFID 175 191 BY SIMILARITY.
FT DISULFID 188 199 BY SIMILARITY.
FT DISULFID 249 263 BY SIMILARITY.
FT DISULFID 366 398 BY SIMILARITY.
FT DISULFID 375 389 BY SIMILARITY.
FT DISULFID 423 702 BY SIMILARITY.
FT DISULFID 443 665 BY SIMILARITY.
FT DISULFID 475 550 BY SIMILARITY.
FT DISULFID 499 693 BY SIMILARITY.
FT DISULFID 509 523 BY SIMILARITY.
FT DISULFID 520 533 BY SIMILARITY.
FT DISULFID 591 605 BY SIMILARITY.
FT DISULFID 643 648 BY SIMILARITY.
FT METAL 78 78 IRON 1 (BY SIMILARITY).
FT METAL 110 110 IRON 1 (BY SIMILARITY).
FT METAL 210 210 IRON 1 (BY SIMILARITY).
FT METAL 271 271 IRON 1 (BY SIMILARITY).
FT METAL 413 413 IRON 2 (BY SIMILARITY).
FT METAL 451 451 IRON 2 (BY SIMILARITY).
FT METAL 544 544 IRON 2 (BY SIMILARITY).
FT METAL 613 613 IRON 2 (BY SIMILARITY).
FT BINDING 139 139 ANION (POTENTIAL).
FT BINDING 481 481 ANION (POTENTIAL).
FT CARBOHYD 118 118 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 494 494 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 1 2 MR -> IQG (IN REF. 1).
FT CONFLICT 25 25 R -> Q (IN REF. 2).
FT CONFLICT 82 82 M -> L (IN REF. 2).
FT CONFLICT 359 359 S -> T (IN REF. 2).
FT CONFLICT 382 382 A -> D (IN REF. 1).
FT CONFLICT 449 449 E -> G (IN REF. 2).
FT CONFLICT 629 629 L -> V (IN REF. 1).
SQ SEQUENCE 707 AA; 77865 MW; F26AE03404C19A8 CRC64;

Query Match 55.7%; Score 39; DB 1; Length 707;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWARMNRKV 11
DB 37 CLRQWNRKV 47

RESULT 9
YNR2_CABEL STANDARD; PRT; 783 AA.
AC Q21988;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein R13G10.2 in chromosome III.
GN R13G10.2.
OS Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
(1)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gardner A.E.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
(2)
RP REVISIONS.
RA Durbin R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: FAD (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
CC -----
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CC -----
CC EMBL; Z35602; CA84671.2; -.
CC WormPep; R13G10.2; CE35088.
CC InterPro; IPR002937; Amino_oxidase.
CC Pfam; PF01593; Amino_oxidase; 1.
CC Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.
FT NP_BIND 311 366 FAD (ADP PART) (POTENTIAL).
FT SEQUENCE 783 AA; 88799 MW; 8D087E96464DC908 CRC64;

Query Match 55.7%; Score 39; DB 1; Length 783;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWARMNRKV 12
DB 540 CIDWGRDQKVK 551

RESULT 10
PAPA_CHICK STANDARD; PRT; 422 AA.
AC Q90678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)
DE (PAF acetylhydrolase) (PAF 2-acylhydrolase) (LDL-associated
DE phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine
DE esterase) (1-alkyl-2-acetyl-glycerophosphocholine esterase).
GN PLA2G7.
OS Gallus gallus (Chicken).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC Gallus.
CC NCBI_TaxID=9031;
(1)
RP SEQUENCE FROM N.A.
RC Tissue=Spleen;
RX MEDLINE=96029630; PubMed=7592717;
RA Tjoelker L.W.; Eberhardt C.; Unger J.; Trong H.L.; Zimmerman G.A.;
RA McIntyre T.M.; Stafforini D.M.; Prescott S.M.; Gray P.W.;
RT "Plasma platelet-activating factor acetylhydrolase is a secreted
RT phospholipase A2 with a catalytic triad.";
J. Biol. Chem. 270:25481-25487 (1995).
CC -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
CC PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: 2-acetyl-1-alkyl-sn-glycero-3-phosphocholine +
CC H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.

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CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
CC
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CC
CC EMBL: U34278; AAC59717.1; --
CC InterPro: IPR000734; Lipase.
CC InterPro: IPR005065; PAF-AH_P_II.
CC InterPro: IPR000379; Serine_site.
CC Pfam: PF03403; PAF-AH_P_II; 1.
CC PROSITE: PS00120; LIPASE_SER; 1.
CC Hydroxylase; Lipid degradation; Glycoprotein; Signal.
CC SIGNAL 1 21 BY SIMILARITY.
CC CHAIN 22 422 PLATELET-ACTIVATING FACTOR
CC FT ACT SITE 266 266 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT SITE 289 289 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT SITE 345 345 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT CARBOHYD 331 331 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 422 AA; 47046 MW; 15A5C794376B9141 CRC64;
Query Match 54.3%; Score 38; DB 1; Length 422;
Best Local Similarity 54.5%; Pred. No. 15;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 FQWARMNRKV 12
DB 316 FQWARMNRKV 326
|||||:|:|:
RESULT 11
SYN CHLTR STANDARD; PRT; 428 AA.
AC O84547;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
(HISRS).
DE HIS OR C7543.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/WW-3/Cx;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kallman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.I., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RA "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis";
RL Science 282:754-759 (1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
CC diphosphate + L-histidyl-tRNA(His).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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CC

CC EMBL: AE001325; AAC68145.1; --
CC HSP: G32422; IQ50.
CC InterPro: IPR002106; AACRNA_ligaseII.
CC InterPro: IPR004154; HGTP_anticonodon.
CC InterPro: IPR004516; His.
CC InterPro: IPR002314; tRNA-synt 2b.
CC Pfam: PF00587; tRNA-synt 2b; 1.
CC Pfam: PF03129; HGTP_anticonodon; 1.
CC TIGRFAMs: TIGR00442; hisS; 1.
CC PROSITE: PS0862; AA_tRNA_LIGASE_II; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
SQ SEQUENCE 428 AA; 49189 MW; 9B9F59A096BD958 CRC64;
Query Match 54.3%; Score 38; DB 1; Length 428;
Best Local Similarity 45.5%; Pred. No. 15;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 CFQWARMNRKV 11
DB 348 CFQWARMNRKV 358
|||||:|:|:
RESULT 12
T100_HUMAN STANDARD; PRT; 989 AA.
ID T100_HUMAN
AC O75448; Q14143;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thyroid hormone receptor-associated protein complex 100 kDa component
(Trap100).
DE TRAP100 OR KIAA0130.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.
RX MEDLINE=98318590; PubMed=9653119;
RA Yuan C.-X., Ito M., Pondell J.D., Fu Z.-Y., Roeder R.G.;
RT "The TRAP220 component of a thyroid hormone receptor-associated
RT protein (TRAP) coactivator complex interacts directly with nuclear
RT receptors in a ligand-dependent fashion";
RL Proc. Natl. Acad. Sci. U.S.A. 95:7939-7944 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96127530; PubMed=8590280;
RA Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. IV.
RT The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by
RT analysis of cDNA clones from human cell line KG-1";
RL DNA Res. 2:167-174 (1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays a role in nuclear hormone receptor-mediated
CC transactivation.
CC -!- SUBUNIT: Does not directly bind nuclear hormone receptors.
CC Interacts and coprecipitates with Trap220.
CC -!- TISSUE SPECIFICITY: Ubiquitous. Abundant in skeletal
CC muscle, heart and placenta.
CC
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CC EMBL; AF055995; AAC39855.1; -.
CC EMBL; D50920; BAA09479.1; -.
CC EMBL; BC011375; AAH11375.1; -.
CC MIM; 607000; -.
KW Transcription regulation; Zinc-finger; Repeat; ATP-binding.
FT DOMAIN 128 861 6 X REPEATS OF L-X-X-L-L.
FT REPEAT 128 132 1.
FT REPEAT 344 348 2.
FT REPEAT 443 452 3.
FT REPEAT 557 561 4.
FT REPEAT 788 792 5.
FT REPEAT 857 861 6.
FT ZN_FING 93 117 POTENTIAL.
FT NP_BIND 436 448 ATP (POTENTIAL).
FT CONFLICT 20 20 D -> Y (IN REF. 2).
FT CONFLICT 204 204 A -> T (IN REF. 2).
SQ SEQUENCE 989 AA; 110304 MW; CCEDE7D4E74D890C CRC64;

Query Match 54.3%; Score 38; DB 1; Length 989;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQWARMRK 10
DB 21 YQWAINMK 29

RESULT 13
DYHB CHLRE STANDARD; PRT; 4568 AA.
AC Q39565;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Dynein beta chain, flagellar outer arm.
GN ODA4 OR ODA-4 OR SUP1.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=219;
RX MEDLINE=94274778; PubMed=8006077;
RA Mitchell D.R., Brown K.S.;
RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
chain genes."
RL J. Cell Sci. 107:635-644 (1994).
CC -!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC -!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
GAMMA). 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
CC -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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-----
CC EMBL; U02963; AAA19956.1; -.
CC InterPro; IPR004273; Dynein heavy.
CC Pfam; PF03028; Dynein heavy; 1.
KW Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
KW Coiled coil.
FT DOMAIN 277 293 COILED COIL (POTENTIAL).
FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).

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FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
FT DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
FT DOMAIN 2831 2848 COILED COIL (POTENTIAL).
FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
FT DOMAIN 3339 3425 COILED COIL (POTENTIAL).
FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
FT NP_BIND 1919 1926 ATP (POTENTIAL).
FT NP_BIND 2202 2209 ATP (POTENTIAL).
FT NP_BIND 2530 2537 ATP (POTENTIAL).
FT NP_BIND 2879 2886 ATP (POTENTIAL).
SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;

Query Match 54.3%; Score 38; DB 1; Length 4568;
Best Local Similarity 41.7%; Pred. No. 17e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWARMNRKVR 12
DB 1852 CFQWQSLRYIQ 1863

RESULT 14
Y708 METJA STANDARD; PRT; 172 AA.
AC Q58118;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0708.
GN MJ0708.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=36337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.B., Geoghegan N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."
RL Science 273:1058-1073 (1996).
CC -!- SIMILARITY: TO S.POMBE SPAC1F3.04C AND S.CEREVISIAE YOR006C.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC EMBL; U67517; AAB98703.1; -.
CC TIGR; MJ0708; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 172 AA; 20029 MW; 01CF25475AD10B2A CRC64;

Query Match 52.9%; Score 37; DB 1; Length 172;
Best Local Similarity 54.5%; Pred. No. 8.9;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWARMNRKV 11
DB 135 CFKWAETFKV 145

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RESULT 15
PDOI_ECOLI
ID_PDOI_ECOLI STANDARD; PRT; 211 AA.
AC P32174;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Formate dehydrogenase, cytochrome b556(FDO) subunit (Formate
DE dehydrogenase-O gamma subunit) (FDO-Z gamma subunit) (Aerobic formate
DE dehydrogenase cytochrome b556 subunit).
GN FDOI OR B3892 OR Z5434 OR ECS4818.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=93347969; PubMed=8346018;
RA Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
RT "Analysis of the Escherichia coli genome. III. DNA sequence of the
RT region from 87.2 to 89.2 minutes."
RL Nucleic Acids Res. 21:3391-3398(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.R., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RN [3]
RP Nature 409:529-533(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
RN [5]
RP CHARACTERIZATION.
RC STRAIN=K12.
RX MEDLINE=9609298; PubMed=8522521;
RA Abaibou H., Pommer J., Giordano G., Mandrand-Berthelot M.-A.;
RT "Expression and characterization of the Escherichia coli fdo locus
RT and a possible physiological role for aerobic formate
RT dehydrogenase."
RL J. Bacteriol. 177:7141-7149(1995).
RN [6]
RP TOPOLOGY.
RX MEDLINE=99069338; PubMed=9852007;
RA Benoit S., Abaibou H., Mandrand-Berthelot M.-A.;
RT "Topological analysis of the aerobic membrane-bound formate
RT dehydrogenase of Escherichia coli."
RL J. Bacteriol. 180:6625-6634(1998).
CC -1- FUNCTION: ALLOWS TO USE FORMATE AS MAJOR ELECTRON DONOR DURING
CC AEROBIC RESPIRATION. SUBUNIT GAMMA IS PROBABLY THE CYTOCHROME
CC B556 (FDO) COMPONENT OF THE FORMATE DEHYDROGENASE.
CC -1- SUBUNIT: FORMATE DEHYDROGENASE IS A MEMBRANE-BOUND COMPLEX, FORMED
CC BY SUBUNITS ALPHA, BETA AND GAMMA.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: STRONG, TO FDOI.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC -----
CC EMBL; LI9201; AAB03025.1; -.
DR EMBL; AF000464; AAD13454.1; -.
DR EMBL; AF005620; AAG59085.1; -.
DR EMBL; AP002567; BAB38241.1; -.
DR FIR; S40836; S40836.
DR EcoGene; Ecol1856; fdoI.
KW Electron transport; Heme; Iron; Transmembrane; Complete proteome.
FT DOMAIN 1 17 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 18 32 PROBABLE.
FT DOMAIN 33 53 PERIPLASMIC (PROBABLE).
FT TRANSMEM 54 72 PROBABLE.
FT DOMAIN 73 112 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 113 130 PROBABLE.
FT DOMAIN 131 151 PERIPLASMIC (PROBABLE).
FT TRANSMEM 152 170 PROBABLE.
FT DOMAIN 171 211 CYTOPLASMIC (PROBABLE).
SQ SEQUENCE 211 AA; 24606 MW; 166ACSA661C738D5 CRC64;
Query Match 52.9%; Score 37; DB 1; Length 211;
Best Local Similarity 62.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 4 WARMNRKV 11
DB 86 WAKNIRKI 95
Search completed: February 21, 2003, 07:27:46
Job time : 6.6 secs
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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	60	85.7	711	4	Q8TCD2	Q8tcd2 homo sapien
2	56	80.0	38	4	Q9UC5	Q9uc5 homo sapien
3	45	64.3	33	6	Q9TR80	Q9tr80 ovis aries
4	40	57.1	148	10	Q9XHL1	Q9xhl1 sesamum ind
5	40	57.1	273	2	Q31090	Q31090 rhizobium l
6	40	57.1	511	16	Q8Z462	Q8z462 salmonella
7	39	55.7	275	5	Q93780	Q93780 caenorhabdi
8	39	55.7	341	11	Q8R2A4	Q8r2a4 mus musculu
9	39	55.7	544	10	Q94921	Q949e1 arya sativa
10	39	55.7	866	10	Q9FHT9	Q9fht9 arabidopsis
11	39	55.7	1213	3	Q98011	Q98011 schizosacch
12	38	54.3	108	9	Q8SC55	Q8sc55 stx2 conver
13	38	54.3	120	4	Q9ETB8	Q9etb8 homo sapien
14	38	54.3	415	5	Q9U4M9	Q9u4m9 leishmania
15	38	54.3	489	16	P96223	P96223 mycobacteri
16	38	54.3	501	3	Q9UUD0	Q9uud0 schizosacch

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96081613; PubMed=8551695;
 RA Sato I.;
 RT "Characterization of the 84-kDa protein with ABH activity in human
 seminal plasma.";
 RL Jpn. J. Legal Med. 49:281-293(1995).
 DR HSP; P02788; IBA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 38 AA; 4459 MW; 0402F4905EBDDDB CRC64;

Query Match 80.0%; Score 56; DB 4; Length 38;
 Best Local Similarity 90.9%; Pred. No. 0.0014;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQWQNRKVR 12
 DB 21 FQWQNRKVR 31
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 ||| |||||

RESULT 3
 Q9TR80 PRELIMINARY; PRT; 33 AA.
 ID Q9TR80;
 AC Q9TR80;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Lactoferrin (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95127729; PubMed=7827104;
 RA Qian Z.Y., Joiles P., Migliore-Samouir D., Fiat A.M.;
 RL Biochim. Biophys. Acta 1243:25-32(1995).
 DR HSP; O77698; ICE2.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 64.3%; Score 45; DB 6; Length 33;
 Best Local Similarity 54.5%; Pred. No. 0.15;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWNRKVR 11
 DB 19 CYQWQNRKVR 29
 ||| : |||
 ||| : |||

RESULT 4
 Q9XHP1 PRELIMINARY; PRT; 148 AA.
 ID Q9XHP1;
 AC Q9XHP1;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE 2S albumin.
 OS Sesamum indicum (Oriental sesame) (Gingelly).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
 OX NCBI_TaxID=4182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TAINAN 1;
 RX MEDLINE=20074970; PubMed=10606554;
 RA Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;

RT "Molecular cloning of 11S globulin and 2S albumin, the two major seed
 storage proteins in sesame";
 RL J. Agric. Food Chem. 47:4932-4938(1999).
 DR EMBL; AF091841; AAD42943.1; -.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR00617; Napin.
 DR InterPro; IPR001768; Try/amy1_inhbr.
 DR Pfam; PF00234; tryp_alpha_aml; 1.
 DR PRINTS; PR00496; NAFIN.
 DR SMART; SM00499; AAI; 1.
 SQ SEQUENCE 148 AA; 17524 MW; BA46B033BA13B3DE CRC64;

Query Match 57.1%; Score 40; DB 10; Length 148;
 Best Local Similarity 66.7%; Pred. No. 6.8;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWNRKVR 9
 DB 54 CMQWNRKVR 62
 ||| |||||
 ||| |||||

RESULT 5
 O31090 PRELIMINARY; PRT; 273 AA.
 ID O31090;
 AC O31090;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Hypothetical 31.0 kDa protein.
 OS Rhizobium leguminosarum (biovar viciae).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=387;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF39;
 RA Ivashina T.V., Sadykov M.R., Kanapin A.A., Ksenzenko V.N.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF39;
 RX MEDLINE=99113394; PubMed=9914965;
 RA Sadykov M.R., Ivashina T.V., Kanapin A.A., Shlyapnikov M.G.,
 Ksenzenko V.N.;
 RT Structural and functional organization of the exopolysaccharide
 biosynthesis genes in Rhizobium leguminosarum bv. viciae VF39.";
 RL Mol. Biol. (Mosk) 32:797-804(1998).
 DR EMBL; AF028810; AAB8891.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 273 AA; 30986 MW; F195D2FEF7AD44D3 CRC64;

Query Match 57.1%; Score 40; DB 2; Length 273;
 Best Local Similarity 60.0%; Pred. No. 13;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWNRKVR 12
 DB 245 RWNRKVR 254
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 ||| : |||

RESULT 6
 Q8Z462 PRELIMINARY; PRT; 511 AA.
 ID Q8Z462;
 AC Q8Z462;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein STY3070.
 GN STY3070.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=601;

```

RN  SEQUENCE FROM N.A.
RP  STRAIN=CT18;
RX  MEDLINE=21534947; PubMed=11677608;
RA  Parhill J., Duggan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA  Churche C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA  Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA  Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA  Fellwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA  Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA  Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA  Whitehead S., Barrell B.G.;
RT  "Complete genome sequence of a multiple drug resistant Salmonella
RT  enterica serovar Typhi CT18."
RL  Nature 413:848-852(2001).
RW  EMBL; AL627276; CAD06049.1; --
KW  Hypothetical protein; Complete proteome.
SQ  SEQUENCE 511 AA; 58126 MW; E2DD124E10D178B CRC64;

Query Match      57.1%; Score 40; DB 16; Length 511;
Best Local Similarity 58.3%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1 CFQWARMKVR 12
    ||| ||| |||
Db  350 CFQWDMKVR 361

RESULT 7
Q93780 PRELIMINARY; PRT; 275 AA.
AC  Q93780;
DT  01-FEB-1997 (TrEMBLrel. 02, Created)
DT  01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  F53H4.4 protein.
GN  F53H4.4
OS  Caenorhabditis elegans.
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC  Rhabditidae; Peloderinae; Caenorhabditis.
OX  NCBI_TaxID=6239;
RN  SEQUENCE FROM N.A.
RP  Dobson R.;
RA  Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN  [2]
SQ  SEQUENCE FROM N.A.
RX  MEDLINE=99069613; PubMed=9851916;
RA  none;
RT  "Genome sequence of the nematode C.elegans: A platform for
RT  investigating biology."
RL  Science 282:2012-2018(1998).
DR  EMBL; Z81089; CAB03137.1; --
SQ  SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;

Query Match      55.7%; Score 39; DB 5; Length 275;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy  2 FQWARMKVR 12
    ||| ||| |||
Db  262 FQWKSMKVR 272

RESULT 8
Q8R2A4 PRELIMINARY; PRT; 341 AA.
AC  Q8R2A4;
DT  01-JUN-2002 (TrEMBLrel. 21, Created)
DT  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Vomeronasal receptor VIRE6.
GN  VIRE6.

```

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OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  STRAIN=129X1/SVJ;
RX  MEDLINE=21676859; PubMed=11802169;
RT  Rodriguez I., Del Punta K., Rothman A., Ishii T., Mombaerts P.;
RT  "Multiple new and isolated families within the mouse superfamily of
RT  V1r vomeronasal receptors."
RL  Nat. Neurosci. 5:134-140(2002).
DR  EMBL; AY065506; AAL47911.1; --
KW  Receptor.
SQ  SEQUENCE 341 AA; 39632 MW; B3D8259F7AD11130 CRC64;

Query Match      55.7%; Score 39; DB 11; Length 341;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy  1 CFQWARMNR 9
    ||| ||| |||
Db  331 CFTWTRNIK 339

RESULT 9
Q949E1 PRELIMINARY; PRT; 544 AA.
AC  Q949E1;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE  Lipase-like protein.
GN  W485ERIPDM.
OS  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC  Ehrhartoideae; Oryzae; Oryza.
OX  NCBI_TaxID=4530;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21329048; PubMed=11435398;
RA  Mayer K., Murphy G., Tarchini R., Wambutt R., Volckaert G., Pohl T.,
RA  Duysterhoeft A., Stiekema W., Entian K.D., Terry N., Lemcke K.,
RA  Haase D., Hall C.R., van Dodeweerd A.M., Tingey S.V., Mewes H.W.,
RA  Bevan M., Bancroft I.;
RT  "Conservation of microstructure between a sequenced region of the
RT  genome of rice and multiple segments of the genome of Arabidopsis
RT  thaliana."
RL  Genome Res. 11:1167-1174(2001).
DR  EMBL; AJ307662; CAC39051.1; --
DR  InterPro; IPR000734; Lipase.
DR  InterPro; IPR002921; Lipase_3.
DR  InterPro; IPR000379; Ser_estrs_site.
DR  Pfam; PF01764; Lipase_3; 1.
DR  PROSITE; PS00120; LIPASE_SER; UNKNOWN 1.
SQ  SEQUENCE 544 AA; 58895 MW; CF42105BPEC29A5B CRC64;

Query Match      55.7%; Score 39; DB 10; Length 544;
Best Local Similarity 55.6%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy  1 CFQWARMNR 9
    ||| ||| |||
Db  290 CLEWAENLR 298

RESULT 10
Q9FHI9 PRELIMINARY; PRT; 866 AA.
AC  Q9FHI9;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Genomic DNA, chromosome 5, pl clone:MFC19.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids 1; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=99397451; PubMed=10470850;
 RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
 RA Miyajima N., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.
 RT Sequence features of the regions of 1,011,550 bp covered by seventeen
 RT pl and TAC clones."
 RL DNA Res. 6:183-195(1999).
 DR EMBL: AB018113; EMB0175.1; -;
 SQ SEQUENCE 866 AA; 100187 MW; 164FAB9B4976D27D CRC64;
 Query Match 55.7%; Score 39; DB 10; Length 866;
 Best Local Similarity 50.0%; Pred. No. 70;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CFQWARMKVR 12
 |||
 Db 389 CFNWLKFKLR 400
 |||
 RESULT 11
 O59801 PRELIMINARY; PRT; 1213 AA.
 ID C59801
 AC C59801; 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Putative DEAD/DEAH box helicase.
 GN SPCC550.03C.
 OS Schizosaccharomyces pombe (Pission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972H-;
 RA Murphy L., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL023592; CAA19107.1; -;
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; Helicase_C; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC; 1.
 KW ATP-binding; Helicase.
 SQ SEQUENCE 1213 AA; 138027 MW; 2F9BE2ABF8068A37 CRC64;
 Query Match 55.7%; Score 39; DB 3; Length 1213;
 Best Local Similarity 62.5%; Pred. No. 18+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWARMN 8
 |||
 Db 1141 CYEWARGM 1148
 |||
 RESULT 12
 Q8SC55 PRELIMINARY; PRT; 108 AA.
 ID Q8SC55
 AC Q8SC55;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 12.3 kDa protein.
 OS Stx2 converting bacteriophage I.
 OC Viruses.
 OX NCBI_TaxID=180816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=STX2 PHAGE-I;
 RA Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T.,
 RA Yanasaki S., Takeda Y.;
 RT "Genomic sequence of Shiga toxin 2-converting phage isolated from
 RT Escherichia coli O157:H7 Okayama strain and comparison with other
 RT Shiga toxin 2-converting phages."
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP004402; BAB87947.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 108 AA; 12279 MW; 2FF2E76690C78BA7 CRC64;
 Query Match 54.3%; Score 38; DB 9; Length 108;
 Best Local Similarity 60.0%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWARMNRK 10
 |||
 Db 31 CFQWISDNRK 40
 |||
 RESULT 13
 Q9BTB8 PRELIMINARY; PRT; 120 AA.
 ID Q9BTB8
 AC Q9BTB8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Similar to laminin, alpha 4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PANCREAS;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC004241; AAH04241.1; -;
 SQ SEQUENCE 120 AA; 12818 MW; 6ABF63CBA663BF3F CRC64;
 Query Match 54.3%; Score 38; DB 4; Length 120;
 Best Local Similarity 60.0%; Pred. No. 13;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 FQWARMNRKV 11
 |||
 Db 104 FTWARSVRKL 113
 |||
 RESULT 14
 Q9U4M9 PRELIMINARY; PRT; 415 AA.
 ID Q9U4M9
 AC Q9U4M9; 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE 7138.2.
 GN 7138.2.
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Ravel C., Dubessay P., Blaineau C., Lignon M.-F., Bastien P.,
 RA Dedet J.-P., Pages M.;

Job time : 21.8 secs

RT "Leishmania major chromosome 5 complete sequence."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF163772; AAP14642.1; -
 DR InterPro; IPR003409; MORN.
 DR Pfam; PF02493; MORN; 4.
 SQ SEQUENCE 415 AA; 46701 MW; 3E3AD710BF23691E CRC64;

Query Match 54.3%; Score 38; DB 5; Length 415;
 Best Local Similarity 66.7%; Pred. No. 49;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWARRNR 9
 Db 272 CGEWFRRNR 280

RESULT 15

P96223 PRELIMINARY; PRT; 489 AA.
 AC P96223;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 55.3 kDa protein (Monooxygenase, flavin-binding family).
 DE RV3854C OR MTCY01A6.14 OR MT3969.
 GN Mycobacterium tuberculosis.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 CX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagers K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / OSHKOSH;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Esmolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z83864; CAB06212.1; -
 DR EMBL; AE007188; AAK48336.1; -
 DR TIGR; MT3969; -
 DR Mycobacterium tuberculosis.
 DR RV3854c; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 489 AA; 55326 MW; 844611B7E831180D CRC64;

Query Match 54.3%; Score 38; DB 16; Length 489;
 Best Local Similarity 54.3%; Pred. No. 59;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWARRNRKV 11
 Db 253 CGKWFRRMRKM 263

Search completed: February 21, 2003, 07:44:24

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds
(without alignments)
56.502 Million cell updates/sec

Title: US-09-743-107b-73

Perfect score: 70

Sequence: 1 CFQWQANRKR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	12	21	AAV78073 Human lactoferrin
2	65	92.9	12	21	AAV78038 Human lactoferrin
3	65	92.9	12	21	AAV78046 Human lactoferrin
4	65	92.9	12	21	AAV78047 Human lactoferrin
5	65	92.9	12	21	AAV78081 Human lactoferrin
6	65	92.9	12	21	AAV78085 Human lactoferrin
7	65	92.9	13	21	AAV78037 Human lactoferrin
8	65	92.9	13	21	AAV78048 Human lactoferrin
9	65	92.9	13	21	AAV78049 Human lactoferrin
10	65	92.9	14	21	AAV78036 Human lactoferrin

11	65	92.9	14	21	AAV78050 Human lactoferrin
12	65	92.9	14	21	AAV78051 Human lactoferrin
13	65	92.9	15	17	AAV78054 Peptide for anti-u
14	65	92.9	15	21	AAV78035 Human lactoferrin
15	65	92.9	15	21	AAV78062 Human lactoferrin
16	65	92.9	15	21	AAV78063 Human lactoferrin
17	65	92.9	16	21	AAV78031 Human lactoferrin
18	65	92.9	16	21	AAV78064 Human lactoferrin
19	65	92.9	16	21	AAV78065 Human lactoferrin
20	65	92.9	17	21	AAV78034 Human lactoferrin
21	65	92.9	17	21	AAV78066 Human lactoferrin
22	65	92.9	17	21	AAV78067 Human lactoferrin
23	65	92.9	18	15	AAV78067 Human lactoferrin
24	65	92.9	18	17	AAV78033 Advanced glycosyla
25	65	92.9	18	21	AAV78033 Human lactoferrin
26	65	92.9	19	21	AAV68867 Amino acid sequenc
27	65	92.9	19	21	AAV78032 Human lactoferrin
28	65	92.9	20	13	AAV21810 Anti microbial pep
29	65	92.9	20	14	AAV44841 Lactoferrin-relate
30	65	92.9	20	14	AAV48530 Lactoferrin derive
31	65	92.9	20	15	AAV48531 Lactoferrin derive
32	65	92.9	20	15	AAV57461 Lactoferrin derive
33	65	92.9	20	15	AAV57462 Lactoferrin derive
34	65	92.9	20	16	AAV84698 Bovine lactoferrin
35	65	92.9	20	16	AAV84699 Bovine lactoferrin
36	65	92.9	20	16	AAV80283 Anti-parasitic lac
37	65	92.9	20	16	AAV80284 Anti-parasitic lac
38	65	92.9	20	17	AAV98553 Peptide for anti-u
39	65	92.9	20	17	AAV91852 Lactoferrin-derive
40	65	92.9	20	17	AAV03045 Lactoferrin-derive
41	65	92.9	20	17	AAV90607 Lactoferrin derive
42	65	92.9	20	17	AAV87621 Lactoferrin-derive
43	65	92.9	20	17	AAV87622 Lactoferrin-derive
44	65	92.9	20	18	AAV26150 Lactoferrin deriva
45	65	92.9	20	18	AAV14036 Anti-parasitic pep

ALIGNMENTS

RESULT 1
AAV78073
ID AAV78073 standard; Peptide; 12 AA.
XX AAV78073;
AC AAV78073;
XX 25-APR-2000 (first entry)
DT Human lactoferrin derived peptide SEQ ID NO:73.
DE Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX Homo sapiens.
OS Synthetic.
XX WO200001730-A1.
FN 13-JAN-2000.
PD 06-JUL-1999; 99WO-SE01230.
PF 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX (ASCI-) A+ SCI INVEST AB.
PI Hanson LA, Matthey-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 PS Claim 22; Page 35; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 70; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFQWQANMKVR 12
 DB 1 CFQWQANMKVR 12
 RESULT 2
 AAY78038
 ID AAY78038 standard; Peptide; 12 AA.
 XX
 AC AAY78038;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human lactoferrin derived peptide SEQ ID NO:38.
 XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 PF 06-JUL-1999; 99WO-SF01230.
 XX
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 PA (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX
 DR WPI; 2000-147388/13.
 XX
 PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 PS Claim 12; Page 70; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 12 AA;
 Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 7.6e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQANMKVR 12
 DB 1 CFQWQANMKVR 12
 RESULT 3
 AAY78046
 ID AAY78046 standard; Peptide; 12 AA.
 XX
 AC AAY78046;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human lactoferrin derived peptide SEQ ID NO:46.
 XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 PF 06-JUL-1999; 99WO-SF01230.
 XX
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 PA (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX
 DR WPI; 2000-147388/13.
 XX
 PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 PS Claim 15; Page 35; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;
 Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 7.6e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQANMKVR 12
 |||||
 DB 1 CFQWQANMKVR 12

RESULT 4
 AAY78047
 ID AAY78047 standard; Peptide; 12 AA.

XX AC AAY78047;
 XX DT 25-APR-2000 (first entry)
 XX DE Human lactoferrin derived peptide SEQ ID NO:47.
 XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200001730-A1.
 XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.
 XX PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1999; 98SE-0004614.
 XX PA (ASCI-) A+ SCI INVEST AB.
 XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 18; Page 73; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;
 Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 7.6e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQANMKVR 12
 |||||
 DB 1 CFQWQANMKVR 12

RESULT 5
 AAY78081
 ID AAY78081 standard; Peptide; 12 AA.

XX AC AAY78081;
 XX DT 25-APR-2000 (first entry)
 XX DE Human lactoferrin derived peptide SEQ ID NO:81.
 XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200001730-A1.
 XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.
 XX PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1999; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.
 XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 22; Page 36; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;
 Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 7.6e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12
 |||||
 Db 1 CFQWQANMKVR 12

RESULT 6

AY78085
 ID AAY78085 standard; Peptide; 12 AA.

XX AAY78085;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:85.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

FN 13-JAN-2000.

PD 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1999; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

PI WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 22; Page 36; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumors. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;

Best Local Similarity 91.7%; Pred. No. 7.6e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12

Db 1 CFQWQANMKVR 12

RESULT 7

AAY78037

ID AAY78037 standard; Peptide; 13 AA.

XX AAY78037;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:37.

XX Human; lactoferrin; modification; infection; inflammation; tumour;

KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

KW urinary tract infection; colitis; Candida infection; fungicidal;

KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

FN 13-JAN-2000.

PD 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

PI WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumors. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. No. 8.2e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12

Db 2 CFQWQANMKVR 13

RESULT 8

AAY78048

ID AAY78048 standard; Peptide; 13 AA.

XX AAY78048;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:48.

XX Human, lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 74; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 13 AA;
 SQ Query Match 92.9%; Score 65; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 8-2e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQNNRKVR 12
 DB 2 CFQWQNNRKVR 13
 RESULT 9
 AAY78049
 ID AAY78049 standard; Peptide; 13 AA.
 AC AAY78049;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:49.
 DE Human, lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS

OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 18; Page 74; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 13 AA;
 SQ Query Match 92.9%; Score 65; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 8-2e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQNNRKVR 12
 DB 2 CFQWQNNRKVR 13
 RESULT 10
 AAY78036
 ID AAY78036 standard; Peptide; 14 AA.
 AC AAY78036;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:36.
 DE Human, lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 PF

XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 12; Page 69; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 14 AA;
 SQ Query Match 92.9%; Score 65; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 8.9e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQANMKVR 12
 DB ||||| |||||
 3 CFQWQANMKVR 14
 RESULT 11
 AAY78050
 ID AAY78050 standard; Peptide; 14 AA.
 XX AC AAY78050;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:50.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 OS WO200001730-A1.
 PN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 12; Page 69; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 14 AA;
 SQ Query Match 92.9%; Score 65; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 8.9e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQANMKVR 12
 DB ||||| |||||
 3 CFQWQANMKVR 14
 RESULT 12
 AAY78051
 ID AAY78051 standard; Peptide; 14 AA.
 XX AC AAY78051;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:51.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 OS WO200001730-A1.
 PN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 75; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 14 AA;
 SQ Query Match 92.9%; Score 65; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 8.9e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQANMKVR 12
 DB ||||| |||||
 3 CFQWQANMKVR 14
 RESULT 12
 AAY78051
 ID AAY78051 standard; Peptide; 14 AA.
 XX AC AAY78051;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:51.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 OS WO200001730-A1.
 PN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

PS Claim 18; Page 75; 102pp; English.

CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX Sequence 14 AA;

SQ Query Match 92.9%; Score 65; DB 21; Length 14;
Best Local Similarity 91.7%; Pred. No. 8.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12
Db ||||| |||||
3 CFQWQANMKVR 14

RESULT 13

AAR98554
ID AAR98554 standard; Peptide; 15 AA.

XX AAR98554;
AC

XX 12-NOV-1996 (first entry)

XX Peptide for anti-ulcer agent.

XX anti-ulcer agent; low toxicity; stable; heat-resistant.

XX Synthetic.

XX JP08143468-A.

XX 04-JUN-1996.

XX 17-NOV-1994; 94JP-0283869.

XX 17-NOV-1994; 94JP-0283869.

XX (MORG) MORINAGA MILK IND CO LTD.

XX WPI; 1996-318857/32.

XX Anti-ulcer agent contg. peptide - has low toxicity, is
PT heat-resistant and water-soluble

XX Claim 1; Page 11; 11pp; Japanese.

XX AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be
CC administered orally and be produced in large amounts.

XX Sequence 15 AA;

SQ Query Match 92.9%; Score 65; DB 17; Length 15;
Best Local Similarity 91.7%; Pred. No. 9.5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12
Db ||||| |||||
2 CFQWQANMKVR 13

RESULT 14

AAY78035

ID AAY78035 standard; Peptide; 15 AA.

XX AAY78035;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:35.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.

XX Homo sapiens.

XX Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 69; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX Sequence 15 AA;

SQ Query Match 92.9%; Score 65; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 9.5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12
Db ||||| |||||
4 CFQWQANMKVR 15

RESULT 15

RAY78062

ID AAY78062 standard; Peptide; 15 AA.

XX

AC AAY78062;

Tue Dec 9 06:51:29 2003

```

XX 25-APR-2000 (first entry)
DT Human lactoferrin derived peptide SEQ ID NO:62.
DE Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX WO200001730-A1.
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-S01230.
XX
XX 06-JUL-1998; 98SE-0002441.
XX 17-JUL-1998; 98SE-0002562.
XX 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI, 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
XX inflammations and tumors and for use in infant formula food -
XX
XX Claim 15; Page 81; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
XX lactoferrin. The peptides are taken up in the intestine through
XX binding to specific lactoferrin receptors and are then transported
XX through the circulation. A medicinal product of the peptide or fragment
XX can be used for treating and/or prevention of infections (such as
XX urinary tract infections, colitis, and Candida infection on a mucosal
XX membrane), inflammations and/or tumors. The peptides can also be used
XX in food stuffs such as infant formula food. The peptides are also
XX fungicidal and bactericidal and may also be used as preservatives.
XX Even though native human lactoferrin have been shown to have desired
XX anti-inflammatory anti-infectious and anti-tumoural properties they
XX cannot be used clinically on a broad basis because of high production
XX costs. Therefore, provision of peptides based on lactoferrin would
XX enable them to be used for the same purposes as lactoferrin at lower
XX cost.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 92.9%; Score 65; DB 21; Length 15;
XX Best Local Similarity 91.7%; Pred. NO. 9.5e-05;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 CFQWQNNRKVR 12
XX |||||
XX Db 4 CFQWQNNRKVR 15
XX
XX Search completed: February 21, 2003, 07:37:12
XX Job time : 29.35 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 Seconds
(without alignments)
40.818 Million cell updates/sec

Title: US-09-743-107B-73
Perfect score: 70
Sequence: 1 CFQWQANMRKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	18	1	US-08-204-487-3
2	65	92.9	18	2	US-08-485-948-8
3	65	92.9	18	2	US-08-628-380-8
4	65	92.9	18	2	US-08-475-055-8
5	65	92.9	20	1	US-07-755-161A-3
6	65	92.9	20	1	US-07-891-174-3
7	65	92.9	20	1	US-08-204-487-1
8	65	92.9	20	1	US-08-256-771-24
9	65	92.9	20	1	US-08-256-771-25
10	65	92.9	20	1	US-08-381-984-24
11	65	92.9	20	1	US-08-381-984-25
12	65	92.9	22	4	US-08-508-734-4
13	65	92.9	24	4	US-08-508-734-6
14	65	92.9	25	1	US-07-755-161A-10
15	65	92.9	25	1	US-07-891-174-10
16	65	92.9	25	1	US-08-204-487-7
17	65	92.9	25	4	US-09-508-734-8
18	65	92.9	35	1	US-07-755-161A-8
19	65	92.9	36	1	US-07-891-174-8
20	65	92.9	36	1	US-08-256-771-30
21	65	92.9	36	1	US-08-381-984-29
22	65	92.9	47	2	US-08-464-182A-6
23	65	92.9	47	2	US-08-406-271-6
24	65	92.9	50	2	US-08-693-274A-7
25	65	92.9	52	4	US-09-017-043A-3
26	65	92.9	53	2	US-08-464-182A-5
27	65	92.9	53	2	US-08-406-271-5

28 65 92.9 54 2 US-08-464-182A-2
29 65 92.9 54 2 US-08-406-271-2
30 65 92.9 694 3 US-08-724-586-2
31 65 92.9 694 4 US-09-421-632-2
32 65 92.9 694 4 US-09-932-190-2
33 65 92.9 705 2 US-08-655-840-2
34 65 92.9 708 2 US-08-655-840-4
35 65 92.9 711 1 US-08-154-019-4
36 65 92.9 711 1 US-08-461-333-4
37 65 92.9 711 3 US-08-464-167-4
38 65 92.9 711 3 US-09-158-313-4
39 65 92.9 711 4 US-08-476-798-4
40 62 88.6 711 1 US-08-145-681-2
41 62 88.6 711 1 US-08-250-308-2
42 62 88.6 711 1 US-08-453-703-2
43 62 88.6 711 2 US-08-456-106-2
44 62 88.6 711 3 US-08-456-108-2
45 62 88.6 711 4 US-09-265-577-2

ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/082044487
; Patent No. 5563425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, TOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: RJN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37) "
US-08-204-487-3

Query Match 92.9%; Score 65; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 3.5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQANRKYR 12
||| |||||
Db 1 CFQWQANRKYR 12

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,948
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,217
; FILING DATE: JUNE 7, 1995
; APPLICATION NUMBER: 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal

US-08-485-948-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 3.5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQANRKYR 12
||| |||||
Db 1 CFQWQANRKYR 12

RESULT 3

US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341
; GENERAL INFORMATION:
; APPLICANT: LI, YONG MING
; APPLICANT: VLASSARA, HELEN
; APPLICANT: CERAMI, ANTHONY
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,380
; FILING DATE: April 4, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal

US-08-628-380-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 3.5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQANRKYR 12
||| |||||
Db 1 CFQWQANRKYR 12

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Klauber & Jackson
;; STREET: 411 Hackensack Avenue
;; CITY: Hackensack
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07601
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: PC-DOS/MS-DOS
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/475,055
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/485,948
;; FILING DATE:
;; APPLICATION NUMBER: 08/488,217
;; FILING DATE: JUNE 7, 1995
;; APPLICATION NUMBER: 08/418,642
;; FILING DATE: APRIL 7, 1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 947-1-008A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; DESCRIPTION: LF-C1, 8-25
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
;; US-08-475-055-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 3.5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12
| | | | | | | | | | | | | | | |
Db 1 CFQWQNNRKVR 12

RESULT 5
US-07-755-161A-3
; Sequence 3, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: DisplayWrite
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/755.161A
;; FILING DATE: 19910905
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX: 202-371-8856
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE:
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; CELL LINE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY: modified site
;; LOCATION: 2
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 19"
;; FEATURE:
;; NAME/KEY: modified site
;; LOCATION: 19
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 2"
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
;; US-07-755-161A-3

Query Match 92.9%; Score 65; DB 1; Length 20;

Best Local Similarity 91.7%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMRKVR 12
| | | | | | | | | |
Db 2 CFQWQANMRKVR 13

RESULT 6
US-07-891-174-3
; Sequence 3, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Creech Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGE:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMRKVR 12
| | | | | | | | | |
Db 2 CFQWQANMRKVR 13

RESULT 7
US-08-204-487-1
; Sequence 1, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGRAKI
; APPLICANT: DOSAKO, SHUN-ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIAKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: RUN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000

```

; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..20
; OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
; OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
; US-08-204-487-1
;
; Query Match 92.9%; Score 65; DB 1; Length 20;
; Best Local Similarity 91.7%; Pred. No. 3.8e-05;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 CFQWQNNRKVR 12
; DB 2 CFQWQNNRKVR 13
;
; RESULT 8
; US-08-256-771-24
; Sequence 24, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,771
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are linked by
; OTHER INFORMATION: disulfide bond"
;
; Query Match 92.9%; Score 65; DB 1; Length 20;
; Best Local Similarity 91.7%; Pred. No. 3.8e-05;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 CFQWQNNRKVR 12
; DB 2 CFQWQNNRKVR 13
;
; RESULT 9
; US-08-256-771-25
; Sequence 25, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,771
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are protected to
; OTHER INFORMATION: prevent disulfide bond"
;
; Query Match 92.9%; Score 65; DB 1; Length 20;
; Best Local Similarity 91.7%; Pred. No. 3.8e-05;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 CFQWQNNRKVR 12
; DB 2 CFQWQNNRKVR 13
;
; RESULT 10
; US-08-381-984-24
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/ Sequence 24, Application US/08381984
/ Patent No. 5804555
/ GENERAL INFORMATION:
/ APPLICANT: Mamoru TOMITA et al.
/ TITLE OF INVENTION: ANTIOXIDANT
/ NUMBER OF SEQUENCES: 32
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Wenderoth, Lind & Ponack
/ STREET: 805 Fifteenth Street, N.W., #700
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: Wordperfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/381.984
/ FILING DATE: April 11, 1995
/ CLASSIFICATION: 252
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warren M. Cheek, Jr.
/ REGISTRATION NUMBER: 33,367
/ REFERENCE/DOCKET NUMBER:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-8850
/ TELEFAX:
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY:
/ LOCATION:
/ IDENTIFICATION METHOD:
/ OTHER INFORMATION: /note= "cysteine residues at positions 2
/ OTHER INFORMATION: and 19 are bonded by disulfide linkage"
/ FEATURE:
/ NAME/KEY:
/ LOCATION:
/ IDENTIFICATION METHOD:
/ OTHER INFORMATION: /note= "the specified peptide as well as
/ OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
/ US-08-381-984-24

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMRKVR 12
DB 2 CFQWQANMRKVR 13

RESULT 11
US-08-381-984-25
/ Sequence 25, Application US/08381984
/ Patent No. 5804555
/ GENERAL INFORMATION:
/ APPLICANT: Mamoru TOMITA et al.
/ TITLE OF INVENTION: ANTIOXIDANT
/ NUMBER OF SEQUENCES: 32
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Wenderoth, Lind & Ponack

/ STREET: 805 Fifteenth Street, N.W., #700
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: Wordperfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/381.984
/ FILING DATE: April 11, 1995
/ CLASSIFICATION: 252
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warren M. Cheek, Jr.
/ REGISTRATION NUMBER: 33,367
/ REFERENCE/DOCKET NUMBER:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-8850
/ TELEFAX:
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 25:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY:
/ LOCATION:
/ IDENTIFICATION METHOD:
/ OTHER INFORMATION: /note= "the specified peptide as well as
/ OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
/ FEATURE:
/ NAME/KEY:
/ LOCATION:
/ IDENTIFICATION METHOD:
/ OTHER INFORMATION: /note= "cysteine residues at positions 2
/ OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
/ US-08-381-984-25

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMRKVR 12
DB 2 CFQWQANMRKVR 13

RESULT 12
US-09-508-734-4
/ Sequence 4, Application US/09508734
/ Patent No. 6423509
/ GENERAL INFORMATION:
/ APPLICANT: Samyang Genex Corporation
/ TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
/ FILE REFERENCE: useful microorganism thereof
/ FILE REFERENCE: PA/SYG/00139
/ CURRENT APPLICATION NUMBER: US/09/508.734
/ CURRENT FILING DATE: 2000-06-01
/ PRIOR APPLICATION NUMBER: PCT/KR99/00373
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: KR1998-299351
/ PRIOR FILING DATE: 1998-07-13
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: Kopatentin 1.71
/ SEQ ID NO 4

; LENGTH: 22

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-508-734-4

Query Match 92.9%; Score 65; DB 4; Length 22;

Best Local Similarity 91.7%; Pred. No. 4.2e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNNRKVR 12

Db 2 CFQWQNNRKVR 13

RESULT 13

US-09-508-734-6

; Sequence 6, Application US/09508734

; Patent No. 6423509

; GENERAL INFORMATION:

; APPLICANT: Samyang Genex Corporation

; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and

; FILE REFERENCE: PA/SYG/00139

; CURRENT APPLICATION NUMBER: US/09/508,734

; PRIOR FILING DATE: 2000-06-01

; PRIOR FILING DATE: 1999-07-14

; PRIOR FILING DATE: 1998-07-13

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: KopatentIn 1.71

; SEQ ID NO 6

; LENGTH: 24

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-508-734-6

Query Match

Best Local Similarity 92.9%; Score 65; DB 4; Length 24;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNNRKVR 12

Db 3 CFQWQNNRKVR 14

RESULT 14

US-07-755-161A-10

; Sequence 10, Application US/07755161A

; Patent No. 5304633

; GENERAL INFORMATION:

; APPLICANT: Mamoru TOMITA et al.

; TITLE OF INVENTION: Antimicrobial Peptides and an

; TITLE OF INVENTION: Antimicrobial Agent

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500KB

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: DisplayWrite

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/755,161A

; FILING DATE: 19910905

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-8850

; TELEFAX: 202-371-8856

; TELEX:

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 25 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE:

; HYPOTHETICAL:

; ANTI-SENSE:

; FRAGMENT TYPE:

; ORIGINAL SOURCE:

; ORGANISM:

; STRAIN:

; INDIVIDUAL ISOLATE:

; DEVELOPMENTAL STAGE:

; HAPLOTYPE:

; TISSUE TYPE:

; CELL TYPE:

; CELL LINE:

; ORGANELLE:

; IMMEDIATE SOURCE:

; LIBRARY:

; CLONE:

; POSITION IN GENOME:

; CHROMOSOME/SEGMENT:

; MAP POSITION:

; UNITS:

; FEATURE:

; NAME/KEY: modified site

; LOCATION: 4

; IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "thiol group of

; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with

; OTHER INFORMATION: thiol group of Cys residue at location 21"

; FEATURE:

; NAME/KEY: modified site

; LOCATION: 21

; IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "thiol group of

; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with

; OTHER INFORMATION: thiol group of Cys residue at location 4"

; PUBLICATION INFORMATION:

; AUTHORS:

; TITLE:

; JOURNAL:

; VOLUME:

; ISSUE:

; PAGES:

; DATE:

; DOCUMENT NUMBER:

; FILING DATE:

; PUBLICATION DATE:

; RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10

Query Match 92.9%; Score 65; DB 1; Length 25;

Best Local Similarity 91.7%; Pred. No. 4.8e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNNRKVR 12

Db 4 CFQWQNNRKVR 15

RESULT 15

US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891.174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21

IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
Query Match 92.9%; Score 65; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFWQANMKVR 12
Db 4 CFWQANMKVR 15
Search completed: February 21, 2003, 07:50:33
Job time : 8.7 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds
(without alignments)
35.508 Million cell updates/sec

Title: US-09-743-107B-73

Perfect score: 70

Sequence: 1 CFQWQNNRKYR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	15	9	US-09-798-869-2
2	65	92.9	25	9	US-09-798-869-20
3	65	92.9	694	9	US-10-023-096-2
4	63	90.0	15	9	US-09-798-869-6
5	48	68.6	15	9	US-09-798-869-3
6	48	68.6	25	9	US-09-798-869-23
7	46	65.7	15	9	US-09-798-869-7
8	43	61.4	15	9	US-09-798-869-4
9	43	61.4	25	9	US-09-798-869-22
10	42	60.0	15	9	US-09-798-869-8
11	42	60.0	15	9	US-09-798-869-29
12	42	60.0	15	9	US-09-798-869-30
13	38	55.7	62	10	US-09-815-242-12129
14	39	55.7	62	10	US-09-815-242-13026
15	39	55.7	747	9	US-10-066-500-58
16	39	55.7	747	9	US-10-002-796-58
17	39	55.7	747	9	US-10-066-273-58
18	39	55.7	747	9	US-10-066-494-58
19	36	51.4	15	9	US-09-798-869-5

20	35	50.0	235	9	US-09-764-868-762	Sequence 762, App
21	34	48.6	49	10	US-09-864-761-47074	Sequence 47074, A
22	34	48.6	239	10	US-09-864-761-37353	Sequence 37353, A
23	34	48.6	484	9	US-10-032-063-27	Sequence 27, Appl
24	34	48.6	1128	10	US-09-888-615-97	Sequence 37, Appl
25	33	47.1	13	9	US-09-798-869-26	Sequence 26, Appl
26	33	47.1	14	9	US-09-798-869-25	Sequence 25, Appl
27	33	47.1	15	9	US-09-798-869-1	Sequence 1, Appl
28	33	47.1	15	9	US-09-798-869-10	Sequence 10, Appl
29	33	47.1	15	9	US-09-798-869-28	Sequence 28, Appl
30	33	47.1	18	9	US-09-798-869-24	Sequence 24, Appl
31	33	47.1	25	9	US-09-798-869-21	Sequence 21, Appl
32	33	47.1	25	10	US-09-909-652-4	Sequence 4, Appl
33	33	47.1	25	10	US-09-030-619-205	Sequence 205, App
34	33	47.1	25	10	US-09-917-340-16	Sequence 16, Appl
35	33	47.1	81	10	US-09-864-761-41887	Sequence 41887, A
36	33	47.1	190	10	US-09-815-242-10092	Sequence 10092, A
37	33	47.1	257	10	US-09-860-232A-19	Sequence 19, Appl
38	33	47.1	579	10	US-09-824-588-2	Sequence 2, Appl
39	33	47.1	1258	10	US-09-867-852-107	Sequence 107, App
40	33	47.1	2273	10	US-09-995-542-12	Sequence 12, Appl
41	33	47.1	2310	10	US-09-995-542-10	Sequence 10, Appl
42	32	45.7	21	10	US-09-864-761-47985	Sequence 47985, A
43	32	45.7	63	9	US-09-984-245-320	Sequence 320, App
44	32	45.7	103	10	US-09-867-550-2054	Sequence 2054, Ap
45	32	45.7	178	9	US-09-738-626-5420	Sequence 5420, Ap

ALIGNMENTS

RESULT 1
US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (VSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ RNSSON
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2

Query Match 92.9% Score 65; DB 9; Length 15;
Best Local Similarity 91.7%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 CFQWQNNRKYR 12
Db 3 CFQWQNNRKYR 14

RESULT 2
US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (VSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ RNSSON

; APPLICANT: LARS VORLAND
 ; TITLE OF INVENTION: BIOACTIVE PEPTIDES
 ; FILE REFERENCE: A34049-PCT-USA-A
 ; CURRENT APPLICATION NUMBER: US/09/798,869
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: PCT/GB99/02851
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: GB9818938.4
 ; PRIOR FILING DATE: 1998-08-28
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-09-798-869-20

Query Match 92.9%; Score 65; DB 9; Length 25;
 Best Local Similarity 91.7%; Pred. No. 3.7e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12
 |||||
 DB 3 CFQWQANMKVR 14

RESULT 3
 US-10-023-096-2
 ; Sequence 2, Application US/10023096
 ; Patent No. US20020160941A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kruzel, Marian L.
 ; APPLICANT: Kurecki, Tomasz
 ; APPLICANT: Gollnick, Paul D.
 ; APPLICANT: Doyle, Darrell J.
 ; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
 ; TITLE OF INVENTION: Lactoferrin
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jacobson, Price, Holman & Stern
 ; STREET: 400 Seventh St. N.W.
 ; CITY: Washington D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/023,096
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/724,586
 FILING DATE: 30-SEPT-1996
 APPLICATION NUMBER: US 08/238,445
 FILING DATE: 05-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Player, William E.
 REGISTRATION NUMBER: 31,409
 REFERENCE/DOCKET NUMBER: 10505/P58185C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 638-8666
 TELEFAX: (202) 393-5350
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 694 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-10-023-096-2

Query Match 92.9%; Score 65; DB 9; Length 694;
 Best Local Similarity 91.7%; Pred. No. 0.00093;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12
 |||||
 DB 22 CFQWQANMKVR 33

RESULT 4
 US-09-798-869-6
 ; Sequence 6, Application US/09798869
 ; Publication No. US20030022821A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN SIGURD SVENDSEN
 ; APPLICANT: (YSTEIN REKDAL
 ; APPLICANT: BALDUR SVEINBJ RNSON
 ; APPLICANT: LARS VORLAND
 ; TITLE OF INVENTION: BIOACTIVE PEPTIDES
 ; FILE REFERENCE: A34049-PCT-USA-A
 ; CURRENT APPLICATION NUMBER: US/09/798,869
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: PCT/GB99/02851
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: GB9818938.4
 ; PRIOR FILING DATE: 1998-08-28
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
 ; OTHER INFORMATION: sequence)
 US-09-798-869-6

Query Match 90.0%; Score 63; DB 9; Length 15;
 Best Local Similarity 91.7%; Pred. No. 5.1e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12
 |||||
 DB 3 CFQWQANMKVR 14

RESULT 5
 US-09-798-869-3
 ; Sequence 3, Application US/09798869
 ; Publication No. US20030022821A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN SIGURD SVENDSEN
 ; APPLICANT: (YSTEIN REKDAL
 ; APPLICANT: BALDUR SVEINBJ RNSON
 ; APPLICANT: LARS VORLAND
 ; TITLE OF INVENTION: BIOACTIVE PEPTIDES
 ; FILE REFERENCE: A34049-PCT-USA-A
 ; CURRENT APPLICATION NUMBER: US/09/798,869
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: PCT/GB99/02851
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: GB9818938.4
 ; PRIOR FILING DATE: 1998-08-28
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: CAPRINE
 US-09-798-869-3

Query Match 68.6%; Score 48; DB 9; Length 15;
 Best Local Similarity 63.6%; Pred. No. 0.02;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQANMKV 11
 : : : : :
 Db 3 CYQWQRMKRL 13
 : : : : :
 : : : : :

RESULT 6
 US-09-798-869-23
 ; Sequence 23, Application US/09798869
 ; Publication No. US20030022821A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN SIGURD SVENDSEN
 ; APPLICANT: (YSTEIN REKDAL
 ; APPLICANT: BALDUR SVEINBJ(RNSSON
 ; APPLICANT: LARS VORLAND
 ; TITLE OF INVENTION: BIOACTIVE PEPTIDES
 ; FILE REFERENCE: A34049-PCT-USA-A
 ; CURRENT APPLICATION NUMBER: US/09/798,869
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: PCT/GB99/02851
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: GB9818938.4
 ; PRIOR FILING DATE: 1998-08-28
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 23
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: CAPRINE
 US-09-798-869-23

Query Match 58.6%; Score 48; DB 9; Length 25;
 Best Local Similarity 63.6%; Pred. No. 0.033;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQANMKV 11
 : : : : :
 Db 3 CYQWQRMKRL 13
 : : : : :
 : : : : :

RESULT 7
 US-09-798-869-7
 ; Sequence 7, Application US/09798869
 ; Publication No. US20030022821A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN SIGURD SVENDSEN
 ; APPLICANT: (YSTEIN REKDAL
 ; APPLICANT: BALDUR SVEINBJ(RNSSON
 ; APPLICANT: LARS VORLAND
 ; TITLE OF INVENTION: BIOACTIVE PEPTIDES
 ; FILE REFERENCE: A34049-PCT-USA-A
 ; CURRENT APPLICATION NUMBER: US/09/798,869
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: PCT/GB99/02851
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: GB9818938.4
 ; PRIOR FILING DATE: 1998-08-28
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens
 ; OTHER INFORMATION: sequence)
 US-09-798-869-7

Query Match 65.7%; Score 46; DB 9; Length 15;
 Best Local Similarity 63.6%; Pred. No. 0.044;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQANMKV 11
 : : : : :
 Db 3 CYQWQRMKRL 13
 : : : : :
 : : : : :

RESULT 8
 US-09-798-869-4
 ; Sequence 4, Application US/09798869
 ; Publication No. US20030022821A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN SIGURD SVENDSEN
 ; APPLICANT: (YSTEIN REKDAL
 ; APPLICANT: BALDUR SVEINBJ(RNSSON
 ; APPLICANT: LARS VORLAND
 ; TITLE OF INVENTION: BIOACTIVE PEPTIDES
 ; FILE REFERENCE: A34049-PCT-USA-A
 ; CURRENT APPLICATION NUMBER: US/09/798,869
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: PCT/GB99/02851
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: GB9818938.4
 ; PRIOR FILING DATE: 1998-08-28
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: MURINE
 US-09-798-869-4

Query Match 61.4%; Score 43; DB 9; Length 15;
 Best Local Similarity 63.6%; Pred. No. 0.15;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQANMKV 11
 : : : : :
 Db 3 CLRQWQNMKRV 13
 : : : : :
 : : : : :

RESULT 9
 US-09-798-869-22
 ; Sequence 22, Application US/09798869
 ; Publication No. US20030022821A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN SIGURD SVENDSEN
 ; APPLICANT: (YSTEIN REKDAL
 ; APPLICANT: BALDUR SVEINBJ(RNSSON
 ; APPLICANT: LARS VORLAND
 ; TITLE OF INVENTION: BIOACTIVE PEPTIDES
 ; FILE REFERENCE: A34049-PCT-USA-A
 ; CURRENT APPLICATION NUMBER: US/09/798,869
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: PCT/GB99/02851
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: GB9818938.4
 ; PRIOR FILING DATE: 1998-08-28
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 22
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: MURINE
 US-09-798-869-22

Query Match 61.4%; Score 43; DB 9; Length 25;
 Best Local Similarity 63.6%; Pred. No. 0.24;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQANMKV 11
 : : : : :
 Db 3 CLRQWQNMKRV 13
 : : : : :
 : : : : :

RESULT 10
US-09-798-869-8
; Sequence 8, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine
; OTHER INFORMATION: sequence)
US-09-798-869-8

Query Match 60.0%; Score 42; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.22;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQANRKY 11
| : || |||
Db 3 CLRQWEMKYL 13

RESULT 11
US-09-798-869-29
; Sequence 29, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29

Query Match 60.0%; Score 42; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.22;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQANRKY 11
| : || |||
Db 3 CFRQWEMKYL 13

RESULT 12
US-09-798-869-30

; Sequence 30, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-30

Query Match 60.0%; Score 42; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.22;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQANRKY 11
| : || |||
Db 3 CFRQWEMKYL 13

RESULT 13
US-09-815-242-12129
; Sequence 12129, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12129
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12129

Query Match 55.7%; Score 39; DB 10; Length 62;

Best Local Similarity 60.0%; Pred. No. 2.8;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QWQANNEKVR 12
Db 28 RWNANLQKVR 37

RESULT 14

US-09-815-242-13026
Sequence 13026 Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 1410
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13026
LENGTH: 62
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-13026

Query Match 55.7%; Score 39; DB 10; Length 62;
Best Local Similarity 60.0%; Pred. No. 2.8;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QWQANNEKVR 12
Db 28 RWNANLQKVR 37

RESULT 15

US-10-066-500-58
Sequence 58 Application US/10066500
Patent No. US2002017165A1
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Oiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerritsen
APPLICANT: Audrey Goddard

APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kljavin
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas P. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3130P1C7
CURRENT APPLICATION NUMBER: US/10/066,500
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066840
PRIOR FILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/095998
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/097000
PRIOR FILING DATE: 1998-08-18
PRIOR APPLICATION NUMBER: 60/099601
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100858
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106032
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/109304
PRIOR FILING DATE: 1998-11-20

;; PRIOR APPLICATION NUMBER: 60/125778
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/139695
;; PRIOR FILING DATE: 1999-08-15
;; PRIOR APPLICATION NUMBER: 60/145070
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: 60/149396
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/169495
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 08/918974
;; PRIOR FILING DATE: 1997-08-26
;; PRIOR APPLICATION NUMBER: 08/933821
;; PRIOR FILING DATE: 1997-09-19
;; PRIOR APPLICATION NUMBER: 08/960507
;; PRIOR FILING DATE: 1997-10-29
;; PRIOR APPLICATION NUMBER: 09/114844
;; PRIOR FILING DATE: 1998-07-14
;; PRIOR APPLICATION NUMBER: 09/136801
;; PRIOR FILING DATE: 1998-08-19
;; PRIOR APPLICATION NUMBER: 09/136804
;; PRIOR FILING DATE: 1998-08-19
;; PRIOR APPLICATION NUMBER: 09/136828
;; PRIOR FILING DATE: 1998-08-19
;; PRIOR APPLICATION NUMBER: 09/158342
;; PRIOR FILING DATE: 1998-09-21
;; PRIOR APPLICATION NUMBER: 09/180997
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 09/202088
;; PRIOR FILING DATE: 1998-12-08
;; PRIOR APPLICATION NUMBER: 09/254311
;; PRIOR FILING DATE: 1999-03-03
;; PRIOR APPLICATION NUMBER: 09/254460
;; PRIOR FILING DATE: 1999-03-09
;; PRIOR APPLICATION NUMBER: 09/254465
;; PRIOR FILING DATE: 1999-03-05
;; PRIOR APPLICATION NUMBER: 09/284663
;; PRIOR FILING DATE: 1999-04-15
;; PRIOR APPLICATION NUMBER: 09/332928
;; PRIOR FILING DATE: 1999-06-14
;; PRIOR APPLICATION NUMBER: 09/332929
;; PRIOR FILING DATE: 1999-06-14
;; PRIOR APPLICATION NUMBER: 09/333075
;; PRIOR FILING DATE: 1999-06-14
;; PRIOR APPLICATION NUMBER: 09/333077
;; PRIOR FILING DATE: 1999-06-14
;; PRIOR APPLICATION NUMBER: 09/380137
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380138
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380139
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/403296
;; PRIOR FILING DATE: 1999-10-18
;; PRIOR APPLICATION NUMBER: 09/403297
;; PRIOR FILING DATE: 1999-10-18
;; PRIOR APPLICATION NUMBER: 09/423741
;; PRIOR FILING DATE: 1999-11-10
;; PRIOR APPLICATION NUMBER: 09/423844
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 09/522342
;; PRIOR FILING DATE: 2000-03-09
;; PRIOR APPLICATION NUMBER: 09/548815
;; PRIOR FILING DATE: 2000-04-13
;; PRIOR APPLICATION NUMBER: 09/664610
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: 09/665350
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: 09/709238
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 09/767609

;; PRIOR FILING DATE: 2001-01-22
;; PRIOR APPLICATION NUMBER: 09/802706
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 09/808689
;; PRIOR FILING DATE: 2001-03-14
;; PRIOR APPLICATION NUMBER: 09/866028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 09/870574
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: 09/872035
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: 09/886342
;; PRIOR FILING DATE: 2001-06-19
;; PRIOR APPLICATION NUMBER: PCT/US98/14552
;; PRIOR FILING DATE: 1998-07-14
;; PRIOR APPLICATION NUMBER: PCT/US98/18824
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: PCT/US98/19093
;; PRIOR FILING DATE: 1998-09-14
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: 1998-09-16
;; PRIOR APPLICATION NUMBER: PCT/US98/19437
;; PRIOR FILING DATE: 1998-09-17
;; PRIOR APPLICATION NUMBER: PCT/US98/24855
;; PRIOR FILING DATE: 1998-11-20
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: 1998-12-01
;; PRIOR APPLICATION NUMBER: PCT/US98/25190
;; PRIOR FILING DATE: 1998-11-25
;; PRIOR APPLICATION NUMBER: PCT/US99/05028
;; PRIOR FILING DATE: 1999-03-08
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: PCT/US99/20111
;; PRIOR FILING DATE: 1999-09-01
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 55.7%; Score 39; DB 9; Length 747;
Best Local Similarity 45.5%; Pred. No. 32;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQANMKV 11
Db 311 CWRQINSRRI 321

Search completed: February 21, 2003, 08:08:04
Job time : 10.55 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 Seconds
(without alignments)
120.168 Million cell updates/sec

Title: US-09-743-107b-73
Perfect score: 70
Sequence: 1 CFQWQNNRRKV 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 731.*
1: Piri1.*
2: Piri2.*
3: Piri3.*
4: Piri4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	92.9	711	1 TFHUL	lactotransferrin p
2	48	68.6	33	2 S52107	lactoferrin - shee
3	48	68.6	708	2 JC2323	lactoferrin - goat
4	46	65.7	4568	2 T08030	dynain beta heavy
5	43	61.4	275	2 T22597	hypothetical prote
6	43	61.4	707	1 A28438	lactoferrin precu
7	42	60.0	511	2 AB0858	hypothetical prote
8	39	55.7	60	2 A48396	ribosomal protein
9	39	55.7	62	2 AH1301	ribosomal protein
10	39	55.7	62	2 AH1673	ribosomal protein
11	39	55.7	62	2 C89895	50S ribosomal prot
12	39	55.7	206	2 H97451	pyridoxamine 5'-ph
13	39	55.7	206	2 AB2670	probable pyridoxam
14	39	55.7	208	2 AG3441	hypothetical prote
15	39	55.7	570	2 T46261	hypothetical prote
16	38	54.3	361	2 T29571	chromosome segrega
17	38	54.3	1154	2 A13431	protein UNC-89 - C
18	38	54.3	6642	2 T29757	cell cycle arrest
19	37	52.9	306	1 A39554	hypothetical prote
20	37	52.9	349	2 T16882	adenosylmethionine
21	37	52.9	433	2 D81164	probable adenosylm
22	37	52.9	433	2 F81940	hypothetical prote
23	37	52.9	464	2 A12343	hypothetical prote
24	37	52.9	475	2 F64151	probable cytochrom
25	37	52.9	518	2 B84514	cell polarity prot
26	37	52.9	522	2 T19536	hypothetical prote
27	37	52.9	601	2 T19429	outer capsid prote
28	37	52.9	749	2 A45687	hypothetical prote
29	37	52.9	962	2 S67385	hypothetical prote

30	37	52.9	2700	2 D88450	protein F21H11.2 [
31	36.5	52.1	235	2 E91097	hypothetical prote
32	36.5	52.1	235	2 A58943	hypothetical prote
33	36	51.4	62	2 S39862	ribosomal protein
34	36	51.4	62	2 D83962	ribosomal protein
35	36	51.4	282	2 F90580	hypothetical prote
36	36	51.4	289	2 G86403	33.3K hypothetical
37	36	51.4	298	2 AD2346	hypothetical prote
38	36	51.4	346	2 T19980	hypothetical prote
39	36	51.4	513	2 F82216	transcription regu
40	36	51.4	517	2 F71417	cytochrome P450 -
41	36	51.4	572	1 DEM5MX	malate dehydrogena
42	36	51.4	572	2 JC4160	malate dehydrogena
43	36	51.4	584	2 C84325	hypothetical prote
44	36	51.4	649	2 AB2154	hypothetical prote
45	36	51.4	703	2 A45543	lactoferrin precu

ALIGNMENTS

RESULT 1

TFHUL
lactotransferrin precursor [validated] - human
N:Alternate names: lactoferrin
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text change 08-Dec-2000
C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74:
R:Cho, Y.
submitted to the EMBL Data Library, March 1994
A:Reference number: G06820
A:Accession: G01394
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-711 <CHO>
A:Cross-references: EMBL:U07643; NID:9467236; PIDN:AAB60324.1; PID:9467237
R:Rev. M.M.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.
Nucleic Acids Res. 18, 5288, 1990
A>Title: Complete nucleotide sequence of human mammary gland lactoferrin.
A:Reference number: S11228; MUID:90384839; PMID:2402455
A:Accession: S11228
A:Molecule type: mRNA
A:Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>
A:Cross-references: EMBL:X53961; NID:934415; PIDN:CAA37914.1; PID:934416
R:Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
Mol. Endocrinol. 6, 1969-1981, 1992
A>Title: Differential molecular mechanism of the estrogen action that regulates lactoferi
A:Reference number: A45401; MUID:93125571; PMID:1480183
A:Accession: A45401
A:Molecule type: DNA
A:Residues: 1-15 <TEN>
A:Cross-references: GB:S52659; NID:9263311; PIDN:AAB24877.1; PID:9263312
A:Experimental source: placenta
A>Note: sequence extracted from NCBI backbone (NCBIP:122202)
R:Powell, M.J.; Ogden, J.E.
Nucleic Acids Res. 18, 4013, 1990
A>Title: Nucleotide sequence of human lactoferrin cDNA.
A:Reference number: S10324; MUID:90326549; PMID:2374734
A:Accession: S10324
A:Molecule type: mRNA
A:Residues: 3-711 <POW>
R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Biochem. J. 276, 349-355, 1991
A>Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A:Reference number: S15853; MUID:91264786; PMID:2049066
A:Accession: S15853
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 20-31 <ST1>
A:Accession: S20841
A:Molecule type: protein
A:Residues: 20-28, 'X', 30-31 <ST2>


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Query Match      68.6%; Score 48; DB 2; Length 33;
Best Local Similarity 63.6%; Pred. No. 0.055;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQANMRKV 11
   |||||
Db 19 CYQWQRRMRKL 29

RESULT 3
JC2323
lactoferrin - goat
C:Species: Capra aegagrus hircus (domestic goat)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C:Accession: JC2323
R:Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A:Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locu
A:Reference number: JC2323; MUID:94380047; PMID:8093048
A:Accession: JC2323
A:Molecule type: mRNA
A:Residues: 1-708 <LEP>
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein
F:359-696/Domain: transferrin repeat homology <TRH2>
P:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      68.6%; Score 48; DB 2; Length 708;
Best Local Similarity 63.6%; Pred. No. 1.1;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQANMRKV 11
   |||||
Db 38 CYQWQRRMRKL 48

RESULT 4
T08030
dyslin beta heavy chain - Chlamydomonas reinhardtii
C:Species: Chlamydomonas reinhardtii
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C:Accession: T08030
R:Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A:Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A:Reference number: Z16302; MUID:94274778; PMID:8006077
A:Accession: T08030
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4568 <MIT>
A:Cross-references: EMBL:U02963; NID:G409965; PIDN:AAA19956.1; PID:G5:4215
A:Experimental source: strain 21gr
C:Genetics:
A:Gene: ODA4
A:Map position: IX
A:Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;
3334/3; 3686/3; 3882/3; 4240/3
C:Superfamily: dynein heavy chain, ciliary
C:Keywords: nucleotide binding; P-loop
F:1919-1926/Region: nucleotide-binding motif A (P-loop)
F:2202-2209/Region: nucleotide-binding motif A (P-loop)
F:2530-2537/Region: nucleotide-binding motif A (P-loop)

Query Match      65.7%; Score 46; DB 2; Length 4568;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQANMRKV 12
   |||||
Db 1852 CFQWQSQLRYIQ 1863

RESULT 5

```

T22597
 Hypothetical protein F53H4.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C:Accession: T22597
 R:Dobson, R.
 Submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19587
 A:Accession: T22597
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-275 <WIL>
 A:Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
 A:Experimental source: clone F53H4
 C:Genetics:
 A:Gene: CESP:F53H4.4
 A:Map position: X
 A:Introns: 67/1; 153/1
 C:Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4

Query Match 61.4%; Score 43; DB 2; Length 275;
 Best Local Similarity 63.6%; Pred. No. 3.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FQWQANMKVR 12
 |||:|||||
 Db 262 FQWKISNRKTR 272

RESULT 6
 A28438
 Lactoferrin precursor - mouse
 N:Alternate names: lactotransferrin
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A28438; A41205
 R:Penetecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A:Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secretory cells
 A:Reference number: A92596; MUID:87280033; PMID:3611056
 A:Accession: A28438
 A:Molecule type: mRNA
 A:Residues: 3-707 <PEN>
 A:Cross-references: EMBL:J03298
 R:Li, Y.; Teng, C.T.
 J. Biol. Chem. 266, 21880-21885, 1991
 A:Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
 A:Reference number: A41205; MUID:92042099; PMID:1939212
 A:Accession: A41205
 A:Molecule type: DNA
 A:Residues: 1-15 <LIU>
 A:Cross-references: GB:M74778
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-707/Product: lactotransferrin #status predicted <MAT>
 F:358-695/Domain: transferrin repeat homology <TRH2>
 F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.4%; Score 43; DB 1; Length 707;
 Best Local Similarity 63.6%; Pred. No. 8.6;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQANMKVR 11
 |||:|||||
 Db 37 CLFQWQANMKVR 47

RESULT 7
 A80858
 Hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
 C:Accession: AB0858
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Paratyphi A
 A:Reference number: AB0502; PMID:11677608
 A:Accession: AB0858
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-511 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:G16504016; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY3070

Query Match 60.0%; Score 42; DB 2; Length 511;
 Best Local Similarity 58.3%; Pred. No. 9.5;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CFQWQANMKVR 12
 |||:|||||
 Db 350 CFANDMKAKVR 361

RESULT 8
 A48396
 Ribosomal protein L28 - Bacillus stearothermophilus
 C:Species: Bacillus stearothermophilus
 C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 21-Aug-1998
 C:Accession: A48396
 R:Kruft, V.; Kapp, U.; Wittmann-Liebold, B.
 Biochimie 73, 855-860, 1991
 A:Title: Characterization and primary structure of proteins L28, L33 and L34 from Bacillus stearothermophilus
 A:Reference number: A48396; MUID:92075758; PMID:1742360
 A:Accession: A48396
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-60 <KRU>
 A:Note: sequence extracted from NCBI backbone (NCBIP:69662)
 C:Superfamily: Escherichia coli ribosomal protein L28

Query Match 55.7%; Score 39; DB 2; Length 60;
 Best Local Similarity 56.7%; Pred. No. 4.1;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WQANMKVR 12
 |||:|||||
 Db 27 WKANLQKVR 35

RESULT 9
 AH1301
 Ribosomal protein L28 [imported] - Listeria monocytogenes (strain EGD-e)
 C:Species: Listeria monocytogenes
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 17-May-2002
 C:Accession: AH1301
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AH1301
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-62 <GLA>
 A:Cross-references: GB:NC_003210; PIDN:CAC99894.1; PID:G16411270; GSPDB:GN00177
 A:Experimental source: strain EGD-e
 C:Genetics:

A:Gene: rpsB
C:Superfamily: Escherichia coli ribosomal protein L28

Query Match 55.7%; Score 39; DB 2; Length 62;
Best Local Similarity 56.7%; Pred. No. 4.2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 WQANMRKVR 12
|:|:|:|:|

DB 29 WKANLQKVR 37
|:|:|:|:|

RESULT 10

AH1673
ribosomal protein L28 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 17-May-2002
C:Accession: AH1673
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schluerer, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, O.; C.; Schluerer, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, O.
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1673
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC97160.1; PID:gl6414431; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: rpsB
C:Superfamily: Escherichia coli ribosomal protein L28

Query Match 55.7%; Score 39; DB 2; Length 62;
Best Local Similarity 56.7%; Pred. No. 4.2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 WQANMRKVR 12
|:|:|:|:|

DB 29 WKANLQKVR 37
|:|:|:|:|

RESULT 11

C89895
50S ribosomal protein L28 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
C:Accession: C89895
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Ma, A.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89759; MUID:21311952; PMID:11418146
A:Accession: C89895
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701024; PIDN:BA842319.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: rpsB
C:Superfamily: Escherichia coli ribosomal protein L28

Query Match 55.7%; Score 39; DB 2; Length 62;
Best Local Similarity 56.0%; Pred. No. 4.2;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 WQANMRKVR 12
|:|:|:|:|

DB 28 RWNANLQKVR 37

RESULT 12

H97451
pyridoxamine 5'-phosphate oxidase (AF179611) [imported] - Agrobacterium tumefaciens (str C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: H97451
R:Godner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorillo, B.; Goldman, A.; Liu, F.; Mollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A:Reference number: A97359; PMID:11743194
A:Accession: H97451
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:gl5155733; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C1381
A:Map position: circular chromosome
C:Superfamily: pyridoxamine-phosphate oxidase

Query Match 55.7%; Score 39; DB 2; Length 206;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQANMRKVR 12
|:|:|:|:|

DB 88 CFHWKSLRRQVR 99
|:|:|:|:|

RESULT 13

AB2670
pyridoxamine 5'-phosphate oxidase [imported] - Agrobacterium tumefaciens (strain C58, Du C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C:Accession: AB2670
R:Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AB2670
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <KUR>
A:Cross-references: GB:AE008698; PIDN:AAL41776.1; PID:gl7739129; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: pdxH
A:Map position: circular chromosome
C:Superfamily: pyridoxamine-phosphate oxidase

Query Match 55.7%; Score 39; DB 2; Length 206;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQANMRKVR 12
|:|:|:|:|

DB 88 CFHWKSLRRQVR 99
|:|:|:|:|

RESULT 14

AG3441
probable pyridoxamine-phosphate oxidase (EC 1.4.3.5) [imported] - Brucella melitensis (s C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
C:Accession: AG3441

R;DeIvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, M.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letee, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
 A;Reference number: AD3252; PMID:1175668
 A;Accession: AC3441
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-208 <KUR>
 A;Cross-references: GB:AE008917; PIDN:AA152698.1; PID:gl7983525; GSPDB:GNO0190
 A;Experimental source: strain 16M
 C;Genetics:
 A;Gene: BME11517
 A;Map position: I
 C;Superfamily: pyridoxamine-phosphate oxidase
 C;Keywords: oxidoreductase

Query Match 55.7%; Score 39; DB 2; Length 208;
 Best Local Similarity 50.0%; Pred.No. 14;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWQANMKVR 12
 |||::|::|::|
 Db 90 CFHWKSLRRQVR 101

RESULT 15
 T46261
 hypothetical protein DKFZp761E1824.1 - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
 C;Accession: T46261
 R;Boecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000
 A;Reference number: Z23032
 A;Accession: T46261
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-570 <AAA>
 A;Cross-references: EMBL:AL137432
 A;Experimental source: adult amygdala, clone DKFZp761E1824
 C;Genetics:
 A;Note: DKFZp761E1824.1

Query Match 55.7%; Score 39; DB 2; Length 570;
 Best Local Similarity 45.5%; Pred.No. 36;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWQANMKVR 11
 |||::|::|::|
 Db 134 CVRWQINSRRI 144

Search completed: February 21, 2003, 07:47:44
 Job time : 11.65 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds
(without alignments)
108.199 Million cell updates/sec

Title: US-09-743-107B-73
Perfect score: 70
Sequence: 1 CFQWQANMRKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	92.9	711	1 TRFL_HUMAN	P02788 homo sapien
2	48	68.6	708	1 TRFL_CAMDR	Q9tun0 camelus dro
3	48	68.6	708	1 TRFL_CAPHI	Q29477 capra hircu
4	45	65.7	4568	1 DYHE_CHLRE	Q39565 chlamydomon
5	43	61.4	707	1 TRFL_MOUSE	P08071 mus musculu
6	40	57.1	695	1 TRFL_HORSE	O77811 equus cabal
7	39	55.7	60	1 RL28_BACST	P23374 bacillus st
8	39	55.7	62	1 RL28_LISMO	Q92aj2 listeria mo
9	39	55.7	62	1 RL28_STAAM	Q99up4 staphylococ
10	38	54.3	62	1 RL28_THETN	Q8r5ul thermomaneer
11	38	54.3	422	1 PAPA_CHICK	Q90678 g platelet-
12	38	54.3	435	1 YKYL_CAEEL	Q19910 caenorhabdi
13	37	52.9	306	1 YUB2_YEAST	P26448 saccharomyc
14	37	52.9	475	1 YEB4_HAEIN	P44693 haemophilus
15	37	52.9	522	1 COR1_SCHPO	O13688 schizosacch
16	37	52.9	749	1 VP4_ROTGA	Q04316 rotavirus (
17	37	52.9	962	1 YBX7_SCHPO	Q10201 schizosacch
18	36	51.4	62	1 RL28_BACHD	Q9K924 bacillus ha
19	36	51.4	62	1 RL28_BACSU	P37807 bacillus su
20	36	51.4	572	1 MAOX_MOUSE	P06801 mus musculu
21	36	51.4	704	1 TRFL_PIG	P14632 sus scrofa
22	36	51.4	1131	1 PHY_FINSY	Q41046 pinus sylve
23	35	50.0	133	1 HS90_PLAEP	P20147 plasmodium
24	35	50.0	401	1 PGK_HALVA	P50315 haloarcula
25	35	50.0	441	1 HS82_ASFFU	P40292 aspergillus
26	35	50.0	457	1 SYS_SULSO	O33780 sulfolobus
27	35	50.0	679	1 HS82_AJECA	P33125 ajelloyobus
28	35	50.0	701	1 HS90_PODAN	P43109 podospora a
29	35	50.0	704	1 HS83_YEAST	P15108 saccharomyc
30	35	50.0	707	1 HS90_CANAL	P45998 candida alb
31	35	50.0	708	1 TRFL_BUBBU	O77698 bubalus bub
32	35	50.0	709	1 HS82_YEAST	P02829 saccharomyc
33	35	50.0	713	1 HS90_EIMTE	Q44001 elmeria ten

RESULT 1

ID	TRFL_HUMAN	STANDARD;	PRT;	711 AA.
AC	P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H1Z3; Q96KZ4;			
AC	Q96KZ5;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactoferrin precursor (Lactoferrin) [Contains: Lactoferrin A;			
DE	Lactoferrin B; Lactoferrin C]			
GN	LTF OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RX	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;			
RT	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RL	Nucleic Acids Res. 18:5288-5288(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cho Y.Y.;			
RL	Theis (1994), Genetic Engineering Research Institute / Taejon, Korea.			
RP	SEQUENCE FROM N.A.			
RA	Connely O.M.;			
RN	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RT	"Molecular cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Rado T.A.;			
RT	"Human neutrophil lactoferrin coding and 5' flanking region DNA			
RL	sequences.";			
RP	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cheng H., Chen X., Huan L.;			
RT	"cDNA cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Straubeberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Straubeberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			

34	35	50.0	716	1	HS83_DROAV	O02192 drosophila
35	35	50.0	717	1	HS83_DROME	P02828 drosophila
36	35	50.0	721	1	HS90_THERA	P24724 theileria p
37	35	50.0	989	1	T100_HUMAN	O75448 homo sapien
38	35	50.0	1019	1	VP3_EDVF	Q98630 rice dwarf
39	35	50.0	1072	1	ITAF6_CHICK	P26007 gallus gall
40	35	50.0	1173	1	GIGA_ORYSA	Q9awl7 oryza sativ
41	34.5	49.3	256	1	VOEC_ECOLI	Q46809 escherichia
42	34.5	49.3	432	1	TRKI_HUMAN	O15756 homo sapien
43	34	48.6	134	1	YA7B_HAEIN	Q57425 haemophilus
44	34	48.6	213	1	IF4E_XENLA	P48597 xenopus lae
45	34	48.6	217	1	IF4E_HUMAN	P06730 homo sapien

ALIGNMENTS

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE-Mammary Gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Oden J.E.;
RT "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
RX Metz-Boutigue M.-H., Jolles J., Jolles P.;
RA Legend D., Spik G., Montreuil J., Jolles P.;
RT "Human lactotransferrin: amino acid sequence and structural
RT comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1984).
RN [10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RA Jolles P.;
RT "The present state of the human lactotransferrin sequence. Study and
RT alignment of the cyanogen bromide fragments and characterization of
RT N- and C-terminal domains.";
RL Biochim. Biophys. Acta 670:243-254(1981).
RN [11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
RA Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
RT lactotransferrin.";
RL FEBS Lett. 142:1107-1110(1982).
RN [12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=8801031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
RN [13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Rang M., Porcel B.M.,
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sagripanti J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2855506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human diferric lactoferrin refined at 2.2-A
RT resolution.";
RL Acta Crystallogr. D 51:629-646(1995).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
RA Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RT 253-->methionine mutant.";
RL Biochemistry 36:341-346(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in Aspergillus
RT awamori.";
RL Acta Crystallogr. D 55:403-407(1999).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
RT and analysis of ligand-induced conformational change.";
RL Acta Crystallogr. D 54:1319-1335(1998).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of opioid antagonist peptides derived
RT from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810(1990).
RN [20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
RA Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
RA El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
RA Hejtmancik J.F., Teng C.T.;
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RL Mol. Vision 4:31-32(1998).
RN [21]
RP FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -I- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -I- SUBUNIT: MONOMER.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -I- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X53961; CAA37914.1; -
CC EMBL; U07643; AAB60324.1; -
CC EMBL; M93150; AAA36159.1; -
CC EMBL; M83202; AAA59511.1; -
CC EMBL; M83205; AAA58656.1; -
CC EMBL; M18642; AAA86665.1; -
CC EMBL; AF332168; AAG48753.1; -
CC EMBL; BC015822; AAH15822.1; -
CC EMBL; BC015823; AAH15823.1; -
CC EMBL; M73700; AAA59479.1; -
CC EMBL; X52941; CAA37116.1; -
CC EMBL; U95626; AAB57795.1; -
CC PIR; S11228; TFHUL.
CC PDB; 1LCP; 31-AUG-94.
CC PDB; 1LCT; 31-OCT-93.
CC PDB; 1LFG; 31-JUL-94.
CC PDB; 1LFH; 31-OCT-93.
CC PDB; 1LFI; 31-OCT-93.
CC PDB; 1LGB; 31-AUG-94.
CC PDB; 1LGC; 31-AUG-94.
CC PDB; 1BKA; 08-NOV-96.
CC PDB; 1DSN; 08-MAR-96.
CC PDB; 1HSE; 12-MAR-97.
CC PDB; 1VFD; 21-APR-97.

Query Match 92.9%; Score 65; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.00017;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKYR 12
 Db 39 CFQWQNNRKYR 50

RESULT 2

TRFL_CAMDR STANDARD; PRT; 708 AA.
 AC QSTUN0; Q9MZS5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Somali; TISSUE=Lactating mammary gland;
 RA Kappeler S.R.; Ackermann M.; Farah Z.; Puhon Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
 RL Int. Dairy J. 9:481-486(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;

RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; A131574; CAB53387.1; -;
 DR EMBL; AF165879; AAF82241.1; -;
 DR HSP; O77811; 1B1X.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 Signal.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 708 LACTOTRANSFERRIN.
 FT REPEAT 20 363 1.
 FT REPEAT 364 708 2.
 FT DISULFID 28 64 BY SIMILARITY.
 FT DISULFID 38 55 BY SIMILARITY.
 FT DISULFID 134 217 BY SIMILARITY.
 FT DISULFID 176 192 BY SIMILARITY.
 FT DISULFID 189 200 BY SIMILARITY.
 FT DISULFID 250 264 BY SIMILARITY.
 FT DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.
 FT DISULFID 424 703 BY SIMILARITY.
 FT DISULFID 444 666 BY SIMILARITY.
 FT DISULFID 476 551 BY SIMILARITY.
 FT DISULFID 500 694 BY SIMILARITY.
 FT DISULFID 510 524 BY SIMILARITY.
 FT DISULFID 521 534 BY SIMILARITY.
 FT DISULFID 592 606 BY SIMILARITY.
 FT DISULFID 644 649 BY SIMILARITY.
 FT METAL 79 79 IRON 1 (BY SIMILARITY).
 FT METAL 111 111 IRON 1 (BY SIMILARITY).
 FT METAL 211 211 IRON 1 (BY SIMILARITY).
 FT METAL 272 272 IRON 1 (BY SIMILARITY).
 FT METAL 414 414 IRON 2 (BY SIMILARITY).
 FT METAL 452 452 IRON 2 (BY SIMILARITY).
 FT METAL 545 545 IRON 2 (BY SIMILARITY).
 FT METAL 614 614 IRON 2 (BY SIMILARITY).
 FT BINDING 140 140 ANION (BY SIMILARITY).
 FT BINDING 482 482 ANION (BY SIMILARITY).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .)
 FT CONFLICT 261 261 F -> S (IN REF. 2).
 FT CONFLICT 304 304 G -> A (IN REF. 2).
 FT CONFLICT 330 330 S -> P (IN REF. 2).
 FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).
 FT CONFLICT 506 506 L -> F (IN REF. 2).
 FT CONFLICT 609 609 A -> P (IN REF. 2).
 FT CONFLICT 642 642 R -> Q (IN REF. 2).
 SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match 68.6%; Score 48; DB 1; Length 708;
 Best Local Similarity 66.7%; Pred. No. 0.25;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNNRKYR 12
 Db 38 CAQWQNNRKYR 49

RESULT 3

TRFL_CAMDR STANDARD; PRT; 708 AA.
 AC Q29477; Q29479;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA MEDLINE=94380047; Pubmed=8093048;
 RA le Provost F., Nocard M., Guerin G., Martin P.;
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the
 RT relevant locus to bovine U12 syntenic group.";
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U53857; AAA97958.1; -
CC EMBL; X78902; CAA55517.1; -
CC HSP; O77698; 1CB2.
CC InterPro; IPR001156; Transferrin.
CC Pfam; PF00405; transferrin; 2.
CC PRINTS; PR00422; TRANSFERRIN.
CC SMART; SM00094; TRFER; 2.
CC PROSITE; PS00205; TRANSFERRIN_1; 2.
CC PROSITE; PS00206; TRANSFERRIN_2; 2.
CC PROSITE; PS00207; TRANSFERRIN_3; 2.
CC Transprot; Iron transport; Metal-binding; Repeat;
CC Signal.
CC -----
CC 1 19 BY SIMILARITY.
CC CHAIN 20 708 LACTOTRANSFERRIN.
CC REPEAT 20 363 1.
CC REPEAT 364 708 2.
CC DISULFID 28 64 BY SIMILARITY.
CC DISULFID 38 55 BY SIMILARITY.
CC DISULFID 134 217 BY SIMILARITY.
CC DISULFID 176 192 BY SIMILARITY.
CC DISULFID 189 200 BY SIMILARITY.
CC DISULFID 250 264 BY SIMILARITY.
CC DISULFID 367 399 BY SIMILARITY.
CC DISULFID 377 390 BY SIMILARITY.
CC DISULFID 424 703 BY SIMILARITY.
CC DISULFID 444 686 BY SIMILARITY.
CC DISULFID 476 551 BY SIMILARITY.
CC DISULFID 500 694 BY SIMILARITY.
CC DISULFID 510 524 BY SIMILARITY.
CC DISULFID 521 534 BY SIMILARITY.
CC DISULFID 592 606 BY SIMILARITY.
CC DISULFID 644 649 BY SIMILARITY.
CC METAL 79 79 IRON 1 (BY SIMILARITY).
CC METAL 111 111 IRON 1 (BY SIMILARITY).
CC METAL 211 211 IRON 1 (BY SIMILARITY).
CC METAL 272 272 IRON 1 (BY SIMILARITY).
CC METAL 414 414 IRON 2 (BY SIMILARITY).
CC METAL 452 452 IRON 2 (BY SIMILARITY).
CC METAL 545 545 IRON 2 (BY SIMILARITY).
CC METAL 614 614 IRON 2 (BY SIMILARITY).
CC BINDING 140 140 ANION (BY SIMILARITY).
CC BINDING 482 482 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CONFLICT 56 56 I -> V (IN REF. 2).
CC CONFLICT 88 88 L -> R (IN REF. 2).
CC CONFLICT 124 124 Q -> K (IN REF. 2).
CC CONFLICT 154 154 F -> P (IN REF. 2).
CC CONFLICT 304 304 S -> R (IN REF. 2).
CC CONFLICT 414 414 D -> G (IN REF. 2).
CC SEQUENCE 708 AA; 77358 MW; F2EDA3C83539960D CRC64;
CC -----
CC Query Match 68.6%; Score 48; DB 1; Length 708;
CC Best Local Similarity 63.6%; Pred. No. 0.25;
CC Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
CC -----
CC QY 1 CFQWQANMRKV 11
CC | : : : : :
CC 38 CFQWQANMRKL 48
CC -----
CC Db

RESULT 4
DYHB CHLRE
ID DYHB CHLRE STANDARD; PRT; 4568 AA.
AC Q39565;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Dynein beta chain, flagellar outer arm.
GN ODA4 OR ODA-4 OR SUP1.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=21gr;
RX MEDLINE=94274778; PubMed=8006077;
RA Mitchell D.R.; Brown K.S.;
RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
chain genes";
RL J. Cell Sci. 107:635-644(1994).
CC -!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
CC FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC -!- DYNEIN HAS ATPASE ACTIVITY.
CC -!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
CC GAMMA). 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
CC -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
CC -----
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CC -----
CC EMBL; U02963; AAA19956.1; -
CC InterPro; IPR004273; Dynein heavy;
CC Pfam; PF03028; Dynein heavy; 1.
CC Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
CC Coiled coil.
CC DOMAIN 277 293 COILED COIL (POTENTIAL).
CC DOMAIN 1158 1175 COILED COIL (POTENTIAL).
CC DOMAIN 1372 1400 COILED COIL (POTENTIAL).
CC DOMAIN 1614 1650 COILED COIL (POTENTIAL).
CC DOMAIN 1778 1825 COILED COIL (POTENTIAL).
CC DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
CC DOMAIN 2831 2848 COILED COIL (POTENTIAL).
CC DOMAIN 3106 3162 COILED COIL (POTENTIAL).
CC DOMAIN 3339 3425 COILED COIL (POTENTIAL).
CC DOMAIN 3648 3728 COILED COIL (POTENTIAL).
CC NP_BIND 1919 1926 ATP (POTENTIAL).
CC NP_BIND 2202 2209 ATP (POTENTIAL).
CC NP_BIND 2530 2537 ATP (POTENTIAL).
CC NP_BIND 2879 2886 ATP (POTENTIAL).
CC SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;
CC -----
CC Query Match 65.7%; Score 46; DB 1; Length 4568;
CC Best Local Similarity 50.0%; Pred. No. 4;
CC Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
CC -----
CC QY 1 CFQWQANMRKV 12
CC | : : : : :
CC 1852 CFQWQANMRKV 1863
CC -----
CC RESULT 5
TRFL_MOUSE
ID TRFL_MOUSE STANDARD; PRT; 707 AA.
AC P08071; P70690; Q61799; Q922P2;
DT 01-AUG-1988 (Rel. 08, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN Lf.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RX MEDLINE=97280033; PubMed=3611056;
 RA Pentecost B.T.; Teng C.T.;
 RT "Lactotransferrin is the major estrogen inducible protein of mouse
 RT uterine secretions.";
 RL J. Biol. Chem. 262:10134-10139(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA Moriishi K.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-14 FROM N.A.
 RX MEDLINE=92042099; PubMed1939212;
 RA Liu Y.; Teng C.T.;
 RT "Characterization of estrogen-responsive mouse lactoferrin promoter.";
 RL J. Biol. Chem. 266:21880-21885(1991).
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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 CC -----
 DR EMBL; J03298; AAA40525.1; -;
 DR EMBL; D88510; BAA13633.1; -;
 DR EMBL; BC006904; AAH06904.1; -;
 DR EMBL; M74778; AAA39427.1; -;
 DR PIR; A28438; A28438.
 DR HSP; P02789; ICB6.
 DR MGD; MGI:96837; Ltf.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TF_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 1.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW signal.
 FT SIGNAL. 1 19 BY SIMILARITY.
 FT CHAIN 20 707 LACTOTRANSFERRIN.
 FT REPEAT 20 357 1.
 FT REPEAT 358 707 2.
 FT DISULFID 27 63 BY SIMILARITY.
 FT DISULFID 37 54 BY SIMILARITY.
 FT DISULFID 133 216 BY SIMILARITY.
 FT DISULFID 175 191 BY SIMILARITY.
 FT DISULFID 188 199 BY SIMILARITY.
 FT DISULFID 249 263 BY SIMILARITY.

FT DISULFID 366 398 BY SIMILARITY.
 FT DISULFID 376 389 BY SIMILARITY.
 FT DISULFID 423 702 BY SIMILARITY.
 FT DISULFID 443 665 BY SIMILARITY.
 FT DISULFID 475 550 BY SIMILARITY.
 FT DISULFID 499 693 BY SIMILARITY.
 FT DISULFID 509 523 BY SIMILARITY.
 FT DISULFID 520 533 BY SIMILARITY.
 FT DISULFID 591 605 BY SIMILARITY.
 FT DISULFID 643 648 BY SIMILARITY.
 FT METAL 78
 FT METAL 110
 FT METAL 210
 FT METAL 271 271
 FT METAL 413 413
 FT METAL 451 451
 FT METAL 544 544
 FT METAL 613 613
 FT BINDING 139 139
 FT BINDING 481 481
 FT CARBOHYD 118 118
 FT CARBOHYD 494 494
 FT CONFLICT 1 2
 FT CONFLICT 25 25
 FT CONFLICT 82 82
 FT CONFLICT 359 359
 FT CONFLICT 382 382
 FT CONFLICT 449 449
 FT CONFLICT 629 629
 SQ SEQUENCE 707 AA; 77865 MW; P26AE0340A4C19A8 CRC64;
 Query Match 61.4%; Score 43; DB 1; Length 707;
 Best Local Similarity 63.6%; Pred. No. 2.1;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWQANNRKV 11
 DB 37 CLRWQNNRKV 47
 RESULT 6
 ID TRFL HORSE STANDARD; PRT; 695 AA.
 AC 077811;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin) (Fragment).
 GN LTF.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Paramasivam M.; Srinivasan A.; Yadav M.P.; Singh T.P.;
 RT "cDNA sequence of mare lactoferrin.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RC TISSUE=Milk;
 RX MEDLINE=99296631; PubMed=10366507;
 RA Sharma A.K.; Paramasivam M.; Srinivasan A.; Yadav M.P.; Singh T.P.;
 RT "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
 RT resolution.";
 RL J. Mol. Biol. 289:303-317(1999).
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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CC -----
CC EMBL; AJ010930; CA009407.1; -.
CC PDB; 1B1X; 02-DEC-98.
CC PDB; 1B7U; 02-FEB-99.
CC PDB; 1B7Z; 02-FEB-99.
CC InterPro; IPR001156; Transferrin.
CC Pfam; PF00405; transferrin; 2.
CC PRINTS; PR00422; TRANSFERRIN.
CC SMART; SM00094; TR FER; 2.
CC PROSITE; PS00205; TRANSFERRIN_1; 2.
CC PROSITE; PS00206; TRANSFERRIN_2; 2.
CC PROSITE; PS00207; TRANSFERRIN_3; 1.
CC Transprot; Iron transport; Glycoprotein; Metal-binding; Repeat;
CC Signal; 3D-structure.
CC -----
CC FT SIGNAL 1 1
CC FT CHAIN 7 695 LACTOTRANSFERRIN.
CC FT REPEAT 7 350 1.
CC FT REPEAT 351 695 2.
CC FT DISULFID 15 51
CC FT DISULFID 25 42
CC FT DISULFID 121 204
CC FT DISULFID 163 179
CC FT DISULFID 166 189
CC FT DISULFID 176 187
CC FT DISULFID 237 251
CC FT DISULFID 354 386
CC FT DISULFID 364 377
CC FT DISULFID 411 690
CC FT DISULFID 431 653
CC FT DISULFID 463 538
CC FT DISULFID 487 681
CC FT DISULFID 497 511
CC FT DISULFID 508 521
CC FT DISULFID 579 593
CC FT DISULFID 631 636
CC FT METAL 66 66 IRON 1 (BY SIMILARITY).
CC FT METAL 98 98 IRON 1 (BY SIMILARITY).
CC FT METAL 198 198 IRON 1 (BY SIMILARITY).
CC FT METAL 259 259 IRON 1 (BY SIMILARITY).
CC FT METAL 401 401 IRON 2 (BY SIMILARITY).
CC FT METAL 439 439 IRON 2 (BY SIMILARITY).
CC FT METAL 532 532 IRON 2 (BY SIMILARITY).
CC FT METAL 601 601 IRON 2 (BY SIMILARITY).
CC FT BINDING 127 127 ANION (BY SIMILARITY).
CC FT BINDING 469 469 ANION (BY SIMILARITY).
CC FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 287 287 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 482 482 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 695 AA; 75991 MW; 07B84D5081B165D CRC64;
CC -----
CC Query Match 57.1%; Score 40; DB 1; Length 695;
CC Best Local Similarity 58.3%; Pred. No. 7.6;
CC Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
CC -----
CC QY 1 CFQWQANMKVIR 12
CC | : : : : |
CC DB 25 CAKFNKKVIR 36
CC -----
CC RESULT 7
CC RL28_BACST STANDARD; PRT; 60 AA.
CC ID RL28_BACST
CC AC P23374;
CC DT 01-NOV-1991 (Rel. 20, Created)

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DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L28.
GN RBM.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE.
RX MEDLINE=92075758; PubMed=1742360;
RA Kruft V., Kapp U., Wittmann-Liebold B.;
RT "Characterization and primary structure of proteins L28, L33 and L34
RT from Bacillus stearothermophilus ribosomes.";
RL Biochimie 73:855-860(1991).
CC -1- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
DR PIR; A48396; A48396.
DR InterPro; IPR001383; Ribosomal L28.
DR Pfam; PF00830; Ribosomal L28; 1.
DR TIGRFAMs; TIGR00009; L28; 1.
KW Ribosomal protein.
FT INIT MET 0
FT SEQUENCE 60 AA; 6810 MW; 2AD9161CD60E82F4 CRC64;
CC -----
CC Query Match 55.7%; Score 39; DB 1; Length 60;
CC Best Local Similarity 66.7%; Pred. No. 0.95;
CC Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 4 WQANMKVIR 12
CC | : : : : |
CC DB 27 WKANLQKVR 35
CC -----
CC RESULT 8
CC RL28_LISMO STANDARD; PRT; 62 AA.
CC ID RL28_LISMO
CC AC Q92AJ2;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L28.
GN RPMB OR LMO1816 OR LMI1930.
OS Listeria monocytogenes, and
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639, 1642;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=L.monocytogenes, and L.innocua;
RC STRAIN=EGD-e / Serovar 1/2a, and CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11796659;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Duesurget O.,
RA Entian K.-D., Fsihi H., Garcia-Gel Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krest J., Kuhn M., Kunst F., Kurapkhat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tisseret A.,
RA Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -1- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
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DR EMBL; AL591981; CAC99894.1; -
 DR EMBL; AL596170; CAC97160.1; -
 DR Listlist; LINO1930; -
 DR Listlist; LMO01816; -
 DR InterPro; IPR001383; Ribosomal_L28.
 DR Pfam; PF00830; Ribosomal_L28; 1.
 DR TIGRFAMs; TIGR00009; L28; 1.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 62 AA; 6991 MW; AA43DE039213C562 CRC64;
 Query Match 55.7%; Score 39; DB 1; Length 62;
 Best Local Similarity 66.7%; Pred. No. 0.98;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 YQ 4 WQANNRKYR 12
 : : : : :
 Db 29 WKANLQKVR 37
 : : : : :
 RESULT 9
 ID RL28 STAAAM STANDARD; PRT; 62 AA.
 AC Q99U64;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L28.
 GN RPMB OR SAV1224 OR SA1067 OR MW1107.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
 OS Staphylococcus aureus (strain N315), and
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878, 158879, 196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699, and N315;
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshina K., Puruya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357:1225-1240 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50;
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 acquired MRSA";
 RL Lancet 359:1819-1827 (2002).
 CC -1- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
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 CC EMBL; AP003361; BAB57386.1; -
 CC EMBL; AP003133; BAB42319.1; -
 CC EMBL; AP004826; BAB94972.1; -
 CC InterPro; IPR001383; Ribosomal_L28.
 CC Pfam; PF00830; Ribosomal_L28; 1.
 CC TIGRFAMs; TIGR00009; L28; 1.

KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 62 AA; 6977 MW; 20042609E7D9C26A CRC64;
 Query Match 55.7%; Score 39; DB 1; Length 62;
 Best Local Similarity 60.0%; Pred. No. 0.98;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 YQ 3 QWQANNRKYR 12
 : : : : :
 Db 28 RWANLQKVR 37
 : : : : :
 RESULT 10
 ID RL28 THETN STANDARD; PRT; 62 AA.
 AC Q8R9U1;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L28.
 GN RPMB OR TTE1495.
 OS Thermoanaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
 OC Thermoanaerobacteriaceae; Thermoanaerobacter.
 OX NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MB4 / JCM 11007;
 RX MEDLINE=21992816; PubMed=1197336;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;
 RA "A complete sequence of T. tengcongensis genome";
 RL Genome Res. 12:689-700 (2002).
 CC -1- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
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 CC EMBL; AE013107; AAM24713.1; -
 CC Ribosomal protein; Complete proteome.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
 Query Match 54.3%; Score 38; DB 1; Length 62;
 Best Local Similarity 60.0%; Pred. No. 1.5;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 YQ 3 QWQANNRKYR 12
 : : : : :
 Db 27 RWKPNIRKYR 36
 : : : : :
 RESULT 11
 ID PAPA CHICK STANDARD; PRT; 422 AA.
 AC Q90678;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)
 DE (PAF acetylhydrolase) (PAF 2-acylhydrolase) (IDL-associated
 DE phospholipase A2) (IDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine
 DE esterase) (1-alkyl-2-acetyl-glycerophosphocholine esterase).
 GN PLAZG7.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.

OX NCBI_TaxID=9031;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA MEDLINE=96029630; PubMed=7592717;
 RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,
 RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted
 RT phospholipase A2 with a catalytic triad";
 RL J. Biol. Chem. 270:25481-25487(1995)
 CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
 CC PHOSPHOLIPIDS.
 CC -!- CATALYTIC ACTIVITY: 2-acetyl-1-alkyl-sn-glycero-3-phosphocholine +
 CC H₂O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: PLASMA.
 CC -!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
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 CC -----
 DR EMBL: U34278; AAC59717.1; -;
 DR InterPro: IPR000734; Lipase.
 DR InterPro: IPR005085; PAF-AH_P_II.
 DR InterPro: IPR000379; Ser estrii_site.
 DR Pfam: PF03403; PAF-AH_P_II; 1.
 DR PROSITE: PS00120; LIPASE_SER; 1.
 KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 422
 FT ACT_SITE 266 266
 FT ACT_SITE 289 289
 FT ACT_SITE 345 345
 FT CARBOHYD 331 331
 FT SEQUENCE 422 AA; 47046 MW; 15A5C794376E9141 CRC64;
 SQ
 Query Match 54.3%; Score 38; DB 1; Length 422;
 Best Local Similarity 54.5%; Pred. No. 11;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 FQWQANRKYR 12
 DB 316 FQWAAILRMK 326
 RESULT 12
 YKYL CAEEL
 ID YKYL CAEEL STANDARD; PRT; 455 AA.
 AC Q19910;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein F30B5.4 in chromosome IV.
 GN F30B5.4
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Miller N., Bradshaw H.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP REVISIONS.
 RA Waterston R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE OKL38 FAMILY.
 CC -----
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 CC -----
 DR EMBL: U42437; AAA83493.2; -;
 DR Wormpup; F30B5.4; CE28552.
 KW Hypothetical protein.
 SQ SEQUENCE 455 AA; 51148 MW; D8E6909408FD6C69 CRC64;
 Query Match 54.3%; Score 38; DB 1; Length 455;
 Best Local Similarity 50.0%; Pred. No. 12;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWQANMRK 10
 DB 102 CIQWELNRRR 111
 RESULT 13
 BUB2 YEAST
 ID BUB2 YEAST STANDARD; PRT; 306 AA.
 AC P26448;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitotic check point protein BUB2 (Cell cycle arrest protein BUB2).
 GN BUB2 OR YMR055C OR YMR9796.08C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 MEDLINE=91330299; PubMed=1651171;
 RA Hoyt M.A., Fotis L., Roberts B.T.;
 RT "S. cerevisiae genes required for cell cycle arrest in response to
 RT loss of microtubule function";
 RL Cell 66:507-517(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP CHARACTERIZATION.
 MEDLINE=21385309; PubMed=11493673;
 RA Lee S.E., Jensen S., Frenz L.M., Johnson A.L., Fesquet D.,
 RA Johnston L.H.;
 RT "The Bub2-dependent mitotic pathway in yeast acts every cell cycle and
 RT regulates cytokinesis";
 RL J. Cell Sci. 114:2345-2354(2001).
 CC -!- FUNCTION: Part of a checkpoint which monitors spindle integrity
 CC and prevents premature exit from mitosis. This cell-cycle arrest
 CC depends upon inhibition of the G-protein Tem1 by the BFA1/BUB2
 CC complex.
 CC -!- SUBUNIT: Interacts with BFA1.
 CC -!- SUBCELLULAR LOCATION: Spindle poles.
 CC -!- SIMILARITY: TO S.POMBE CDC16.
 CC -----
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DR ENBL; M64706; AAA16885.1; -;
 DR ENBL; M249703; CAA89765.1; -;
 DR PIR; A39654; A39654.
 DR SGD; S0004659; BUR2.
 DR InterPro; IPR000195; RabGAP_TBC.
 DR Pfam; PF00566; TBC; 1.
 DR SMART; SM00164; TBC; 1.
 KW Cell cycle; Mitosis.
 SQ SEQUENCE 306 AA; 35027 MW; A1DBFB548E81EA3 CRC64;

Query Match 52.9%; Score 37; DB 1; Length 306;
 Best Local Similarity 50.0%; Pred. No. 12;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNMKX 10
 DB 108 CFQWQNMKX 117

RESULT 14

YEBB_HAEIN STANDARD; PRT; 475 AA.
 AC P44693;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein H10409.
 GN H10409.
 OS Haemophilus influenzae.
 CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Haemophilus.
 CC NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE=95305630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kieravage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RL Rd".
 RL Science 269:496-512(1995).
 CC -!- FUNCTION: COULD BE INVOLVED IN CELL WALL DEGRADATION OR
 CC FORMATION (BY SIMILARITY).
 CC -!- SIMILARITY: STRONG, TO E.COLI YEBB.
 CC -!- SIMILARITY: TO STAPHYLOCOCCUS LYSOSTAPHIN.
 CC -----

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DR ENBL; U32724; AAC22068.1; -;
 DR MEROPS; M37.UFW; -;
 DR TIGR; H10409; -;
 DR InterPro; IPR002886; Peptidase M37.
 DR Pfam; PF01551; Peptidase M37; 1.
 KW Hypothetical protein; Cell wall; Complete proteome.
 SQ SEQUENCE 475 AA; 53255 MW; 143C10F92233939D CRC64;

Query Match 52.9%; Score 37; DB 1; Length 475;
 Best Local Similarity 50.0%; Pred. No. 19;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWQNMKXVR 12
 DB 251 QWQNMKXVR 160

RESULT 15

CORL_SCHPO STANDARD; PRT; 522 AA.
 AC O13688;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Core protein 1.
 GN CORL OR SPAC1E3.08C.
 OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 CC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sawin K.E., Hajibagheri M., Nurse P.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds R., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Waleh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
 RA Welter J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Sipakowski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe".
 RL Nature 415:871-880(2002).
 CC -----

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 CC -----

DR ENBL; AJ002494; CAA05501.1; -;
 DR ENBL; Z98595; CAB11187.1; -;
 SQ SEQUENCE 522 AA; 59898 MW; 36CF241DD74AF0F5 CRC64;

Query Match 52.9%; Score 37; DB 1; Length 522;
 Best Local Similarity 45.5%; Pred. No. 21;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPWOANRKY 11
| : | : | :
Db 203 CSEWIANLEKI 213

Search completed: February 21, 2003, 07:27:47
Job time : 5.6 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds
(without alignments)
118.873 Million cell updates/sec

Title: US-09-743-107b-73

Perfect score: 70

Sequence: 1 CFQWQANMRKV 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mbc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	85.7	711	4 Q8TCD2	Q8TCD2 homo sapien
2	56	80.0	38	4 Q9UCY5	Q9UCY5 homo sapien
3	48	68.6	33	6 Q9TR80	Q9TR80 ovis aries
4	43	61.4	275	5 Q93780	Q93780 caenorhabdi
5	42	60.0	511	16 Q8Z462	Q8Z462 salmonella
6	42	60.0	514	10 Q9SP27	Q9SP27 callistephu
7	41	58.6	306	4 Q8TAX2	Q8TAX2 homo sapien
8	41	58.6	466	4 Q9NUS2	Q9NUS2 homo sapien
9	39	55.7	205	16 Q986A0	Q986A0 rhizobium l
10	39	55.7	206	16 Q8UHC2	Q8UHC2 agrobacteri
11	39	55.7	208	16 Q92RH8	Q92RH8 rhizobium m
12	39	55.7	208	16 Q8YFK3	Q8YFK3 brucella me
13	39	55.7	274	4 Q96M21	Q96M21 homo sapien
14	39	55.7	270	4 Q9NTA7	Q9NTA7 homo sapien
15	39	55.7	570	4 Q96DM9	Q96DM9 homo sapien
16	39	55.7	620	4 Q8WX60	Q8WX60 homo sapien

17	39	55.7	866	10 Q9FHI9	Q9FHI9 arabidopsis
18	38	54.3	62	16 Q8R9U1	Q8R9U1 thermocane
19	38	54.3	108	9 Q8SC55	Q8SC55 stx2 conver
20	38	54.3	333	17 Q975Y9	Q975Y9 sulfobus
21	38	54.3	433	5 Q83A2	Q83A2 ciona intes
22	38	54.3	471	16 Q99Z05	Q99Z05 streptococc
23	38	54.3	513	10 Q9LJY8	Q9LJY8 arabidopsis
24	38	54.3	531	10 Q9LTD4	Q9LTD4 arabidopsis
25	38	54.3	557	10 Q9LOH7	Q9LOH7 arabidopsis
26	38	54.3	1154	16 Q8YF11	Q8YF11 brucella me
27	38	54.3	6632	5 Q17362	Q17362 caenorhabdi
28	38	54.3	6632	5 Q01761	Q01761 caenorhabdi
29	37	52.9	279	16 Q8XSE2	Q8XSE2 raietonia s
30	37	52.9	349	5 Q22512	Q22512 caenorhabdi
31	37	52.9	424	5 Q9VT09	Q9VT09 drosophila
32	37	52.9	433	16 Q9K086	Q9K086 neisseria m
33	37	52.9	433	16 Q8JV96	Q8JV96 neisseria m
34	37	52.9	464	16 Q8YF95	Q8YF95 anabaena sp
35	37	52.9	469	9 Q38115	Q38115 bacteriophag
36	37	52.9	518	10 Q9SI49	Q9SI49 arabidopsis
37	37	52.9	681	5 Q9XVD1	Q9XVD1 caenorhabdi
38	37	52.9	737	5 Q95QJ8	Q95QJ8 caenorhabdi
39	37	52.9	940	10 Q9AV70	Q9AV70 oryza sativ
40	37	52.9	1121	10 Q9SM86	Q9SM86 lycopersico
41	37	52.9	2858	5 Q8GYP6	Q8GYP6 caenorhabdi
42	36.5	52.1	235	16 Q8XEI9	Q8XEI9 escherichia
43	36	51.4	48	6 Q77558	Q77558 sus scrofa
44	36	51.4	125	5 Q26115	Q26115 pseudaletia
45	36	51.4	134	13 Q98UD4	Q98UD4 xenopus lae

ALIGNMENTS

RESULT 1

Q8TCD2 PRELIMINARY; PRT; 711 AA.
 ID Q8TCD2; PRELIMINARY; PRT; 711 AA.
 AC Q8TCD2;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Lactotransferrin.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PROSTATE;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC022347; AAH22347.1; --
 SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;

Query Match 85.7%; Score 60; DB 4; Length 711;
 Best Local Similarity 90.9%; Pred. No. 0.0052;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMRKV 11
 |||||
 Db 39 CFQWQANMRKV 49

RESULT 2

Q9UCY5 PRELIMINARY; PRT; 38 AA.
 ID Q9UCY5; PRELIMINARY; PRT; 38 AA.
 AC Q9UCY5;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Lactoferrin homolog (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96081613; PubMed=8551695;
RX Sato I.;
RT "Characterization of the 84-kDa protein with ABH activity in human
  seminal plasma.";
RL Jpn. J. Legal Med. 49:281-293(1995).
DR HSP; P02788; 18KA.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDEB CRC64;

  Query Match      80.0%; Score 56; DB 4; Length 38;
  Best Local Similarity 90.9%; Pred. No. 0.0013;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQWQNNRKVR 12
Db 21 FQWQNNRKVR 31

RESULT 3
Q9TR80 PRELIMINARY; PRT; 33 AA.
AC Q9TR80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Lactoferrin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=95127729; PubMed=7827104;
RA Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
RL Biochim. Biophys. Acta 1243:25-32(1995).
DR HSP; O77698; 1CE2.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

  Query Match      68.6%; Score 48; DB 6; Length 33;
  Best Local Similarity 63.6%; Pred. No. 0.037;
  Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 11
Db 19 CYQWQNNRKVL 29

RESULT 4
Q93780 PRELIMINARY; PRT; 275 AA.
AC Q93780;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F53H4.4 protein.
GN F53H4.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Dobson R.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96069613; PubMed=9851916;
RX none;
RT "Genome sequence of the nematode C.elegans: A platform for
  investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81089; CAB03137.1; -.
SQ SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;

  Query Match      61.4%; Score 43; DB 5; Length 275;
  Best Local Similarity 63.6%; Pred. No. 3.4;
  Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNNRKVR 12
Db 262 FQWQNNRKVR 272

RESULT 5
Q82462 PRELIMINARY; PRT; 511 AA.
AC Q82462;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein STY3070.
GN STY3070.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks R., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies K.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagers K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
  enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL627276; CAD06049.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 511 AA; 58126 MW; E2DD124E10D178B CRC64;

  Query Match      60.0%; Score 42; DB 16; Length 511;
  Best Local Similarity 58.3%; Pred. No. 10;
  Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12
Db 350 CFQWQNNRKVR 361

RESULT 6
Q9SP27 PRELIMINARY; PRT; 514 AA.
AC Q9SP27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Flavone synthase II.
GN CYP93B5.
OS Callistephus chinensis (China aster).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
OC Astereae; Callistephus.

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OX NCBI_TaxID=113379;
RN [1]
RP SEQUENCE FROM N.A.
RA Martens S., Forkmann G.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AF188612; AAF04115.1; -.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 514 AA; 58412 MW; 90B631B28952A5E7 CRC64;

Query Match 60.0%; Score 42; DB 10; Length 514;
Best Local Similarity 54.5%; Pred. No. 10;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFOWQANMKV 11
Db 470 CFENANDKEV 480
|||||:|:|

RESULT 7
Q8TAX2 PRELIMINARY; PRT; 306 AA.
ID Q8TAX2
AC Q8TAX2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to hypothetical protein FLJ11175.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PANCREAS;
RA Strauberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025708; AAH25708.1; -.
KW Hypothetical protein.
SQ SEQUENCE 306 AA; 43D9AD722566B343 CRC64;

Query Match 58.6%; Score 41; DB 4; Length 306;
Best Local Similarity 55.6%; Pred. No. 9.1;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFOWQANMR 9
Db 269 CFQWESTLR 277
|||||:|:|

RESULT 8
Q9NUS2 PRELIMINARY; PRT; 466 AA.
ID Q9NUS2
AC Q9NUS2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CDNA FLJ11175 fis, clone PLACE1007375, weakly similar to phorbol
ester/diacylglycerol-binding protein UNC-13.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isogai T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagaatsuna M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

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RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK002037; BAA92048.1; -.
DR HSSP; P21707; 1BYN.
DR InterPro; IPR000008; C2.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00168; C2; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR SMART; SM00239; C2; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; UNKNOWN_1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00030; RNP_RNP_1; UNKNOWN_1.
SQ SEQUENCE 466 AA; 53192 MW; E4113A5062F58D6E CRC64;

Query Match 58.6%; Score 41; DB 4; Length 466;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFOWQANMR 9
Db 269 CFQWESTLR 277
|||||:|:|

RESULT 9
Q986A0 PRELIMINARY; PRT; 205 AA.
ID Q986A0
AC Q986A0;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Pyridoxamine 5'-phosphate oxidase.
GN MLJ7454.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214969;
RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003011; BAB53553.1; -.
DR InterPro; IPR000659; Pyridox_oxidase.
DR Pfam; PF01243; Pyridox_oxidase; 1.
DR ProDom; PD008312; Pyridox_oxidase; 1.
DR TIGRFAMs; TIGR00558; pdxH; 1.
DR PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
KW Complete proteome.
SQ SEQUENCE 205 AA; 23300 MW; 0BADE4CD312327EA CRC64;

Query Match 55.7%; Score 39; DB 16; Length 205;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFOWQANMKVR 12
Db 88 CFHWKSLERQVR 99
|||||:|:|

RESULT 10
Q8UHC2 PRELIMINARY; PRT; 206 AA.
ID Q8UHC2
AC Q8UHC2;

```

DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Pyridoxamine 5'-phosphate oxidase.
 GN Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Bisen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liaw L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58.";
 RL Science 294:2317-2323 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmel K., Gordon J., Vaudin D., Iartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursun J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RA "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328 (2001).
 DR EMBL; AE009043; AAL41776.1; -;
 DR EMBL; AE008009; AAK8569.1; -;
 KW Complete proteome.
 SQ SEQUENCE 206 AA; 23720 MW; 3B8488AE5307C0C1 CRC64;
 Query Match 55.7%; Score 39; DB 16; Length 206;
 Best Local Similarity 50.0%; Pred. No. 14;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWQANMKVR 12
 DB 88 CFHWKSLRRQVR 99
 RESULT 11
 Q92RH8 PRELIMINARY; PRT; 206 AA.
 ID Q92RH8
 AC Q92RH8
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Probable pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase) protein
 DE (EC 1.4.3.5).
 GN PDHX OR R00895 OR SMC000069.
 OS Rhizobium meliloti (sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=1021.
 RA Capela D., Barloy-Hubler F., Guzy J., Bothe G., Ampe F., Batut J.,
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
 RA Pohl T., Portetellette D., Puehler A., Purnelle B., Ramsperger U.,

RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 RT Sinorhizobium meliloti strain 1021.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
 DR EMBL; AL591785; CAC45467.1; -;
 DR InterPro; IPR000659; Pyridox oxidase.
 DR Pfam; PF01243; Pyridox oxidase; 1.
 DR ProDom; PD006312; Pyridox oxidase; 1.
 DR TIGRFAMs; TIGR00558; pdxH; 1.
 DR PROSITE; PS01084; PYRIDOX_OXIDASE; UNKNOWN_1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 206 AA; 23900 MW; A2DB74229DACA97A CRC64;
 Query Match 55.7%; Score 39; DB 16; Length 206;
 Best Local Similarity 50.0%; Pred. No. 14;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWQANMKVR 12
 DB 88 CFHWKSLRRQVR 99
 RESULT 12
 Q8YFK3 PRELIMINARY; PRT; 208 AA.
 ID Q8YFK3
 AC Q8YFK3
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Probable pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5).
 GN BMEI1517.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=16M / ATCC 23456 / BIOTYPE 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA DelVecchio V.G., Kaprat V., Redkar R.J., Patra G., Mujar C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
 RA Selkov E., Eizer F.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyrides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
 DR EMBL; AE009587; AAL52698.1; -;
 DR InterPro; IPR000659; Pyridox oxidase.
 DR Pfam; PF01243; Pyridox oxidase; 1.
 DR ProDom; PD006312; Pyridox oxidase; 1.
 DR TIGRFAMs; TIGR00558; pdxH; 1.
 DR PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 208 AA; 23866 MW; CB1F50BC9612DE28 CRC64;
 Query Match 55.7%; Score 39; DB 16; Length 208;
 Best Local Similarity 50.0%; Pred. No. 14;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWQANMKVR 12
 DB 90 CFHWKSLRRQVR 101
 RESULT 13
 Q96M21 PRELIMINARY; PRT; 274 AA.
 ID Q96M21
 AC Q96M21
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE CDNA FLJ32891 fis, clone TESTI2004929.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahori K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK057453; BAB71493.1; -
DR InterPro; IPR000436; SUSHI_SCR_CCP.
DR Pfam; PF00084; SUSHI; 2.
SQ SEQUENCE 274 AA; 30083 MW; 1DD43654D4135B2F CRC64;

Query Match 55.7%; Score 39; DB 4; Length 274;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQANMRKV 12
Db |||||:|:|:|
66 CFQWRGVRYLR 77

RESULT 14
Q9NTA7 PRELIMINARY; PRT; 570 AA.
ID Q9NTA7
AC Q9NTA7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Hypothetical 63.7 kDa protein (Fragment).
GN DKFZP761E1824.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=AMYGDALA;
RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Gassenhuber J.,
RA Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137432; CAB70735.1; -
DR InterPro; IPR000436; SUSHI_SCR_CCP.
DR Pfam; PF00084; SUSHI; 2.
DR SMART; SM00032; CCP; 2.
KW Hypothetical protein.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 570 AA; 63713 MW; 66B1A4B4096C3A1B CRC64;

Query Match 55.7%; Score 39; DB 4; Length 570;
Best Local Similarity 45.5%; Pred. No. 43;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQANMRKV 11
Db |||||:|:|:|
134 CVRWQINSRRI 144

RESULT 15
Q96DM9 PRELIMINARY; PRT; 570 AA.
ID Q96DM9
AC Q96DM9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CDNA FLJ32142 fis, clone PLACE5000068, weakly similar to C4B-binding
DE protein precursor (C4BP).

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahori K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK056704; BAB71259.1; -
DR InterPro; IPR000436; SUSHI_SCR_CCP.
DR Pfam; PF00084; SUSHI; 2.
SQ SEQUENCE 570 AA; 64211 MW; E67489C3A38B868A CRC64;

Query Match 55.7%; Score 39; DB 4; Length 570;
Best Local Similarity 45.5%; Pred. No. 43;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQANMRKV 11
Db |||||:|:|:|
159 CVRWQINSRRI 169

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Search completed: February 21, 2003, 07:44:26
Job time : 22.8 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds
(without alignments)
56.502 Million cell updates/sec

Title: US-09-743-107B-74
Perfect score: 69
Sequence: 1 CFQWRMRKVR 12

Scoring table: BLOSUM62
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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	12	21	AAV78074 Human lactoferrin
2	65	94.2	12	21	AAV78089 Human lactoferrin
3	65	94.2	12	21	AAV78090 Human lactoferrin
4	65	94.2	12	21	AAV78093 Human lactoferrin
5	64	92.8	12	21	AAV78086 Human lactoferrin
6	63	91.3	12	21	AAV78038 Human lactoferrin
7	63	91.3	12	21	AAV78046 Human lactoferrin
8	63	91.3	12	21	AAV78047 Human lactoferrin
9	63	91.3	12	21	AAV78095 Human lactoferrin
10	63	91.3	13	21	AAV78037 Human lactoferrin

11	63	91.3	13	21	AAV78048 Human lactoferrin
12	63	91.3	13	21	AAV78049 Human lactoferrin
13	63	91.3	14	21	AAV78036 Human lactoferrin
14	63	91.3	14	21	AAV78050 Human lactoferrin
15	63	91.3	14	21	AAV78051 Human lactoferrin
16	63	91.3	15	17	AAV78054 Peptide for anti-u
17	63	91.3	15	21	AAV78035 Human lactoferrin
18	63	91.3	15	21	AAV78062 Human lactoferrin
19	63	91.3	15	21	AAV78063 Human lactoferrin
20	63	91.3	16	21	AAV78031 Human lactoferrin
21	63	91.3	16	21	AAV78064 Human lactoferrin
22	63	91.3	16	21	AAV78065 Human lactoferrin
23	63	91.3	17	21	AAV78034 Human lactoferrin
24	63	91.3	17	21	AAV78066 Human lactoferrin
25	63	91.3	17	21	AAV78067 Human lactoferrin
26	63	91.3	18	15	AAV78067 Human lactoferrin
27	63	91.3	18	17	AAV78032 Advanced glycosyla
28	63	91.3	18	21	AAV78033 Human lactoferrin
29	63	91.3	19	21	AAV78067 Amino acid sequenc
30	63	91.3	19	21	AAV78032 Human lactoferrin
31	63	91.3	20	13	AAV78032 Anti microbial pep
32	63	91.3	20	14	AAV78032 Lactoferrin-relate
33	63	91.3	20	15	AAV78032 Lactoferrin-derive
34	63	91.3	20	15	AAV78032 Lactoferrin-derive
35	63	91.3	20	15	AAV78032 Lactoferrin-derive
36	63	91.3	20	15	AAV78032 Lactoferrin-derive
37	63	91.3	20	16	AAV78032 Bovine lactoferrin
38	63	91.3	20	16	AAV78032 Bovine lactoferrin
39	63	91.3	20	16	AAV78032 Anti-parasitic lac
40	63	91.3	20	16	AAV78032 Anti-parasitic lac
41	63	91.3	20	17	AAV78032 Peptide for anti-u
42	63	91.3	20	17	AAV78032 Lactoferrin-derive
43	63	91.3	20	17	AAV78032 Lactoferrin-derive
44	63	91.3	20	17	AAV78032 Lactoferrin-derive
45	63	91.3	20	17	AAV78032 Lactoferrin-derive

ALIGNMENTS

RESULT 1
AAV78074
ID AAV78074 standard; Peptide; 12 AA.
XX AAV78074;
AC AAV78074;
XX 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:74.
DE Human lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX Homo sapiens.
OS Synthetic.
XX WO200001730-A1.
XX 13-JAN-2000.
XX 06-JUL-1999; 99WO-SE01230.
XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX (ASCI-) A+ SCI INVEST AB.
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX Claim 22; Page 35; 102pp; English.
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX SQ Sequence 12 AA;
Query Match 100.0%; Score 69; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFQWQRMKVR 12
| | | | | | | | | | | |
Db 1 CFQWQRMKVR 12
RESULT 2
AAY78089
ID AAY78089 standard; Peptide; 12 AA.
XX AAY78089;
AC AAY78089;
XX 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:89.
XX Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.
XX Homo sapiens.
XX OS Synthetic.
XX WO200001730-A1.
XX 13-JAN-2000.
XX 06-JUL-1999; 99WO-SB01230.
XX 06-JUL-1998; 98SE-0002441.
XX 17-JUL-1998; 98SE-0002562.
XX 29-DEC-1998; 98SE-0004614.
XX (ASCI-) A+ SCI INVEST AB.
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX Claim 22; Page 37; 102pp; English.
XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX SQ Sequence 12 AA;
Query Match 94.2%; Score 65; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.00014;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWQRMKVR 12
| | | | | | | | | | | |
Db 1 CFQWQRMKVR 12
RESULT 3
AAY78090
ID AAY78090 standard; Peptide; 12 AA.
XX AAY78090;
AC AAY78090;
XX 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:90.
XX Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.
XX Homo sapiens.
XX OS Synthetic.
XX WO200001730-A1.
XX 13-JAN-2000.
XX 06-JUL-1999; 99WO-SB01230.
XX 06-JUL-1998; 98SE-0002441.
XX 17-JUL-1998; 98SE-0002562.
XX 29-DEC-1998; 98SE-0004614.
XX (ASCI-) A+ SCI INVEST AB.
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX Claim 22; Page 37; 102pp; English.
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 94.2%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00014;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQRAVRKVR 12
 DB 1 CFQWQRAVRKVR 12

RESULT 4

AAV78093
 ID AAV78093 standard; Peptide; 12 AA.

XX AC AAV78093;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:93.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;
 XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Matsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections.

XX PS Claim 22; Page 38; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations, colitis, and Candida infection on a mucosal
 CC in food stuffs such as infant formula food. The peptides can also be used
 CC fungicidal and bactericidal and may also be used as preservatives.

XX CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 94.2%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00014;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFQWQRAVRKVR 12
 DB 1 CFQWQRAVRKVR 12

RESULT 5

AAV78086

ID AAY78086 standard; Peptide; 12 AA.

XX AC AAY78086;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:85.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;
 XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Matsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,

XX PS Claim 22; Page 36; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations, colitis, and Candida infection on a mucosal
 CC in food stuffs such as infant formula food. The peptides can also be used
 CC fungicidal and bactericidal and may also be used as preservatives.

XX CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.8%; Score 64; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00021;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRAVRKVR 12
 |||||
 Db 1 CFQWQRAVRKVR 12

RESULT 6

AAV78038
 ID AAY78038 standard; Peptide; 12 AA.

XX AAY78038;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:38.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 DE food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX

OS Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

PD 06-JUL-1999; 99WO-SE01230.

PF 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food

XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumors. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 12 AA;

SQ

Query Match 91.3%; Score 63; DB 21; Length 12;

Best Local Similarity 91.7%; Pred. No. 0.00031;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRAVRKVR 12

|||||

Db 1 CFQWQRAVRKVR 12

|||||

RESULT 7

AAV78046

ID AAY78046 standard; Peptide; 12 AA.

XX AAY78046;

XX 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:46.

DE Human; lactoferrin; modification; infection; inflammation; tumour;

DE food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

KW urinary tract infection; colitis; Candida infection; fungicidal;

KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

PD 06-JUL-1999; 99WO-SE01230.

PF 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food

XX Claim 15; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumors. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 12 AA;

SQ

Query Match 91.3%; Score 63; DB 21; Length 12;

Best Local Similarity 91.7%; Pred. No. 0.00031;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRAVRKVR 12

|||||

Db 1 CFQWQRAVRKVR 12

|||||

RESULT 8

AAV78047

ID AAY78047 standard; Peptide; 12 AA.

XX AAY78047;

XX 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:47.

DE

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 18; Page 73; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 12 AA;
 SQ Query Match 91.3%; Score 63; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00031;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRAMRKVR 12
 Db 1 CFQWQRAMRKVR 12
 RESULT 9
 AAY78095
 ID AAY78095 standard; Peptide; 12 AA.
 XX AAY78095;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:95.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS

OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 22; Page 38; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 12 AA;
 SQ Query Match 91.3%; Score 63; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00031;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRAMRKVR 12
 Db 1 CFQWQRAMRKVR 12
 RESULT 10
 AAY78037
 ID AAY78037 standard; Peptide; 13 AA.
 XX AAY78037;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:37.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 PF


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XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 12; Page 70; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX SQ Sequence 13 AA;
Query Match 91.3%; Score 63; DB 21; Length 13;
Best Local Similarity 91.7%; Pred. No. 0.00033;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
DB 2 CFQWQRMKVR 13

RESULT 11
AAY78048
ID AAY78048 standard; Peptide; 13 AA.
XX
XX AAY78048;
XX
XX 25-APR-2000 (first entry)
XX
XX Human lactoferrin derived peptide SEQ ID NO:48.
XX
XX Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
XX
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 98WO-SE01230.
XX
XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX

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PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 15; Page 74; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX SQ Sequence 13 AA;
Query Match 91.3%; Score 63; DB 21; Length 13;
Best Local Similarity 91.7%; Pred. No. 0.00033;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
DB 2 CFQWQRMKVR 13

RESULT 12
AAY78049
ID AAY78049 standard; Peptide; 13 AA.
XX
XX AAY78049;
XX
XX 25-APR-2000 (first entry)
XX
XX Human lactoferrin derived peptide SEQ ID NO:49.
XX
XX Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
XX
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 98WO-SE01230.
XX
XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX

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PS Claim 18; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 13 AA;

SQ Query Match 91.3%; Score 63; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. NO. 0.00033;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKVR 12

Db 2 CFQWQRMNRKVR 13

RESULT 13

AAAY78036

ID AAY78036 standard; Peptide; 14 AA.

XX AC AAY78036;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:36.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;

XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

XX KW urinary tract infection; colitis; Candida infection; fungicidal;

XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,

XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 12; Page 69; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 14 AA;

SQ Query Match 91.3%; Score 63; DB 21; Length 14;

Best Local Similarity 91.7%; Pred. NO. 0.00036;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKVR 12

Db 3 CFQWQRMNRKVR 14

RESULT 14

AAAY78050

ID AAY78050 standard; Peptide; 14 AA.

XX AC AAY78050;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:50.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;

XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

XX KW urinary tract infection; colitis; Candida infection; fungicidal;

XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,

XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 15; Page 75; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 14 AA;

Query Match 91.3%; Score 63; DB 21; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.00036;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKVR 12

DB 3 CFQWQRNMRKVR 14

RESULT 15

AA78051

ID AA78051 standard; Peptide; 14 AA.

XX AC AA78051;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:51.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections, -
 PT inflammations and tumors and for use in infant formula food -

XX PS Claim 18; Page 75; 102pp; English.

XX AA78001 to AA78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 14 AA;

Query Match 91.3%; Score 63; DB 21; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.00036;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKVR 12

DB 3 CFQWQRNMRKVR 14

Search completed: February 21, 2003, 07:37:12

Job time: 28.35 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 Seconds
(without alignments)
40.818 Million cell updates/sec

Title: US-09-743-107B-74
Perfect score: 69
Sequence: 1 CFQWRAMKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCOTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	91.3	18	1	US-08-204-487-3
2	63	91.3	18	2	US-08-485-948-8
3	63	91.3	18	2	US-08-428-380-8
4	63	91.3	18	2	US-08-475-055-8
5	63	91.3	20	1	US-07-755-161A-3
6	63	91.3	20	1	US-07-891-174-3
7	63	91.3	20	1	US-08-204-487-1
8	63	91.3	20	1	US-08-256-771-24
9	63	91.3	20	1	US-08-256-771-25
10	63	91.3	20	1	US-08-381-984-24
11	63	91.3	20	1	US-08-381-984-25
12	63	91.3	22	4	US-09-508-734-4
13	63	91.3	24	4	US-09-508-734-6
14	63	91.3	25	1	US-07-755-161A-10
15	63	91.3	25	1	US-07-891-174-10
16	63	91.3	25	1	US-08-204-487-7
17	63	91.3	29	4	US-09-508-734-8
18	63	91.3	36	1	US-07-755-161A-8
19	63	91.3	36	1	US-07-891-174-8
20	63	91.3	36	1	US-08-256-771-30
21	63	91.3	36	1	US-08-381-984-29
22	63	91.3	47	2	US-08-464-182A-6
23	63	91.3	47	2	US-08-406-271-6
24	63	91.3	50	2	US-08-893-274A-7
25	63	91.3	52	4	US-09-017-043A-3
26	63	91.3	53	2	US-08-464-182A-5
27	63	91.3	53	2	US-08-406-271-5

28	63	91.3	54	2	US-08-464-182A-2
29	63	91.3	54	2	US-08-406-271-2
30	63	91.3	694	3	US-08-724-586-2
31	63	91.3	694	4	US-09-421-632-2
32	63	91.3	694	4	US-09-932-190-2
33	63	91.3	705	2	US-08-655-640-2
34	63	91.3	708	2	US-08-655-640-4
35	63	91.3	711	1	US-08-154-019-4
36	63	91.3	711	1	US-08-461-333-4
37	63	91.3	711	3	US-08-464-167-4
38	63	91.3	711	3	US-09-158-313-4
39	63	91.3	711	4	US-08-476-798-4
40	60	87.0	711	1	US-08-145-681-2
41	60	87.0	711	1	US-08-250-308-2
42	60	87.0	711	1	US-08-453-703-2
43	60	87.0	711	2	US-08-456-106-2
44	60	87.0	711	3	US-08-456-108-2
45	60	87.0	711	4	US-09-265-577-2

ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESS: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FJN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "HUMAN LACTOPERRIN PEPTIDE"

OTHER INFORMATION: (20-37)"
US-08-204-487-3

Query Match 91.3%; Score 63; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.00012;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMKVR 12
| | | | | | | | | |
Db 1 CFQWQRMKVR 12

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/485,948
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,217
; FILING DATE: JUNE 7, 1995
; APPLICATION NUMBER: 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008A
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LP-C1, 8-25
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal

US-08-485-948-8

Query Match 91.3%; Score 63; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.00012;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMKVR 12
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Db 1 CFQWQRMKVR 12

OTHER INFORMATION: (20-37)"
US-08-204-487-3

Query Match 91.3%; Score 63; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.00012;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMKVR 12
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Db 1 CFQWQRMKVR 12

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/485,948
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,217
; FILING DATE: JUNE 7, 1995
; APPLICATION NUMBER: 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008A
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LP-C1, 8-25
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal

US-08-485-948-8

Query Match 91.3%; Score 63; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.00012;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMKVR 12
| | | | | | | | | |
Db 1 CFQWQRMKVR 12

RESULT 3

US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341
; GENERAL INFORMATION:
; APPLICANT: LI YONG MING
; APPLICANT: VLASSARA, HELEN
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/628,380
; FILING DATE: April 4, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LP-C1, 8-25
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal

US-08-628-380-8

Query Match 91.3%; Score 63; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.00012;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMKVR 12
| | | | | | | | | |
Db 1 CFQWQRMKVR 12

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; NUMBER OF SEQUENCES: 9

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LP-CI, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8

Query Match          91.3%; Score 63; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.00012;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRKVR 12
Db 1 CFQWQRMRKVR 12

RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURES:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

Query Match          91.3%; Score 63; DB 1; Length 20;
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Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRAMRKVR 12
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Db 2 CFQWQRAMRKVR 13

RESULT 6
US-07-891-174-3
; Sequence 3, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHEICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURES:
; NAME/KEY: modified site

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 91.3%; Score 63; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRAMRKVR 12
| | | | | | | | | |
Db 2 CFQWQRAMRKVR 13

RESULT 7
US-08-204-487-1
; Sequence 1, Application US/08204487
; Patent No. 5563425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FJN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1-20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
US-08-204-487-1

Query Match 91.3%; Score 63; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRKVR 12
DB 2 CFQWQRMRKVR 13

RESULT 8
US-08-256-771-24
Sequence 24, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"

US-08-256-771-24

Query Match 91.3%; Score 63; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRKVR 12
DB 2 CFQWQRMRKVR 13

RESULT 9
US-08-256-771-25
Sequence 25, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are protected to
OTHER INFORMATION: prevent disulfide bond"

US-08-256-771-25
Query Match 91.3%; Score 63; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRKVR 12
DB 2 CFQWQRMRKVR 13

RESULT 10
US-08-381-984-24


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; Sequence 24, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at positions 2
; OTHER INFORMATION: and 19 are bonded by disulfide linkage"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
; US-08-381-984-24

Query Match 91.3%; Score 63; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRKVR 12
DB 2 CFQWQRMRKVR 13

RESULT 11
US-08-381-984-25
; Sequence 25, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
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; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at positions 2
; OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
; US-08-381-984-25

Query Match 91.3%; Score 63; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRKVR 12
DB 2 CFQWQRMRKVR 13

RESULT 12
US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; TITLE OF INVENTION: useful microorganism thereof
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 4
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RESULT 15
US-07-891-174-10
Sequence 10, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
LOCATION: 21

IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
Query Match 91.3%; Score 63; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.00017;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CFQWRMRKVR 12
Db 4 CFQWRMRKVR 15
Search completed: February 21, 2003, 07:50:34
Job time : 9.7 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds
(without alignments)
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Title: US-09-743-107b-74
Perfect score: 69
Sequence: 1 CFQWQRMRKVR 12

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Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	63	91.3	25	9	US-09-798-869-20
3	63	91.3	694	9	US-10-023-098-2
4	55	79.7	15	9	US-09-798-869-6
5	53	76.8	15	9	US-09-798-869-3
6	53	76.8	25	9	US-09-798-869-23
7	45	65.2	15	9	US-09-798-869-7
8	44	63.8	15	9	US-09-798-869-4
9	44	63.8	25	9	US-09-798-869-22
10	41	59.4	15	9	US-09-798-869-8
11	41	59.4	15	9	US-09-798-869-29
12	41	59.4	15	9	US-09-798-869-30
13	37	53.6	21	10	US-09-864-761-47985
14	37	53.6	489	9	US-09-888-320-2
15	36	52.2	209	10	US-09-904-536-8
16	36	52.2	209	10	US-09-904-536-9
17	36	52.2	209	10	US-09-904-536-11
18	36	52.2	209	10	US-09-904-536-12
19	36	52.2	209	10	US-09-904-536-13

20	36	52.2	209	10	US-09-904-536-14	Sequence 14, Appl
21	36	52.2	209	10	US-09-904-536-15	Sequence 15, Appl
22	36	52.2	209	10	US-09-904-536-16	Sequence 16, Appl
23	36	52.2	209	10	US-09-904-536-17	Sequence 17, Appl
24	36	52.2	209	10	US-09-904-536-18	Sequence 18, Appl
25	36	52.2	212	10	US-09-904-536-10	Sequence 10, Appl
26	36	52.2	235	9	US-10-095-449-6	Sequence 6, Appl
27	36	52.2	235	10	US-09-448-378-1	Sequence 1, Appl
28	36	52.2	235	10	US-09-983-806-6	Sequence 6, Appl
29	36	52.2	235	10	US-09-904-536-1	Sequence 1, Appl
30	35	50.7	86	9	US-09-738-626-5715	Sequence 5715, Ap
31	35	50.7	1192	9	US-10-170-102-2	Sequence 2, Appl
32	34	49.3	95	10	US-09-764-864-1031	Sequence 1031, Ap
33	34	49.3	846	9	US-10-051-409-4	Sequence 4, Appl
34	34	49.3	1617	9	US-10-090-453A-2	Sequence 2, Appl
35	33	47.8	15	9	US-09-798-869-5	Sequence 5, Appl
36	33	47.8	46	10	US-09-864-761-48879	Sequence 48879, A
37	33	47.8	138	9	US-10-013-373-14	Sequence 14, Appl
38	33	47.8	411	10	US-09-764-864-899	Sequence 899, App
39	33	47.8	411	10	US-09-764-864-1346	Sequence 1346, Ap
40	33	47.8	978	9	US-09-938-901-8	Sequence 8, Appl
41	32.5	47.1	124	10	US-09-864-761-44327	Sequence 44327, A
42	32	46.4	13	9	US-09-798-869-26	Sequence 26, Appl
43	32	46.4	14	9	US-09-798-869-25	Sequence 25, Appl
44	32	46.4	15	9	US-09-798-869-1	Sequence 1, Appl
45	32	46.4	15	9	US-09-798-869-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication No. US2003022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2

Query Match 91.3%; Score 63; DB 9; Length 15;
Best Local Similarity 91.7%; Pred. NO. 7.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMRKVR 12
| | | | | | | | | | | | | |
Db 3 CFQWQRMRKVR 14

RESULT 2
US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US2003022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON

Tue Dec 9 06:51:31 2003

```

; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-798-869-20

Query Match          91.3%; Score 63; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
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DB 3 CFQWQRMKVR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-023-096-2

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Query Match          91.3%; Score 63; DB 9; Length 694;
Best Local Similarity 91.7%; Pred. No. 0.0036;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
   |||||
DB 22 CFQWQRMKVR 33

RESULT 4
US-09-798-869-6
; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
; OTHER INFORMATION: sequence)
; US-09-798-869-6

Query Match          79.7%; Score 55; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
   |||||
DB 3 CFQWQRMKVR 14

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
; US-09-798-869-3

Query Match          76.8%; Score 53; DB 9; Length 15;
Best Local Similarity 72.7%; Pred. No. 0.0037;

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Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMKV 11
|:|||||:
Db 3 CYQWQRMKL 13

RESULT 6
US-09-798-869-23
; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23

Query Match 76.8%; Score 53; DB 9; Length 25;
Best Local Similarity 72.7%; Pred. No. 0.0062;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMKV 11
|:|||||:
Db 3 CYQWQRMKL 13

RESULT 7
US-09-798-869-7
; Sequence 7, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-7

Query Match 65.2%; Score 45; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.084;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQRMKV 11
|:|||||:
Db 3 CYQWQRMKL 13

RESULT 8
US-09-798-869-4
; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4

Query Match 63.8%; Score 44; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.12;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQRMKV 11
|:|||||:
Db 3 CLRWQNMKV 13

RESULT 9
US-09-798-869-22
; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-22

Query Match 63.8%; Score 44; DB 9; Length 25;
Best Local Similarity 63.6%; Pred. No. 0.21;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQRMKV 11
|:|||||:
Db 3 CLRWQNMKV 13

RESULT 10

US-09-798-869-8
; Sequence 8, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine
; OTHER INFORMATION: sequence)
US-09-798-869-8

Query Match 59.4%; Score 41; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.4;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 11
|:|:|:|:|
DB 3 CLRQWQWEMKV 13

RESULT 11

US-09-798-869-29
; Sequence 29, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29

Query Match 59.4%; Score 41; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.4;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 11
|:|:|:|:|
DB 3 CFRQWQRMKXL 13

RESULT 12

US-09-798-869-30

; Sequence 30, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-30

Query Match 59.4%; Score 41; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.4;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 11
|:|:|:|:|
DB 3 CFRQWQRMKXL 13

RESULT 13

US-09-864-761-47985
; Sequence 47985, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47985
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL096701.14
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EST_HUMAN HIT: AW294800.1, EVALUATE 1.00e-06
US-09-864-761-47985

Query Match 53.6%; Score 37; DB 10; Length 21;
Best Local Similarity 83.3%; Pred. No. 2.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQR 6
| | | | |
Db 16 CFQWRR 21

RESULT 14
US-09-888-320-2
; Sequence 2, Application US/09888320
; Publication No. US20030013090A1
; GENERAL INFORMATION:
; APPLICANT: Barry III, Clifton E.
; APPLICANT: DeBarber, Andrea E.
; APPLICANT: Mdluli, Khisimuzi
; APPLICANT: Bekker, Linda-Gail
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
; FILE REFERENCE: 015280-413100US
; CURRENT APPLICATION NUMBER: US/09/888,320
; CURRENT FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/214,187
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: wild-type EtAa monooxygenase (Rv3854c, EtAa)
US-09-888-320-2

Query Match 53.6%; Score 37; DB 9; Length 489;
Best Local Similarity 54.5%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRKV 11
| : | | | |
Db 253 CQWPRRMRKM 263

RESULT 15
US-09-904-536-8
; Sequence 8, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:

; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-8

Query Match 52.2%; Score 36; DB 10; Length 209;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMRK 10
| | | | |
Db 178 CLHWQTRRR 187

Search completed: February 21, 2003, 08:08:04
Job time : 10.55 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 Seconds
(without alignments)
120.168 Million cell updates/sec

Title: US-09-743-107B-74

Perfect score: 69

Sequence: 1 CFQWQRAMKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	91.3	711	1 TFHUL	lactotransferrin p
2	53	76.8	708	2 JC323	lactoferrin - goat
3	50	72.5	33	2 S52107	lactoferrin - sheep
4	44	63.8	707	1 A28438	lactoferrin precursor
5	43	62.3	4568	2 T08030	dynein beta heavy
6	42	60.9	1135	2 T14803	phytochrome C - so
7	41	59.4	275	2 T2597	hypothetical prote
8	41	59.4	932	2 T28820	hypothetical prote
9	40	58.0	1391	2 T20642	hypothetical prote
10	40	58.0	1397	2 H97451	protein F09C3.1 [i
11	39	56.5	206	2 E87998	pyridoxamine 5'-ph
12	39	56.5	206	2 AB3670	pyridoxamine 5'-ph
13	39	56.5	208	2 AG3441	probable pyridoxam
14	39	56.5	1746	2 D83181	hypothetical prote
15	39	56.5	2594	2 A35774	kinase-related pro
16	38	55.1	275	2 A36415	32K protein - vacc
17	38	55.1	377	2 T28558	hypothetical prote
18	38	55.1	377	2 T37403	35K myristylprotei
19	38	55.1	377	2 F72165	17L protein - var
20	38	55.1	378	2 T42518	A16L protein - vac
21	38	55.1	433	2 T34605	hypothetical prote
22	38	55.1	500	2 T71633	ADP/ATP carrier pr
23	38	55.1	515	2 T00510	probable cytochrom
24	38	55.1	543	2 T00513	cytochrome P450 ho
25	37	53.6	85	2 AG0794	polymyxin B resist
26	37	53.6	121	2 AH1147	hypothetical prote
27	37	53.6	202	2 T71306	hypothetical prote
28	37	53.6	289	2 G86403	33.3K hypothetical
29	37	53.6	294	2 T00104	probable dUDP-4-de

ALIGNMENTS

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

A/Alternate names: lactoferrin

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence, revision 21-Nov-1997 #text, change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74:

R/Cho, Y.

submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A/Status: preliminary; translated from GE/EMBL/DBD

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237

R/Rev, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5289, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; MUID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-148, 'T', 150-422, 'C', 424-711 <REV>

A/Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactoferi

A/Reference number: A45401; MUID:93125571; PMID:1480183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <TEN>

A/Cross-references: GB:S52559; NID:G263311; PIDN:AAB24877.1; PID:G263312

A/Experimental source: placenta

A/Note: sequence extracted from NCBI backbone (NCBIIP:122202)

R/Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; MUID:90326549; PMID:2374734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POW>

A/Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A/Reference number: S15853; MUID:91264786; PMID:2049066

A/Accession: S15853

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 20-31 <ST1>

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-28, 'X', 30-31 <ST2>

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
 Blood 70, 989-993, 1987
 A>Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
 A;Reference number: S07160; PMID:88001031; PMID:3477300
 A;Accession: S07160
 A;Molecule type: mRNA
 A;Residues: 436-487, 'A', 489-711 <RAD>
 A;Cross-references: EMBL:M18642; NID:G186815; PIDN:AAA86665.1; PID:G386855
 R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
 Cancer Res. 51, 3037-3043, 1991
 A>Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
 A;Reference number: A61169; PMID:91235214; PMID:167448
 A;Accession: A61169
 A>Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 3-701, 'SWKPVN' <PAN>
 A;Experimental source: normal breast tissue
 R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
 Eur. J. Biochem. 145, 659-666, 1984
 A>Title: Human lactotransferrin: amino acid sequence and structural comparisons with other
 A;Reference number: A31000; PMID:85076667; PMID:6510420
 A;Accession: A31000
 A;Molecule type: protein
 A;Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4
 A;Note: this is the final paper in a series
 R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
 Eur. J. Biochem. 241, 303-308, 1996
 A>Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity
 A;Reference number: S74119; PMID:97054624; PMID:8898921
 A;Accession: S74119
 A;Molecule type: protein
 A;Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>
 A;Experimental source: neutrophil granulocytes
 C;Genetics:
 A;Gene: GDB:17F
 A;Cross-references: GDB:119368; OMIM:150210
 A;Map position: 3q21-3q23
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication; glycoprotein; iron binding; milk
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-711/Product: lactotransferrin #status experimental <MAT>
 F;21-356/Domain: transferrin repeat homology <TRH1>
 F;360-699/Domain: transferrin repeat homology <TRH2>
 F;29-65, 39-55, 135-218, 177-193, 190-201, 251-265, 503-697, 695-609/Disulfide bonds: #status
 F;157-490/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #stat

Query Match 91.3%; Score 63; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.0023;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 12
 DB 39 CFQWQRMKRV 50

RESULT 2
 JC2323
 lactoferrin - goat
 C;Species: Capra aegagrus hircus (domestic goat)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 C;Accession: JC2323
 R;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A>Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
 A;Reference number: JC2323; PMID:94380047; PMID:8093048
 A;Accession: JC2323
 A;Molecule type: mRNA
 A;Residues: 1-708 <LEP>
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication; glycoprotein
 F;359-696/Domain: transferrin repeat homology <TRH2>
 F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.8%; Score 53; DB 2; Length 708;
 Best Local Similarity 72.7%; Pred. No. 0.14;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 11
 DB 38 CYQWQRMKRL 48

RESULT 3

S52107
 lactoferrin - sheep (fragment)
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
 C;Accession: S52107
 R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
 Biochim. Biophys. Acta 1243, 25-32, 1995
 A>Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet
 A;Reference number: S52107; PMID:95127729; PMID:7827104
 A;Accession: S52107
 A>Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-33 <QIA>
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication

Query Match 72.5%; Score 50; DB 2; Length 33;
 Best Local Similarity 63.6%; Pred. No. 0.024;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 11
 DB 19 CYQWQRMKRL 29

RESULT 4

A28438
 lactoferrin precursor - mouse
 N;Alternate names: lactotransferrin
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A28438; A41205
 R;Pentecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A>Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret
 A;Reference number: A92596; PMID:87280033; PMID:3611056
 A;Accession: A28438
 A;Molecule type: mRNA
 A;Residues: 3-707 <PEN>
 A;Cross-references: EMBL:J03298
 R;Liu, Y.; Teng, C.T.
 J. Biol. Chem. 266, 21880-21885, 1991
 A>Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
 A;Reference number: A41205; PMID:92042099; PMID:1939212
 A;Accession: A41205
 A;Molecule type: DNA
 A;Residues: 1-15 <LIU>
 A;Cross-references: GB:M74778
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication; glycoprotein
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-707/Product: lactotransferrin #status predicted <MAT>
 F;358-695/Domain: transferrin repeat homology <TRH2>
 F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.8%; Score 44; DB 1; Length 707;
 Best Local Similarity 63.8%; Pred. No. 5.7;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 11
 DB 37 CLRQWQRMKRV 47

Nature 406, 959-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83181
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1746 <STO>
A;Cross-references: GB:AE004791; GB:AE004091; NID:g9949882; PIDN:AAG07115.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3728

Query Match 56.5%; Score 39; DB 2; Length 1746;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQWQAMRKV 11
|:|||||:
Db 205 FEWQATREM 214

RESULT 15

A35774
Kinase-related protein sevenless - fruit fly (*Drosophila virilis*)
C;Species: *Drosophila virilis*
C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 24-Apr-1998
C;Accession: A35774
R;Michael, W.M.; Bowtell, D.D.L.; Rubin, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 5351-5353, 1990
A;Title: Comparison of the sevenless genes of *Drosophila virilis* and *Drosophila melanogaster*
A;Reference number: A35774; MUID:90319110; PMID:2115169
A;Accession: A35774
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2594 <MIC>
A;Cross-references: GB:M34543
C;Genetics:
A;Gene: FlyBase:Dvir/sev
A;Cross-references: FlyBase:FBgn0013140
C;Superfamily: sevenless; fibronectin type III repeat homology; LDL receptor YWTD-containing
C;Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
E;9-26/Region: glutamine-rich
E;465-555/Domain: fibronectin type III repeat homology <FN3>
F;2222-2499/Domain: protein kinase homology <KIN>
F;2230-2238/Region: protein kinase ATP-binding motif

Query Match 56.5%; Score 39; DB 2; Length 2594;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQAMRKV 11
|:|||||:
Db 305 CAQWYALKKEI 315

Search completed: February 21, 2003, 07:47:45
Job time : 10.65 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds
(without alignments)
108.199 Million cell updates/sec

Title: US-09-743-107B-74

Perfect score: 69

Sequence: 1 CFQWRAMRKR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	63	91.3	711	1 TRFL_HUMAN
2	53	76.8	708	1 TRFL_CAMDR
3	53	76.8	708	1 TRFL_CAPHI
4	44	63.8	707	1 TRFL_MOUSE
5	43	62.3	4568	1 DYHB_CHLRE
6	42	60.9	1135	1 PHYC_SORBI
7	40	58.0	1137	1 PHYC_ORYSA
8	39	56.5	292	1 NLA_DROME
9	39	56.5	2594	1 7LES_DROVI
10	38	55.1	146	1 RPOB_LIBAF
11	38	55.1	275	1 VA16_VACCV
12	38	55.1	378	1 VA16_VACCC
13	38	55.1	500	1 TLCE_RICPR
14	38	55.1	695	1 TRFL_HORSE
15	37	53.6	85	1 PMRD_SALTY
16	37	53.6	1131	1 PHY_PINSV
17	37	53.6	2554	1 7LES_DROME
18	36	52.2	214	1 YFCF_ECOLI
19	36	52.2	235	1 FL3L_HUMAN
20	36	52.2	275	1 IL2A_BOVIN
21	36	52.2	275	1 IL2A_SHEEP
22	36	52.2	303	1 UL24_HSVSA
23	36	52.2	538	1 RO60_HUMAN
24	36	52.2	538	1 RO60_MOUSE
25	36	52.2	538	1 RO60_XENIA
26	36	52.2	1111	1 PHYC_ARATH
27	36	52.2	1156	1 PHYC_SOYEN
28	36	52.2	1164	1 PHYD_ARATH
29	36	52.2	1172	1 PHYB_ARATH
30	36	52.2	1179	1 ATX1_ARATH
31	35	50.7	211	1 LOLS_VIBCH
32	35	50.7	270	1 PDHX_MYXXA
33	35	50.7	306	1 BUB2_YEAST

RESULT 1

ID	TRFL_HUMAN	STANDARD;	PRT;	711 AA.
AC	P02788;	Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96K24;		
AC	Q96K25;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin A;			
DE	Lactoferrin B; Lactoferrin C]			
GN	LTF OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary Gland;			
RX	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;			
RT	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RL	Nucleic Acids Res. 18:5288-5288(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cho Y.Y.;			
RL	Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Connely O.M.;			
RL	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary Gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RT	"Molecular cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Rado T.A.;			
RT	"Human neutrophil lactoferrin coding and 5' flanking region DNA sequences.";			
RL	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary Gland;			
RA	Cheng H., Chen X., Huan L.;			
RT	"cDNA cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Straussberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN	[8]			

34	35	50.7	317	1	MOCA_RHIME	P49307 rhizobium m
35	35	50.7	363	1	CTNS_DROME	O9YCR7 drosophila
36	35	50.7	435	1	DCOR_PANRE	P43725 arabidopsis
37	35	50.7	502	1	C911_ARATH	Q9EG65 arabidopsis
38	35	50.7	558	1	NCAP_LYCV	P09992 lymphocytic
39	35	50.7	558	1	NCAP_LYCV	P07400 lymphocytic
40	35	50.7	601	1	WD66_PHYPO	P90587 physarum po
41	35	50.7	805	1	L100_ADE02	P24932 human adeno
42	35	50.7	807	1	L100_ADE05	P24933 human adeno
43	35	50.7	1121	1	PHY2_CERPU	Q39557 ceratodon p
44	35	50.7	1132	1	PHY1_PHYPA	P36505 physcomitre
45	35	50.7	1355	1	ATC3_YEAS	P39524 saccharomyc

ALIGNMENTS

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ouden J.E.;
RL "Nucleotide sequence of human lactoferrin cDNA.";
RN Nucleic Acids Res. 18:4013-4013(1990).
[9]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
RA Legrand D., Spik G., Montreuil J., Jolles P.;
RL "Human lactotransferrin: amino acid sequence and structural
RT comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1994).
[10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RA Jolles P.;
RL "The present state of the human lactotransferrin sequence. Study and
RT alignment of the cyanogen bromide fragments and characterization of
RT N- and C-terminal domains.";
RL Biochim. Biophys. Acta 670:243-254(1981).
[11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
RA Jolles P.;
RL "An 88 amino acid long C-terminal sequence of human
RT lactotransferrin.";
RL FEBS Lett. 142:107-110(1982).
[12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RL "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
[13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie M.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang X., Porcel B.M.,
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sagripanti J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
[14]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RL "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
[15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.;
RL "Structure of human diferric lactoferrin refined at 2.2-A
RT resolution.";
RL Acta Crystallogr. D 51:629-646(1995).
[16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
RA Baker E.N.;
RL "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RT 253->methionine mutant.";
RL Biochemistry 36:1341-1346(1997).
[17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RL "Structure of recombinant human lactoferrin expressed in Aspergillus
RT awamori.";
RL Acta Crystallogr. D 55:403-407(1999).
[18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RL "Structure of human apolactoferrin at 2.0-A resolution. Refinement
RT and analysis of ligand-induced conformational change.";
RL Acta Crystallogr. D 54:1319-1335(1998).
[19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani E., Iio K., Chiba H., Yoshikawa M.;
RL "Isolation and characterization of opioic antagonist peptides derived
RT from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810(1990).
[20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
RA Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
RA El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
RA Hejmancik J.F., Teng C.T.;
RL "Familial subepithelial corneal amyloidosis (gelatinous drop-like
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RL Mol. Vision 4:31-32(1998).
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC ACTIVITY: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
CC FOR XAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC EMBL; X53961; CAA37914.1; -;
CC EMBL; U07643; AAB60324.1; -;
CC EMBL; M93150; AAA36159.1; -;
CC EMBL; M83202; AAA59511.1; -;
CC EMBL; M83205; AAA58656.1; -;
CC EMBL; M18642; AAA86665.1; -;
CC EMBL; AF332168; AAG48753.1; -;
CC EMBL; BC015822; AAH15822.1; -;
CC EMBL; BC015823; AAH15823.1; -;
CC EMBL; M73700; AAA59479.1; -;
CC EMBL; X52941; CAA37116.1; -;
CC EMBL; U95626; AAB57795.1; -;
CC PIR; S11228; TFHUL.
CC PDB; 1LCT; 31-AUG-94.
CC PDB; 1LCT; 31-OCT-93.
CC PDB; 1LFG; 31-JUL-94.
CC PDB; 1LFI; 31-OCT-93.
CC PDB; 1LFI; 31-OCT-93.
CC PDB; 1LGB; 31-AUG-94.
CC PDB; 1LGC; 31-AUG-94.
CC PDB; 1BKA; 08-NOV-96.
CC PDB; 1DSN; 08-MAR-96.
CC PDB; 1HSE; 12-MAR-97.
CC PDB; 1VFD; 21-APR-97.

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Query Match          91.3%; Score 63; DB 1; Length 711;
Best Local Similarity 91.7%; Pred. No. 0.00073;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQAMRKVR 12
    |||||
Db 39 CFQWQAMRKVR 50

RESULT 2
TRFL CAMDR          STANDARD;          PRT; 708 AA.
AC Q9TUMG; Q9MZS5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN Capra.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Somali; TISSUE=Lactating mammary gland;
RA Kappeler S.R.; Ackermann M.; Farah Z.; Puhan Z.;
RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
RN Int. Dairy J. 9:481-486(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Paramasivam M.; Srinivasan A.; Singh R.; Sahani M.S.; Singh T.P.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION. USUALLY BICARBONATE (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC -----
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CC -----
DR EMBL; AJ131674; CAB53387.1; -.
DR EMBL; AF165879; AAF82241.1; -.
DR HSSP; 077811; 1B1X.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER_2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
Signal.
FT SIGNAL. 1 19 BY SIMILARITY.
FT CHAIN 20 708 LACTOTRANSFERRIN.
FT REPEAT 20 363 1.
FT REPEAT 364 708 2.
FT REPEAT 28 64 BY SIMILARITY.
FT DISULFID 38 55 BY SIMILARITY.
FT DISULFID 134 217 BY SIMILARITY.
FT DISULFID 176 192 BY SIMILARITY.
FT DISULFID 189 200 BY SIMILARITY.
FT DISULFID 250 264 BY SIMILARITY.
FT DISULFID 367 399 BY SIMILARITY.
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FT DISULFID 377 390 BY SIMILARITY.
FT DISULFID 424 703 BY SIMILARITY.
FT DISULFID 444 666 BY SIMILARITY.
FT DISULFID 476 551 BY SIMILARITY.
FT DISULFID 500 694 BY SIMILARITY.
FT DISULFID 510 524 BY SIMILARITY.
FT DISULFID 521 534 BY SIMILARITY.
FT DISULFID 592 606 BY SIMILARITY.
FT DISULFID 644 649 BY SIMILARITY.
FT METAL 79 79 IRON 1 (BY SIMILARITY).
FT METAL 111 111 IRON 1 (BY SIMILARITY).
FT METAL 211 211 IRON 1 (BY SIMILARITY).
FT METAL 272 272 IRON 1 (BY SIMILARITY).
FT METAL 414 414 IRON 2 (BY SIMILARITY).
FT METAL 452 452 IRON 2 (BY SIMILARITY).
FT METAL 545 545 IRON 2 (BY SIMILARITY).
FT METAL 614 614 IRON 2 (BY SIMILARITY).
FT BINDING 140 140 ANION (BY SIMILARITY).
FT BINDING 482 482 ANION (BY SIMILARITY).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 261 261 F -> S (IN REF. 2).
FT CONFLICT 304 304 G -> A (IN REF. 2).
FT CONFLICT 330 330 S -> P (IN REF. 2).
FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).
FT CONFLICT 506 506 L -> F (IN REF. 2).
FT CONFLICT 609 609 A -> P (IN REF. 2).
FT CONFLICT 642 642 R -> Q (IN REF. 2).
SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match          76.8%; Score 53; DB 1; Length 708;
Best Local Similarity 75.0%; Pred. No. 0.046;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQAMRKVR 12
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Db 38 CAQWQRMKKVR 49

RESULT 3
TRFL CAPHI          STANDARD;          PRT; 708 AA.
ID TRFL CAPHI
AC Q29477; Q29479;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN LTF.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Lee T.; Yu S.; Kim S.; Lee K.; Yu D.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary Gland;
RX MEDLINE=94380047; PubMed=9093048;
RA le Provost F.; Noca M.; Guerin G.; Martin P.;
RT "Characterization of the goat lactoferrin cDNA. Assignment of the
RT relevant locus to bovine U12 syntenic group.";
RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION. USUALLY BICARBONATE.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
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FT REPEAT 358 707
FT DISULFID 27 63
FT DISULFID 37 54
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FT DISULFID 188 199
FT DISULFID 249 263
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FT DISULFID 423 702
FT DISULFID 443 665
FT DISULFID 475 550
FT DISULFID 499 693
FT DISULFID 509 523
FT DISULFID 520 533
FT DISULFID 591 605
FT DISULFID 643 648
FT METAL 78 78
FT METAL 110 110
FT METAL 210 210
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FT METAL 413 413
FT METAL 451 451
FT METAL 544 544
FT METAL 613 613
FT METAL 139 139
FT BINDING 481 481
FT CARBOHYD 118 118
FT CARBOHYD 494 494
FT CONFLICT 1 2
FT CONFLICT 25 25
FT CONFLICT 82 82
FT CONFLICT 359 359
FT CONFLICT 382 382
FT CONFLICT 449 449
FT CONFLICT 629 629
SQ SEQUENCE 707 AA; 77865 MW; F26AE03404C19A8 CRC64;

Query Match 63.8%; Score 44; DB 1; Length 707;
Best Local Similarity 63.6%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWRMRKV 11
Db 37 CLRQWNRKV 47

RESULT 5
ID_DYHB_CHLRE STANDARD; PRT; 4568 AA.
AC Q39565;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Dynein beta chain, flagellar outer arm.
GN ODA4 OR ODA-4 OR SUP1.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadales; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=21gr;
RX MEDLINE=94274778; PubMed=8006077;
RA Mitchell D.R., Brown K.S.;
RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes";
RL J. Cell Sci. 107:635-644(1994).
CC -1- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC DYNEIN HAS ATPASE ACTIVITY.
CC -1- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.

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CC -1- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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CC -----
DR EMBL; U02963; AAA19956.1; -.
DR InterPro; IPR004273; Dynein heavy.
DR Pfam; PF03028; Dynein heavy; 1.
KW Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
KW Coiled coil.
FT DOMAIN 277 293 COILED COIL (POTENTIAL).
FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).
FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
FT DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
FT DOMAIN 2831 2848 COILED COIL (POTENTIAL).
FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
FT DOMAIN 3339 3425 COILED COIL (POTENTIAL).
FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
FT NP_BIND 1919 1926 ATP (POTENTIAL).
FT NP_BIND 2202 2209 ATP (POTENTIAL).
FT NP_BIND 2530 2537 ATP (POTENTIAL).
FT NP_BIND 2879 2886 ATP (POTENTIAL).
SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;

Query Match 62.3%; Score 43; DB 1; Length 4568;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQSRMRKV 12
Db 1852 CFQWQSLRYIQ 1863

RESULT 6
ID_PHYC_SORBI STANDARD; PRT; 1135 AA.
AC P93528;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phytochrome C.
GN PHYC.
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Sorghum.
OX NCBI_TaxID=4558;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97198556; PubMed=9046599;
RA Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
RA Morgan P.W., Millet J.E.;
RT "The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a phytochrome B.";
RL Plant Physiol. 113:611-619(1997).
CC -1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCOVERSION OF PR IN PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RUBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION (BY

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CC SIMILARITY).

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

CC -1- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.

CC -1- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.

CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.

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CC EMBL: U56731; AAB41399.1; -

DR InterPro: IPR003594; ATPbind_ATPase.

DR InterPro: IPR003018; GAF.

DR InterPro: IPR004359; HIS_KIN sig.

DR InterPro: IPR003661; His_kinA.

DR InterPro: IPR001610; PAC.

DR InterPro: IPR000014; PAS domain.

DR InterPro: IPR001294; Phytochrome.

DR Pfam: PF00360; Phytochrome; 1.

DR Pfam: PF00512; signal; 1.

DR Pfam: PF00989; PAS; 2.

DR Pfam: PF01590; GAF; 1.

DR Pfam: PF02518; HATPase_c; 1.

DR PRINTS: PR01033; PHYTOCHROME.

DR SMART: SM00065; GAF; 1.

DR SMART: SM00387; HATPase_c; 1.

DR SMART: SM00388; Hiska; 1.

DR SMART: SM00086; PAC; 1.

DR SMART: SM00091; PAS; 2.

DR TIGRFS: TIGR00229; sensory_box; 2.

DR PROSITE: PS50109; HIS_KIN; 1.

DR PROSITE: PS00245; PHYTOCHROME_1; FALSE_NEG.

DR PROSITE: PS0046; PHYTOCHROME_2; 1.

KW Transcription regulation; Photoreceptor; Phytochrome; Chromophore;

KW Repeat; Multigene family.

FT DOMAIN 618 688 PAS 1.

FT DOMAIN 748 822 PAS 2.

FT DOMAIN 902 1122 HISTIDINE KINASE.

FT BINDING 321 321 CHROMOPHORE (BY SIMILARITY).

SQ SEQUENCE 1135 AA; 126315 MW; AFCC934B7592DE4D CRC64;

Query Match 60.9%; Score 42; DB 1; Length 1135;

Best Local Similarity 45.5%; Pred. No. 7.2;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPQWQRMKRV 11

Db 775 CLEWKMQRKI 785

RESULT 7

ID PHYC_ORYSA STANDARD; PRT; 1137 AA.

AC Q92W19; P93429;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Phytochrome C.

GN PHYC.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Cryzeae; Oryza.

OX NCBI_TaxID=4530;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;

RA Tahir M., Kanegae H., Takano M.;

RT "Phytochrome C (PHYC) gene in rice: isolation and characterization of

RT a complete coding sequence.";

RL (In) Plant Gene Register FGR98-210.

RN [2]

RP SEQUENCE OF 275-378 FROM N.A.

RX MEDLINE=97019052; PubMed=8865668;

RA Mathews S., Sharrock R.A.;

RT "The phytochrome gene family in grasses (Poaceae): a phylogeny and

RT evidence that grasses have a subset of the loci found in dicot

RT angiosperms";

RL Mol. Biol. Evol. 13:1141-1150(1996).

CC -1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT

CC ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS

CC MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT

CC ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN

CC PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS

CC RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE

CC RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR

CC GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-

CC BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,

CC PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS

CC THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

CC -1- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.

CC -1- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.

CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.

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CC EMBL: AB018442; BAB74448.1; -

DR EMBL: U61207; AAB41996.1; -

DR InterPro: IPR003594; ATPbind_ATPase.

DR InterPro: IPR003018; GAF.

DR InterPro: IPR004359; HIS_KIN sig.

DR InterPro: IPR003661; His_kinA.

DR InterPro: IPR001610; PAC.

DR InterPro: IPR000014; PAS domain.

DR InterPro: IPR001294; Phytochrome.

DR Pfam: PF00360; phytochrome; 1.

DR Pfam: PF00512; signal; 1.

DR Pfam: PF00989; PAS; 2.

DR Pfam: PF01590; GAF; 1.

DR Pfam: PF02518; HATPase_c; 1.

DR PRINTS: PR01033; PHYTOCHROME.

DR SMART: SM00065; GAF; 1.

DR SMART: SM00387; HATPase_c; 1.

DR SMART: SM00388; Hiska; 1.

DR SMART: SM00086; PAC; 1.

DR SMART: SM00091; PAS; 2.

DR TIGRFS: TIGR00229; sensory_box; 2.

DR PROSITE: PS50109; HIS_KIN; 1.

DR PROSITE: PS00245; PHYTOCHROME_1; 1.

DR PROSITE: PS0046; PHYTOCHROME_2; 1.

KW Transcription regulation; Photoreceptor; Phytochrome; Chromophore;

KW Repeat; Multigene family.

FT DOMAIN 620 690 PAS 1.

FT DOMAIN 750 824 PAS 2.

FT DOMAIN 904 1124 HISTIDINE KINASE.

FT BINDING 322 322 CHROMOPHORE (BY SIMILARITY).

FT CONFLICT 279 279 F -> S (IN REF. 2).

FT CONFLICT 292 292 C -> S (IN REF. 2).

SQ SEQUENCE 1137 AA; 125982 MW; F2A520181CFE7B32 CRC64;

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Query Match      58.0%; Score 40; DB 1; Length 1137;
Best Local Similarity 45.5%; Pred. No. 17;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWRMRKV 11
   | | | | |
DB 777 CLEWNEAQKI 787

RESULT 8
NLA DROME
ID NLA DROME STANDARD; PRT; 292 AA.
AC Q9XZL8; Q9V391;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nebula protein.
OS NLA OR CG6072.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP
RP SEQUENCE FROM N.A.
RA McCormick A.V., Goldberg M.L.;
RT "Gene required for elongation of meiosis I spindle in Drosophila females."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RC MEDLINE=20196005; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananidis P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fessler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murty D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Sanders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.

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CC -1- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.
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CC
DR EMBL; AF147700; AAD33987.1; -
DR EMBL; AE003712; AAF55285.1; -
DR Flybase; FBGN0026629; nla.
SQ SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;

Query Match      56.5%; Score 39; DB 1; Length 292;
Best Local Similarity 54.5%; Pred. No. 62; 2; Indels 0; Gaps 0;
Matches 6; Conservative 3; Mismatches 3;

QY 2 FQWRMRKV 12
   | | | | |
DB 150 FQWLSFRRLR 160

RESULT 9
7LES DROVI
ID 7LES DROVI STANDARD; PRT; 2594 AA.
AC P20806;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sevenless protein (EC 2.7.1.112).
OS SEV.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90319110; PubMed=2115169;
RA Michael W.M., Bowtell D.D.L., Rubin G.M.;
RT "Comparison of the sevenless genes of Drosophila virilis and
RT Drosophila melanogaster."
RL Proc. Natl. Acad. Sci. U.S.A. 87:5351-5353(1990).
CC -1- FUNCTION: RECEPTOR FOR AN EXTRACELLULAR SIGNAL REQUIRED TO
CC INDUCE A CELL TO DIFFERENTIATE INTO A R7 PHOTORECEPTOR. THE
CC LIGAND FOR SEV IS THE BOSS (BRIDE OF SEVENLESS) PROTEIN.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC RECEPTOR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 7 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- CAUTION: UNCLEAR WHETHER THE POTENTIAL MEMBRANE SPANNING REGION
CC NEAR THE N-TERMINUS IS PRESENT AS A TRANSMEMBRANE DOMAIN IN THE
CC NATIVE PROTEIN OR SERVES AS A CLEAVED SIGNAL SEQUENCE.
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CC
DR EMBL; M34545; AAA28883.1; -
DR EMBL; M34544; AAA28883.1; JOINED.
DR EMBL; M34543; AAA28883.1; JOINED.
DR PIR; A35774; A35774.
DR HSP; P11362; 1FGK.
DR Flybase; FBGN0031140; Dvir\sev.
DR InterPro; IPR000719; Euk_kinase.
DR InterPro; IPR003961; FN_III.

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DR InterPro; IPR000033; Ldl receptor_rep.
DR InterPro; IPR002011; RTKinaseI.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00041; fn3; 6.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk pkinase; 1.
DR SMART; SM00060; FN3; 5.
DR SMART; SM00135; LY; 1.
DR SMART; SM00219; TyrK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR Transferrase; Tyrosine-protein kinase; Receptor; Vision; Transmembrane;
KW Glycoprotein; ATP-binding; Phosphorylation; Repeat.
FT DOMAIN 1 2139
FT TRANSMEM 2140 2163
FT DOMAIN 2164 2594
FT DOMAIN 9 26
FT DOMAIN 356 459
FT DOMAIN 464 555
FT DOMAIN 835 935
FT DOMAIN 1328 1421
FT DOMAIN 1706 1816
FT DOMAIN 1817 1916
FT DOMAIN 1917 2007
FT DOMAIN 2057 2063
FT DOMAIN 2224 2495
FT NP_BIND 2230 2238
FT BINDING 2257 2257
FT MOD_RES 2391 2391
FT CARBOHYD 77 77
FT CARBOHYD 401 401
FT CARBOHYD 508 508
FT CARBOHYD 532 532
FT CARBOHYD 641 641
FT CARBOHYD 667 667
FT CARBOHYD 778 778
FT CARBOHYD 797 797
FT CARBOHYD 874 874
FT CARBOHYD 980 980
FT CARBOHYD 1257 1257
FT CARBOHYD 1344 1344
FT CARBOHYD 1382 1382
FT CARBOHYD 1577 1577
FT CARBOHYD 1587 1587
FT CARBOHYD 1665 1665
FT CARBOHYD 1752 1752
FT CARBOHYD 1776 1776
FT CARBOHYD 1824 1824
FT CARBOHYD 1908 1908
FT CARBOHYD 1966 1966
FT CARBOHYD 2088 2088
FT CARBOHYD 2594 AA; 289130 MW; 77D8A356CBAD0BBD CRC64;
SQ SEQUENCE 2594 AA; 289130 MW; 77D8A356CBAD0BBD CRC64;

Query Match 56.5%; Score 39; DB 1; Length 2594;
Best Local Similarity 45.5%; Pred. No. 58;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWRMRKV 11
DB 305 CAQWYRLKEI 315

RESULT 10
RPOB LIBAF
ID RPOB LIBAF STANDARD; PRT; 146 AA.
AC P41187;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase
beta chain) (RNA polymerase beta subunit) (Fragment).

Query Match 55.1%; Score 38; DB 1; Length 146;
Best Local Similarity 60.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWRMRKV 10
DB 10 CVQWSRGARK 19

RESULT 11
ID VAL16 VACCV STANDARD; PRT; 275 AA.
AC P16710;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein A16 (Fragment).
GN A16L
OS Vaccinia virus (strain WR).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OC NCBI_TaxID=10254;
OX 1
RP SEQUENCE FROM N.A.
RX MEDLINE=90317884; PubMed=2370683;
RA Pacha R.F., Meis R.J., Condit R.C.;
RT "Structure and expression of the vaccinia virus gene which prevents
virus-induced breakdown of RNA.";
RL J. Virol. 64:3853-3863(1990).
CC -1- SIMILARITY: BELONGS TO THE POXVIRUSES A16 FAMILY.
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CC -----
DR EMBL; M32064; AAA48348.2; -.
DR PIR; A36415; A36415.
DR InterPro; IPR004251; DUF230.
DR Pfam; PF03003; DUF230; 1.
FT NON TER 275 275
SQ SEQUENCE 275 AA; 31811 MW; E2461AB1DB7B93A3 CRC64;

Query Match 55.1%; Score 38; DB 1; Length 275;
Best Local Similarity 60.0%; Pred.No. 8.8;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRAVRK 10
| | | | |
DB 185 CLEWLRVRK 194

RESULT 12

ID VA16 VACCC STANDARD; PRT; 378 AA.
AC P20923;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein A16.
GN A16L.
OS Vaccinia virus (strain Copenhagen).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10249;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91021027; PubMed=2219722;
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA Paolletti E.;
RT "The complete DNA sequence of vaccinia virus.";
RL Virology 179:247-266(1990).
CC [2]
CC COMPLETE GENOME.
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA Paolletti E.;
RT "Appendix to 'The complete DNA sequence of vaccinia virus'.";
RL Virology 179:517-563(1990).
CC -1- SIMILARITY: BELONGS TO THE POXVIRUSES A16 FAMILY.

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CC -----
DR EMBL; M35027; AAA48138.1; -.
DR PIR; I42518; I42518.
DR InterPro; IPR004251; DUF230.
DR Pfam; PF03003; DUF230; 1.
SQ SEQUENCE 378 AA; 43561 MW; 05ED614AA1D11A19 CRC64;

Query Match 55.1%; Score 38; DB 1; Length 378;
Best Local Similarity 60.0%; Pred.No. 12;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRAVRK 10
| | | | |
DB 185 CLEWLRVRK 194

RESULT 13

TLCE RICPR
ID TLCE RICPR STANDARD; PRT; 500 AA.
AC O05962;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP, ATP carrier protein 5 (ADP/ATP translocase 5).
GN TLCE OR TLCS OR RP739.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O., Naeslund A.K.,
RA Scharitz-Ponten T., Alsmark U.C.M., Podowski R.M., Kurland C.G.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
RN [2]
RP SEQUENCE OF 325-500 FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=97419517; PubMed=9274032;
RA Andersson J.O., Andersson S.G.E.;
RT "Genomic rearrangements during evolution of the obligate
RT intracellular parasite Rickettsia prowazekii as inferred from an
RT analysis of 52015 bp nucleotide sequence.";
RL Microbiology 143:2783-2795(1997).
CC -1- FUNCTION: PROVIDES THE RICKETTSIAL CELL WITH HOST ATP IN
CC EXCHANGE FOR RICKETTSIAL ADP. THIS IS AN OBLIGATE EXCHANGE SYSTEM.
CC THIS ENERGY ACQUIRING ACTIVITY IS AN IMPORTANT COMPONENT OF
CC RICKETTSIAL PARASITISM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE ADP/ATP TRANSLOCASE TLC FAMILY.

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CC -----
DR EMBL; AJ235273; CAA15167.1; -.
DR EMBL; Y11778; CAA72457.1; -.
DR InterPro; IPR004667; ADP_ATP_car.
DR Pfam; PF03219; TLC; 1.
DR TIGRfam; TIGR00769; AAA; 1.
KW Transmembrane; Transport; ATP-binding; Multigene family;
KW Complete proteome.
FT TRANSMEM 26 46 POTENTIAL.
FT TRANSMEM 62 82 POTENTIAL.
FT TRANSMEM 94 114 POTENTIAL.
FT TRANSMEM 149 169 POTENTIAL.
FT TRANSMEM 184 204 POTENTIAL.
FT TRANSMEM 224 244 POTENTIAL.
FT TRANSMEM 287 307 POTENTIAL.
FT TRANSMEM 328 348 POTENTIAL.
FT TRANSMEM 357 377 POTENTIAL.
FT TRANSMEM 381 401 POTENTIAL.
FT TRANSMEM 469 489 POTENTIAL.
SQ SEQUENCE 500 AA; 57073 MW; FE3DB48D08CF5F72 CRC64;

Query Match 55.1%; Score 38; DB 1; Length 500;
Best Local Similarity 54.5%; Pred.No. 16;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRAVRK 11
| | | | |
DB 482 CFATYAVRK 492

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CC -----
DR EMEL; U02281; AAA21322.1; --
DR EMEL; AE008803; AAL21205.1; --
DR StyGene; SG10304; pmrD.
KW Antibiotic resistance; Complete proteome.
SQ SEQUENCE 85 AA; 9749 MW; 1E1922419EA50CCA CRC64;

Query Match 53.6%; Score 37; DB 1; Length 85;
Best Local Similarity 60.0%; Pred. No. 4;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy 1 CFQWQRAWRK 10
| : | | |
Db 74 CDEWQLTRK 83

Search completed: February 21, 2003, 07:27:48
Job time : 5.6 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 seconds
(without alignments)
118.873 Million cell updates/sec

Title: US-09-743-107B-74

Perfect score: 69

Sequence: 1 CFQWQAMRKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	84.1	711	4 Q8TCD2	Q8tcd2 homo sapien
2	54	78.3	38	4 Q9UCY5	Q9ucy5 homo sapien
3	50	72.5	33	6 Q9TR80	Q9tr80 ovis aries
4	42	60.9	1121	10 Q9SW56	Q9sws6 lycopersico
5	41	59.4	105	10 Q9XFD5	Q9xfds oxyza sativ
6	41	59.4	148	10 Q9XHP1	Q9xhpl sesamum ind
7	41	59.4	275	5 Q93780	Q93780 caenorhabdi
8	41	59.4	932	5 Q19153	Q19153 caenorhabdi
9	40	58.0	279	16 Q8XSE2	Q8xse2 ralistaonia s
10	40	58.0	830	10 Q945T7	Q945t7 hordeum vul
11	40	58.0	1137	10 Q9M7A9	Q9m7a9 oxyza sativ
12	40	58.0	1139	10 Q9VMN1	Q9vmn1 triticum ae
13	40	58.0	1391	5 O17772	O17772 caenorhabdi
14	39	56.5	205	16 Q986A0	Q986a0 rhizobium l
15	39	56.5	206	16 Q8UHC2	Q8uhc2 agrobacteri
16	39	56.5	206	16 Q92RH8	Q92rh8 rhizobium m

17	39	56.5	208	16 Q8YFK3	Q8yfk3 brucella me
18	39	56.5	274	4 Q96M21	Q96m21 homo sapien
19	39	56.5	306	4 Q8TAX2	Q8tax2 homo sapien
20	39	56.5	466	4 Q9NUS2	Q9nus2 homo sapien
21	39	56.5	1746	16 Q9HXR4	Q9hxr4 pseudomonas
22	38	55.1	57	4 Q96I36	Q96i36 homo sapien
23	38	55.1	91	15 Q77855	Q77855 human immun
24	38	55.1	91	15 Q77856	Q77856 human immun
25	38	55.1	377	12 Q89164	Q89164 variola vir
26	38	55.1	377	12 Q85389	Q85389 variola maj
27	38	55.1	377	12 Q93122	Q93122 vaccinia vi
28	38	55.1	377	12 Q8V2N9	Q8v2n9 camelpox vir
29	38	55.1	377	12 Q8QMT7	Q8qmt7 cowpox viru
30	38	55.1	396	17 Q8ZUT0	Q8zut0 pyrobaculum
31	38	55.1	433	5 Q44473	Q44473 caenorhabdi
32	38	55.1	509	10 Q9LHA1	Q9lha1 arabidopsis
33	38	55.1	515	10 Q22185	Q22185 arabidopsis
34	38	55.1	543	10 Q22188	Q22188 arabidopsis
35	38	55.1	1444	5 Q9GY67	Q9gy67 leishmania
36	37	53.6	85	16 Q8Z536	Q8z536 salmonella
37	37	53.6	109	15 Q9YQC1	Q9yqc1 human immun
38	37	53.6	109	15 Q9YOC0	Q9yoc0 human immun
39	37	53.6	109	15 Q9YOB9	Q9yob9 human immun
40	37	53.6	109	15 Q9YQB8	Q9yqb8 human immun
41	37	53.6	109	15 Q9YJ17	Q9yj17 human immun
42	37	53.6	109	15 Q9YIJ2	Q9yij2 human immun
43	37	53.6	115	15 Q9Q9L0	Q9q9l0 human immun
44	37	53.6	119	15 Q8Q454	Q8q454 human immun
45	37	53.6	121	16 Q8U6K3	Q8u6k3 agrobacteri

ALIGNMENTS

RESULT 1

Q8TCD2 PRELIMINARY; PRT; 711 AA.
AC Q8TCD2; 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Lactotransferrin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022347; AAH22347.1; -.
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAP CRC64;

Query Match 84.1%; Score 58; DB 4; Length 711;
Best Local Similarity 90.9%; Pred. No. 0.038; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 1;

QY 1 CFQWQAMRKV 11
|||
Db 39 CFQWQAMRKV 49

RESULT 2

Q9UCY5 PRELIMINARY; PRT; 38 AA.
ID Q9UCY5
AC Q9UCY5; 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE Lactoferrin homolog (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96081613; PubMed=8551695;
 RX Sato I.;
 RT "Characterization of the 84-kDa protein with ABH activity in human
 seminal plasma.";
 RL Jpn. J. Legal Med. 49:281-293 (1995).
 DR HSP; P02788; IRLA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDD5B CRC64;
 Query Match 78.3%; Score 54; DB 4; Length 38;
 Best Local Similarity 90.9%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0;
 QY 2 FQWQNRKVR 12
 Db 21 FQWQNRKVR 31
 RESULT 3
 Q9TR80 PRELIMINARY; PRT; 33 AA.
 AC Q9TR80;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Lactoferrin (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95127729; PubMed=7827104;
 RL Qian X.Y., Jolles P., Migliore-Samouri D., Fiat A.M.;
 RA Biochim. Biophys. Acta 1243:25-32 (1995).
 DR HSP; O77698; ICE2.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
 Query Match 72.5%; Score 50; DB 6; Length 33;
 Best Local Similarity 63.6%; Pred. No. 0.045; Mismatches 3; Indels 0; Gaps 0;
 Matches 7; Conservative 3;
 QY 1 CFQWQNRKVR 11
 Db 19 CYQWQNRKVR 29
 RESULT 4
 Q9SW56 PRELIMINARY; PRT; 1121 AA.
 AC Q9SW56;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Phytochrome B2.
 GN PHYB2.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99413290; PubMed=10485280;
 RA Kerckhoffs L.H., Kelmenson P.M., Schreuder M.E., Kendrick C.I.,

PA Kendrick R.E., Hanhart C.J., Koornneef M., Pratt L.H.,
 RA Cordonnier-Pratt M.M.;
 RT "Characterization of the gene encoding the apoprotein of phytochrome
 B2 in tomato, and identification of molecular lesions in two mutant
 alleles.";
 RL Mol. Gen. Genet. 261:901-907 (1999).
 DR EMBL; AF122901; AAD50631.1; -.
 DR InterPro; IPR002198; ADH short.
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR003018; GAF.
 DR InterPro; IPR003661; His_kinA.
 DR InterPro; IPR004359; HIS_KIN_sig.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS domain.
 DR InterPro; IPR001294; Phytochrome.
 DR Pfam; PF01590; GAF; 1.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF00989; PAS; 2.
 DR Pfam; PF00360; phytochrome; 1.
 DR Pfam; PF00512; signal; 1.
 DR PRINTS; PR01033; PHYTOCHROME.
 DR SMART; SM00065; GAF; 1.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00388; HisKA; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR TIGRfams; TIGR00229; sensory_box; 2.
 DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
 DR PROSITE; PS00245; PHYTOCHROME_1; 1.
 DR PROSITE; PS00046; PHYTOCHROME_2; 1.
 SQ SEQUENCE 1121 AA; 125308 MW; ED9EDA704BB37F27 CRC64;
 Query Match 60.9%; Score 42; DB 10; Length 1121;
 Best Local Similarity 54.5%; Pred. No. 44;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWQNRKVR 11
 Db 777 CFQWQNRKVR 787
 RESULT 5
 Q9XFD5 PRELIMINARY; PRT; 105 AA.
 AC Q9XFD5;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Cytochrome P450 (Fragment).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PANICLE;
 RA Liu J., Yang J.;
 RT "Suppression subtractive hybridization (SSH) identified candidate
 genes that are differentially expressed at rice young panicle.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR EMBL; AF140486; AAD29699.1; -.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR Pfam; PF00067; P450; 1.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
 KW Heme; Monooxygenase; Oxidoreductase.
 FT NON TER 1
 SQ SEQUENCE 105 AA; 11912 MW; B0EEFCD487E19F9 CRC64;
 Query Match 59.4%; Score 41; DB 10; Length 105;
 Best Local Similarity 60.0%; Pred. No. 5.9;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWRMRK 10
 |||||:|:
 Db 61 CFQWRMRK 70

RESULT 6

ID Q9XHP1 PRELIMINARY; PRT; 148 AA.
 AC Q9XHP1 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE 2S albumin.
 OS Sesamum indicum (Oriental sesame) (Gingelly).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
 OX NCBI_TaxID=4182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TAINAN 1;
 RX MEDLINE=20074970; PubMed=10606554;
 RA Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;
 RT "Molecular cloning of 11S globulin and 2S albumin, the two major seed
 storage proteins in sesame.";
 RL J. Agric. Food Chem. 47:4932-4938(1999).
 DR EMBL: AF091841; AAD42943.1; -;
 DR InterPro; IPR003612; AAI;
 DR InterPro; IPR000617; RapiN.
 DR InterPro; IPR001768; try/amy1 inhbr.
 DR Pfam; PF00234; tryf_alpha_amy1; 1.
 DR PRINTS; PR00496; NAFIN.
 DR SMART; SMO0499; AAI; 1.
 SQ SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;

Query Match 59.4%; Score 41; DB 10; Length 148;
 Best Local Similarity 66.7%; Pred. No. 8.4;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWRMRK 9
 |||||:|:
 Db 54 CFQWRMRK 62

RESULT 7

ID Q93780 PRELIMINARY; PRT; 275 AA.
 AC Q93780 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE F53H4.4 protein.
 DE F53H4.4.
 GN F53H4.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Dobson R.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; Z81089; CAB03137.1; -;
 SQ SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;

Query Match 59.4%; Score 41; DB 5; Length 275;
 Best Local Similarity 63.6%; Pred. No. 16;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWRMRKVR 12
 |||||:|:
 Db 262 FQWRMRKVR 272

RESULT 8

ID Q19153 PRELIMINARY; PRT; 932 AA.
 AC Q19153 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical 105.1 kDa protein.
 GN F07C3.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Favello A., Gattung S.;
 RT "The sequence of C. elegans cosmid F07C3.";
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U50308; AAG24025.1; -;
 DR InterPro; IPR000731; HMGR/patch_5TM.
 DR PROSITE; PS50156; SSD; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 932 AA; 105144 MW; 66680619ADACBFD5 CRC64;

Query Match 59.4%; Score 41; DB 5; Length 932;
 Best Local Similarity 63.6%; Pred. No. 55;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWRMRKVR 12
 |||||:|:
 Db 579 FQWRMRKVR 589

RESULT 9

ID Q8XSE2 PRELIMINARY; PRT; 279 AA.
 AC Q8XSE2 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative ICC protein homolog.
 GN ICC OR RSP0534 OR RS00414.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.

AC	Q9MTA9;
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Phytochrome C.
GN	PHYC.
OS	Oryza sativa (Rice).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC	Eriharcoideae; Oryzaceae; Oryza.
OX	NCBI_TaxID=4530;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-CV. IR36;
RX	MEDLINE=20544086; PubMedId1094977;
RA	Basu D., Dehesen K.; Schneider-Poetsch H.J., Harrington S.E.,
RT	"Rice PHYC gene: structure, expression, map position and evolution."
RL	Plant Mol. Biol. 44:27-42(2000).
DR	EMBL; AF141942; AAF66603.1; -
DR	InterPro; IPR003594; ATPbind_ATPase.
DR	InterPro; IPR003018; GAF.
DR	InterPro; IPR003661; His_KinA.
DR	InterPro; IPR004359; HIS_KIN_sig.
DR	InterPro; IPR001610; PAC.
DR	InterPro; IPR000014; PAS domain.
DR	InterPro; IPR001294; PHYTOCHROME.
DR	Pfam; PF01590; GAF. 1
DR	Pfam; PF03518; HATPase_c; 1.
DR	Pfam; PF00989; PAS; 2.
DR	Pfam; PF00360; phytochrome; 1.
DR	Pfam; PF0512; signal; 1.
DR	PRINTS; PR01033; PHYTOCHROME.
DR	SMART; SM00065; GAF. 1.
DR	SMART; SM00387; HATPase_c; 1.
DR	SMART; SM00388; HSKA; 1.
DR	SMART; SM00086; PAC; 1.
DR	SMART; SM00091; PAS; 2.
DR	TIGRFAMs; TIGR00229; sensory_box; 2.
DR	PROSITE; PS00245; PHYTOCHROME_1; 1.
DR	PROSITE; PS00046; PHYTOCHROME_2; 1.
SQ	SEQUENCE 1137 AA; 125937 MW; 782B0B75B904370A CRC64;
Qy	Query Match 58.0%; Score 40; DB 10; Length 1137;
Dd	Best Local Similarity 45.5%; Pred.No. 1e+02;
	Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps
QY	1 CFOWCFAMRKV 11 Dd 777 CLEWNEAQKI 787
RESULT 12	
Q8VWN1	PRELIMINARY; PRT; 1139 AA.
ID Q8VWN1	
AC Q8VWN1	
DT	01-MAR-2002 (TREMBLrel. 20, Created)
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Phytochrome C.
GN	PHYC.
OS	Triticum aestivum (wheat).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC	Triticeae; Triticum.
OX	NCBI_TaxID=4565;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-ETIOLOGICAL SHOOT;
RA	Kulshrestha R., Khurana J.P.;
RT	"Nucleotide sequence and characterization of a gene encoding
RL	phytochrome C from wheat (Triticum aestivum)."; Submitted (NOV-2000) to the EMBL/GenBank/DDJ databases

RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58",
 RL Science 294:2317-2323(2001).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu P.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Iappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58",
 RL Science 294:2323-2328(2001).
 DR EMBL; AF009043; AAL41776.1; -;
 DR EMBL; AF008009; AAK8569.1; -;
 KW Complete proteome.
 SQ SEQUENCE 206 AA; 23720 MW; 3BE488AE5307C0C1 CRC64;

Query Match 56.5%; Score 39; DB 16; Length 206;
 Best Local Similarity 50.0%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRAMRKVR 12
 |||:|:
 Db 88 CFHWKSLRQVR 99

Search completed: February 21, 2003, 07:44:27
 Job time : 21.8 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds
(without alignments)
56.502 Million cell updates/sec

Title: US-09-743-107B-75
Perfect score: 70
Sequence: 1 CFQWQNRKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*
1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
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19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	12	21	AAV78075 Human lactoferrin
2	65	92.9	12	21	AAV78038 Human lactoferrin
3	65	92.9	12	21	AAV78046 Human lactoferrin
4	65	92.9	12	21	AAV78047 Human lactoferrin
5	65	92.9	12	21	AAV78082 Human lactoferrin
6	65	92.9	13	21	AAV78037 Human lactoferrin
7	65	92.9	13	21	AAV78048 Human lactoferrin
8	65	92.9	13	21	AAV78049 Human lactoferrin
9	65	92.9	14	21	AAV78036 Human lactoferrin
10	65	92.9	14	21	AAV78050 Human lactoferrin

11	65	92.9	14	21	AAV78051 Human lactoferrin
12	65	92.9	15	17	AAV78054 Peptide for anti-u
13	65	92.9	15	21	AAV78035 Human lactoferrin
14	65	92.9	15	21	AAV78062 Human lactoferrin
15	65	92.9	15	21	AAV78083 Human lactoferrin
16	65	92.9	16	21	AAV78031 Human lactoferrin
17	65	92.9	16	21	AAV78064 Human lactoferrin
18	65	92.9	16	21	AAV78065 Human lactoferrin
19	65	92.9	17	21	AAV78034 Human lactoferrin
20	65	92.9	17	21	AAV78066 Human lactoferrin
21	65	92.9	17	21	AAV78067 Human lactoferrin
22	65	92.9	17	21	AAV78067 Human lactoferrin
23	65	92.9	18	15	AAV78032 Advanced Glycosyla
24	65	92.9	18	17	AAV78033 Human lactoferrin
25	65	92.9	19	21	AAV78067 Amino acid sequenc
26	65	92.9	19	21	AAV78032 Human lactoferrin
27	65	92.9	20	13	AAV78032 Anti microbial pep
28	65	92.9	20	14	AAV78032 Lactoferrin-relate
29	65	92.9	20	15	AAV78032 Lactoferrin-derive
30	65	92.9	20	15	AAV78032 Lactoferrin-derive
31	65	92.9	20	15	AAV78032 Lactoferrin-derive
32	65	92.9	20	15	AAV78032 Lactoferrin-derive
33	65	92.9	20	16	AAV78032 Bovine lactoferrin
34	65	92.9	20	16	AAV78032 Bovine lactoferrin
35	65	92.9	20	16	AAV78032 Anti-parasitic lac
36	65	92.9	20	16	AAV78032 Anti-parasitic lac
37	65	92.9	20	17	AAV78032 Peptide for anti-u
38	65	92.9	20	17	AAV78032 Lactoferrin-derive
39	65	92.9	20	17	AAV78032 Lactoferrin-derive
40	65	92.9	20	17	AAV78032 Lactoferrin-derive
41	65	92.9	20	17	AAV78032 Lactoferrin-derive
42	65	92.9	20	17	AAV78032 Lactoferrin-derive
43	65	92.9	20	18	AAV78032 Lactoferrin-derive
44	65	92.9	20	18	AAV78032 Anti-parasitic pep
45	65	92.9	20	19	AAV78032 Thrombus formation

ALIGNMENTS

RESULT 1
AAV78075
ID AAV78075 standard; Peptide; 12 AA.
XX AAV78075;
AC AAV78075;
XX
XX 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:75.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.

XX Homo sapiens.
OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattaby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 22; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 12 AA;
 SQ Query Match 100.0%; Score 70; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.3e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
 DB |||||

RESULT 2
 AAY78038
 ID AAY78038 standard; Peptide; 12 AA.
 XX AAY78038;
 AC AAY78038;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:38.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 PN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 12 AA;
 SQ Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00022;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
 DB |||||

RESULT 3
 AAY78046
 ID AAY78046 standard; Peptide; 12 AA.
 XX AAY78046;
 AC AAY78046;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:46.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 PN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00022;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
 |||||
 DB 1 CFQWQNRNARKVR 12

RESULT 4

AAV78047
 ID AAV78047 standard; Peptide; 12 AA.

XX AC AAV78047;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:47.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;
 XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,

XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 18; Page 73; 102pp; English.

XX CC AAV78001 to AAV78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00022;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
 |||||
 DB 1 CFQWQNRNARKVR 12

RESULT 5

AAV78082
 ID AAV78082 standard; Peptide; 12 AA.

XX AC AAV78082;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:82.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;
 XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,

XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 22; Page 36; 102pp; English.

XX CC AAV78001 to AAV78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00022;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
 DB 1 CFQWQNRNARKVR 12

RESULT 6

ID AAY78037
 ID AAY78037 standard; Peptide; 13 AA.

XX AC AAY78037;
 XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:37.

XX DE Human lactoferrin derived peptide SEQ ID NO:37.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX OS Homo sapiens.
 OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCII-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX PS Claim 12; Page 70; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 0.00024;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
 DB 2 CFQWQNRNARKVR 13

RESULT 7

AAY78048

ID AAY78048 standard; Peptide; 13 AA.

XX AC AAY78048;
 XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:48.

XX DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX OS Homo sapiens.
 OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCII-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX PS Claim 15; Page 74; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 0.00024;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
 DB 2 CFQWQNRNARKVR 13

RESULT 8

AAY78049

ID AAY78049 standard; Peptide; 13 AA.

XX AC AAY78049;
 XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:49.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 OS
 OS Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PT Claim 18; Page 74; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 13 AA;
 SQ Query Match 92.9%; Score 65; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 0.00024;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRNARKVR 12
 Db |||||
 2 CFQWQRNARKVR 13
 RESULT 9
 AAY78036
 ID AAY78036 standard; Peptide; 14 AA.
 XX AAY78036;
 AC AAY78036;
 DT 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:36.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.

OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PT Claim 12; Page 69; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 14 AA;
 SQ Query Match 92.9%; Score 65; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00026;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRNARKVR 12
 Db |||||
 3 CFQWQRNARKVR 14
 RESULT 10
 AAY78050
 ID AAY78050 standard; Peptide; 14 AA.
 XX AAY78050;
 AC AAY78050;
 DT 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:50.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 PF

XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 75; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 14 AA;
 SQ Query Match 92.9%; Score 65; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00026;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRNARKVR 12
 DB |||||
 3 CFQWQRNARKVR 14
 RESULT 11
 AAY78051
 ID AAY78051 standard; Peptide; 14 AA.
 XX AAY78051;
 AC AAY78051;
 DT 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:51.
 DE Human, lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 PN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 DR WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 18; Page 75; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 14 AA;
 SQ Query Match 92.9%; Score 65; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00026;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRNARKVR 12
 DB |||||
 3 CFQWQRNARKVR 14
 RESULT 12
 AAR98554
 ID AAR98554 standard; Peptide; 15 AA.
 XX AAR98554;
 AC AAR98554;
 DT 12-NOV-1996 (first entry)
 XX Peptide for anti-ulcer agent.
 DE anti-ulcer agent; low toxicity; stable; heat-resistant.
 XX Synthetic.
 OS JP08143468-A.
 PN 04-JUN-1996.
 PD 17-NOV-1994; 94JP-0283869.
 XX 17-NOV-1994; 94JP-0283869.
 PR (MORG) MORINAGA MILK IND CO LTD.
 XX WPI; 1996-318857/32.
 DR Anti-ulcer agent contg. peptide - has low toxicity, is
 PT heat-resistant and water-soluble
 PS Claim 1; Page 11; 11pp; Japanese.
 XX AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
 CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be
 CC administered orally and be produced in large amounts.
 XX Sequence 15 AA;

Query Match 92.9%; Score 65; DB 17; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.00028;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12
 DB 2 CFQWQNRKVR 13

RESULT 13

AAV78035
 ID AAV78035 standard; Peptide; 15 AA.

XX AC AAV78035;
 XX DT 25-APR-2000 (first entry)
 XX DE Human lactoferrin derived peptide SEQ ID NO:35.
 XX KW Human, lactoferrin; modification; infection; inflammation; tumour;
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;
 XX KW bactericidal; preservative.

XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200001730-A1.
 XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-S01230.
 XX PR 06-JUL-1998; 98SE-0002441.
 XX PR 17-JUL-1998; 98SE-0002562.
 XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX CC New peptides used for treatment and prevention of infections,
 XX PT inflammations and tumors and for use in infant formula food -
 XX PS Claim 12; Page 69; 102pp; English.

XX CC AAV78001 to AAV78100 represent peptides having sequences based on human
 XX CC lactoferrin. The peptides are taken up in the intestine through
 XX CC binding to specific lactoferrin receptors and are then transported
 XX CC through the circulation. A medicinal product of the peptide or fragment
 XX CC can be used for treating and/or prevention of infections (such as
 XX CC urinary tract infections, colitis, and Candida infection on a mucosal
 XX CC membrane), inflammations, colitis, and Candida infection on a mucosal
 XX CC in food stuffs such as infant formula food. The peptides can also be used
 XX CC fungicidal and bactericidal and may also be used as preservatives.
 XX CC Even though native human lactoferrin have been shown to have desired
 XX CC anti-inflammatory anti-infectious and anti-tumoural properties they
 XX CC cannot be used clinically on a broad basis because of high production
 XX CC costs. Therefore, provision of peptides based on lactoferrin would
 XX CC enable them to be used for the same purposes as lactoferrin at lower
 XX CC cost.

XX SQ Sequence 15 AA;

Query Match 92.9%; Score 65; DB 21; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.00028;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12
 DB 4 CFQWQNRKVR 15

RESULT 14

AAV78062
 ID AAV78062 standard; Peptide; 15 AA.

XX AC AAV78062;
 XX DT 25-APR-2000 (first entry)
 XX DE Human lactoferrin derived peptide SEQ ID NO:62.
 XX KW Human, lactoferrin; modification; infection; inflammation; tumour;
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;
 XX KW bactericidal; preservative.

XX OS Homo sapiens.
 XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-S01230.

XX PR 06-JUL-1998; 98SE-0002441.
 XX PR 17-JUL-1998; 98SE-0002562.
 XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
 XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 15; Page 81; 102pp; English.

XX CC AAV78001 to AAV78100 represent peptides having sequences based on human
 XX CC lactoferrin. The peptides are taken up in the intestine through
 XX CC binding to specific lactoferrin receptors and are then transported
 XX CC through the circulation. A medicinal product of the peptide or fragment
 XX CC can be used for treating and/or prevention of infections (such as
 XX CC urinary tract infections, colitis, and Candida infection on a mucosal
 XX CC membrane), inflammations, colitis, and Candida infection on a mucosal
 XX CC in food stuffs such as infant formula food. The peptides can also be used
 XX CC fungicidal and bactericidal and may also be used as preservatives.
 XX CC Even though native human lactoferrin have been shown to have desired
 XX CC anti-inflammatory anti-infectious and anti-tumoural properties they
 XX CC cannot be used clinically on a broad basis because of high production
 XX CC costs. Therefore, provision of peptides based on lactoferrin would
 XX CC enable them to be used for the same purposes as lactoferrin at lower
 XX CC cost.

XX SQ Sequence 15 AA;

Query Match 92.9%; Score 65; DB 21; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.00028;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12
 DB 4 CFQWQNRKVR 15

RESULT 15

AAV78063
 ID AAV78063 standard; Peptide; 15 AA.

XX AC AAV78063;

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XX 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:63.
XX
XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
XX
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-SE01230.
XX
XX 06-JUL-1998; 98SE-0002441.
XX 17-JUL-1998; 98SE-0002562.
XX 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX Hanson LA, Matsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
XX inflammations and tumors and for use in infant formula food -
XX Claim 18; Page 81; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
XX lactoferrin. The peptides are taken up in the intestine through
XX binding to specific lactoferrin receptors and are then transported
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XX membrane), inflammations and/or tumors. The peptides can also be used
XX in food stuffs such as infant formula food. The peptides are also
XX fungicidal and bactericidal and may also be used as preservatives.
XX Even though native human lactoferrin have been shown to have desired
XX anti-inflammatory anti-infectious and anti-tumoural properties they
XX cannot be used clinically on a broad basis because of high production
XX costs. Therefore, provision of peptides based on lactoferrin would
XX enable them to be used for the same purposes as lactoferrin at lower
XX cost.
XX
XX Sequence 15 AA;
XX
XX Query Match 92.9%; Score 65; DB 21; Length 15;
XX Best Local Similarity 91.7%; Pred. No. 0.00028;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 CFQWQNRNARKVR 12
XX | | | | |
XX Db 4 CFQWQNRNARKVR 15

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Search completed: February 21, 2003, 07:37:12
 Job time : 28.35 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 Seconds
(without alignments)
40.818 Million cell updates/sec

Title: US-09-743-107B-75
Perfect score: 70
Sequence: 1 CFQQRNARKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCUTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	18	1	US-08-204-487-3
2	65	92.9	18	2	US-08-485-948-8
3	65	92.9	18	2	US-08-628-380-8
4	65	92.9	18	2	US-08-475-055-8
5	65	92.9	20	1	US-07-755-161A-3
6	65	92.9	20	1	US-07-891-174-3
7	65	92.9	20	1	US-08-204-487-1
8	65	92.9	20	1	US-08-256-771-24
9	65	92.9	20	1	US-08-256-771-25
10	65	92.9	20	1	US-08-381-984-24
11	65	92.9	20	1	US-08-381-984-25
12	65	92.9	22	4	US-09-508-734-4
13	65	92.9	24	4	US-09-508-734-6
14	65	92.9	25	1	US-07-755-161A-10
15	65	92.9	25	1	US-07-891-174-10
16	65	92.9	25	1	US-08-204-487-7
17	65	92.9	29	4	US-09-508-734-8
18	65	92.9	26	1	US-07-755-161A-8
19	65	92.9	36	1	US-07-891-174-8
20	65	92.9	36	1	US-08-256-771-30
21	65	92.9	36	1	US-08-381-984-29
22	65	92.9	47	2	US-08-464-182A-6
23	65	92.9	47	2	US-08-406-271-6
24	65	92.9	50	2	US-08-693-274A-7
25	65	92.9	52	4	US-09-017-043A-3
26	65	92.9	53	2	US-08-464-182A-5
27	65	92.9	53	2	US-08-406-271-5

28	65	92.9	54	2	US-08-464-182A-2
29	65	92.9	54	2	US-08-406-271-2
30	65	92.9	694	3	US-08-724-586-2
31	65	92.9	694	4	US-08-421-632-2
32	65	92.9	694	4	US-09-932-190-2
33	65	92.9	705	2	US-08-655-640-2
34	65	92.9	708	2	US-08-655-640-4
35	65	92.9	711	1	US-08-154-019-4
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37	65	92.9	711	3	US-08-464-167-4
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39	65	92.9	711	4	US-08-476-798-4
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44	62	88.6	711	3	US-08-456-108-2
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ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/082044487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FUN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37)"
US-08-204-487-3

Query Match 92.9%; Score 65; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 8.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRKVR 12
| | | | | | | | | | | | | | | | | |
Db 1 CFQWQNRKVR 12

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,948
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,217
; FILING DATE: JUNE 7, 1995
; APPLICATION NUMBER: 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-485-948-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 8.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRKVR 12
| | | | | | | | | | | | | | | | | |
Db 1 CFQWQNRKVR 12

RESULT 3

US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341
; GENERAL INFORMATION:
; APPLICANT: LI, YONG MING
; APPLICANT: VLASSARA, HELEN
; APPLICANT: CERAMI, ANTHONY
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,380
; FILING DATE: April 4, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-628-380-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 8.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRKVR 12
| | | | | | | | | | | | | | | | | |
Db 1 CFQWQNRKVR 12

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURES:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURES:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3
Query Match 92.9%; Score 65; DB 1; Length 20;
US-08-475-055-8
Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 8.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CFQWRNARKVR 12
Db 1 CFQWRNARKVR 12
RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KB
COMPUTER: IBM Compatible
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Best Local Similarity 91.7%; Pred. No. 9e-05; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNARKVR 12
| | | | | | | | | |
Db 2 CFQWQRNARKVR 13

RESULT 6
US-07-891-174-3
; Sequence 3, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 905 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Displaywrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 08-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNARKVR 12
| | | | | | | | | |
Db 2 CFQWQRNARKVR 13

RESULT 7
US-08-204-487-1
; Sequence 1, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEAKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIAKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESS: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: RJN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
DERIVED FROM HUMAN LACTOFERRIN"
US-08-204-487-1

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
DB 2 CFQWQNRNARKVR 13

RESULT 8

US-08-256-771-24
Sequence 24, Application US/08256771
Patent No. 5656591

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "Cys residues are linked by

OTHER INFORMATION: disulfide bond"

US-08-256-771-24

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
DB 2 CFQWQNRNARKVR 13

RESULT 9

US-08-256-771-25
Sequence 25, Application US/08256771
Patent No. 5656591

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/256,771

FILING DATE: July 22, 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "Cys residues are protected to

OTHER INFORMATION: prevent disulfide bond"

US-08-256-771-25

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
DB 2 CFQWQNRNARKVR 13

RESULT 10

US-08-381-984-24

; Sequence 24, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:

INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "cysteine residues at positions 2
; OTHER INFORMATION: and 19 are bonded by disulfide linkage".
; FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
; US-08-381-984-24

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNARKVR 12

DB 2 CFQWQRNARKVR 13

RESULT 11

US-08-381-984-25
; Sequence 25, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:

INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
; FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "cysteine residues at positions 2
; OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
; US-08-381-984-25

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNARKVR 12

DB 2 CFQWQRNARKVR 13

RESULT 12

US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 4

; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4

Query Match 92.9%; Score 65; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 9.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRNARKVR 12
Db 2 CFQWQNRNARKVR 13

RESULT 13

US-09-508-734-6
; Sequence 6, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-6

Query Match 92.9%; Score 65; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRNARKVR 12
Db 3 CFQWQNRNARKVR 14

RESULT 14

US-07-755-161A-10
; Sequence 10, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755,161A
; FILING DATE: 19910905
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHEetical:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
Query Match 92.9%; Score 65; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CFQWQNRNARKVR 12
Db 4 CFQWQNRNARKVR 15

RESULT 15

US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21

; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-07-891-174-10
; Query Match 92.9%; Score 65; DB 1; Length 25;
; Best Local Similarity 91.7%; Pred. No. 0.00011;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
; Cys 1 CFQWQNRNARKVR 12
; Db 4 CFQWQNRNARKVR 15
; Search completed: February 21, 2003, 07:50:34
; Job time : 8.7 secs


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; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match      92.9%; Score 65; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
   |||||
Db 3 CFQWQNRNARKVR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; TITLE OF INVENTION: Lactoferrin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-023-096-2
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Query Match      92.9%; Score 65; DB 9; Length 694;
Best Local Similarity 91.7%; Pred. No. 0.0028;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
   |||||
Db 22 CFQWQNRNARKVR 33

RESULT 4
US-09-798-869-6
; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON)
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-6

Query Match      81.4%; Score 57; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
   |||||
Db 3 CFQWQNRNARKVR 14

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON)
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-3

Query Match      58.6%; Score 48; DB 9; Length 15;
Best Local Similarity 63.8%; Pred. No. 0.043;
```

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRKRV 11
|:|:|:|:|:
Db 3 CYQWQNRKRL 13

RESULT 6
US-09-798-869-23
; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23

Query Match 69.6%; Score 48; DB 9; Length 25;
Best Local Similarity 63.6%; Pred. No. 0.07;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRKRV 11
|:|:|:|:|:
Db 3 CYQWQNRKRL 13

RESULT 7
US-09-798-869-7
; Sequence 7, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-7

Query Match 57.1%; Score 40; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.89;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNRKRV 11
|:|:|:|:|:
Db 3 CYQWQNRKRL 13

RESULT 8
US-09-798-869-4
; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4

Query Match 55.7%; Score 39; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.3;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNRKRV 11
|:|:|:|:|:
Db 3 CLRWQNRKRV 13

RESULT 9
US-09-798-869-22
; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-22

Query Match 55.7%; Score 39; DB 9; Length 25;
Best Local Similarity 54.5%; Pred. No. 2.1;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNRKRV 11
|:|:|:|:|:
Db 3 CLRWQNRKRV 13

RESULT 10
US-10-066-500-58
; Sequence 58, Application US/10066500
; Patent No. US2002017165A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kijavlin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas P. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C7
; CURRENT APPLICATION NUMBER: US/10/066,500
; CURRENT FILING DATE: 2002-02-01
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063733
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066840
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: 60/069694
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074092
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/095998
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/097000
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/099601
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100858
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106032
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/109304
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/125778
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/139695
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/145070
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/149396
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 08/918874
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 08/933821
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 08/960507
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 09/114844
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: 09/136801
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: 09/136804
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: 09/136828
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: 09/158342
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: 09/180997
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/202088
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: 09/254311
; PRIOR FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: 09/254460
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/254465
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: 09/284663
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 09/332928
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: 09/332929
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: 09/333075
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: 09/333077
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380139
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/403296
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/403297

PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/423741
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 09/423844
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 09/522342
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 09/548815
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 09/664610
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/665350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/709238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/767609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/808699
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/866028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/870574
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: 09/872035
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/886342
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: PCT/US98/14552
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: PCT/US98/18824
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/US98/19093
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/24855
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: 1998-12-01
PRIOR APPLICATION NUMBER: PCT/US98/25190
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 55.7%; Score 39; DB 9; Length 747;

Best Local Similarity 45.5%; Pred. No. 57;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFOWQNRKRV 11

Db 311 CWRQWNSREI 321

RESULT 11

US-10-002-796-58
; Sequence 58, Application US/10002796
; Publication No. US20030032057A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker

APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerritsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kljavin
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TEANSMEMERANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3130RIC1
CURRENT APPLICATION NUMBER: US/10/002,796
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062285
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PRIOR APPLICATION NUMBER: 60/081049
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PRIOR APPLICATION NUMBER: 60/095998
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PRIOR FILING DATE: 1998-11-25
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PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: PCT/US99/12252
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PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28301

Query Match 55.7%; Score 39; DB 9; Length 747;

Best Local Similarity 45.5%; Pred. No. 57;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWNRKV 11

Db 311 CVRWQNSRI 321

RESULT 12

US-10-066-273-58
Sequence 58, Application US/10066273
Publication No. US20030032062A1
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleon Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber

APPLICANT: Mary E. Gerritsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kljavin
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: F31301C2
CURRENT APPLICATION NUMBER: US/10/066,273
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 55.7%; Score 39; DB 9; Length 747;

Best Local Similarity 45.5%; Pred. No. 57;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRKRV 11

Db 311 CVMQINSRRI 321

RESULT 13

US-10-066-494-58

Sequence 58, Application US/10066494

Publication No. US20030032063A1

GENERAL INFORMATION:

APPLICANT: Avi J. Ashkenazi

APPLICANT: Kevin P. Baker

APPLICANT: David A. Botstein

APPLICANT: Luc Desnoyers

APPLICANT: Dan L. Eaton

APPLICANT: Napoleone Ferrara

APPLICANT: Sherman Fong

APPLICANT: Wei-Qiang Gao

APPLICANT: Hanspeter Gerber

APPLICANT: Mary E. Gerritsen

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APPLICANT: James Pan
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APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3130R1C9
CURRENT APPLICATION NUMBER: US/10/066,494
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
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;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 55.7%; Score 39; DB 9; Length 747;
Best Local Similarity 45.5%; Pred No. 57;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQMQRNARKV 11

DB 311 CVRWQINSRRI 321

RESULT 14

US-09-738-626-5071
; Sequence 5071, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5071

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/ LENGTH: 255
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/ ORGANISM: Corynebacterium glutamicum
US-09-738-626-5071

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Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QWQNRARK 10
    |||||:
Db 110 QWQNRARR 117

RESULT 15
US-09-978-295A-119
/ Sequence 119, Application US/09978295A
/ Patent No. US2002015606A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavini, Ivar J.
/ APPLICANT: Kuc, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630PIC11
/ CURRENT APPLICATION NUMBER: US/09/978,295A
/ CURRENT FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: 09/918595
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/064249
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69 PRIOR FILING DATE: 1998-05-15
70 PRIOR APPLICATION NUMBER: 60/085697

Query Match 54.3%; Score 38; DB 9; Length 338;
Best Local Similarity 45.5%; Pred. No. 39;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CFOWORNARKY 11
Db 50 CYGWRNRNSKGV 60

Search completed: February 21, 2003, 08:08:05
Job time : 11.55 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 Seconds
(without alignments)
120.168 Million cell updates/sec

Title: US-09-743-107B-75
Perfect score: 70
Sequence: 1 CFQWQNRKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 73:.*
1: Pirl:.*
2: Pirl:.*
3: Pirl:.*
4: Pirl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	65	92.9	711	1 TFHUL	lactotransferrin p
2	48	68.6	708	2 JC2323	lactoferrin - goat
3	46	65.7	932	2 T28820	hypothetical prote
4	45	64.3	33	2 S52107	lactoferrin - shee
5	43	61.4	1432	2 B85431	trichohyalin like
6	42	60.0	289	2 G86403	33.3K hypothetical
7	42	60.0	511	2 AB0858	hypothetical prote
8	41	58.6	228	2 AD2346	hypothetical prote
9	41	58.6	4568	2 T08030	dyein beta heavy
10	40	57.1	255	2 T87515	signal peptidase I
11	40	57.1	681	2 T19429	hypothetical prote
12	39	55.7	518	2 B84514	probable cytochrom
13	39	55.7	570	2 T46261	hypothetical prote
14	39	55.7	707	1 A28438	lactoferrin precu
15	38	54.3	121	2 AH3147	hypothetical prote
16	38	54.3	283	2 D72378	sugar ABC transpo
17	38	54.3	340	2 T51386	probable protein w
18	38	54.3	365	2 T37477	MHC class I histoc
19	38	54.3	515	2 T00510	probable cytochrom
20	38	54.3	536	2 T24218	hypothetical prote
21	38	54.3	543	2 T00513	cytochrome P450 ho
22	38	54.3	558	2 T17324	hypothetical prote
23	38	54.3	749	2 A45687	outer capsid prote
24	38	54.3	6642	2 T29757	protein UNC-89 - C
25	37	52.9	89	2 G97365	hypothetical prote
26	37	52.9	194	2 AF1269	hypothetical GTP b
27	37	52.9	194	2 AH1631	hypothetical GTP b
28	37	52.9	206	2 H97451	pyridoxamine 5'-ph
29	37	52.9	206	2 AB2670	pyridoxamine 5'-ph

30 37 52.9 208 2 AG3441
31 37 52.9 223 2 T37974
32 37 52.9 238 2 T40568
33 37 52.9 287 1 S70810
34 37 52.9 287 2 B82546
35 37 52.9 361 2 T29571
36 37 52.9 367 2 S15716
37 37 52.9 367 2 G97649
38 37 52.9 374 1 WZWCPC
39 37 52.9 374 2 JC1313
40 37 52.9 374 2 S49306
41 37 52.9 479 2 T16130
42 37 52.9 493 1 S17663
43 37 52.9 500 2 S42867
44 37 52.9 510 2 S62545
45 37 52.9 517 2 F71417

probable pyridoxam
probable peroxisom
hypothetical prote
type IV prelin p
pre-pilin leader p
hypothetical prote
pectate lyase (EC
glutamine syntheta
pectate lyase (EC
pectate lyase (EC
pectase lyase 2 pr
hypothetical prote
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protein kinase (EC
hypothetical prote
cytochrome P450 -

ALIGNMENTS

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N/Alternate names: lactoferrin

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74

R/Cho, Y.

submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:U07643; NID:G467236; PIDN:AA60324.1; PID:G467237

R/Rev. M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; MUID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>

A/Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactoferi

A/Reference number: A45401; MUID:93125571; PMID:1480183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <TEN>

A/Cross-references: GB:S52659; NID:G263311; PIDN:AA624877.1; PID:G263312

A/Experimental source: placenta

A/Note: sequence extracted from NCBI backbone (NCBIP:122202)

R/Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; MUID:90326549; PMID:2374734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POW>

A/Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA371116.1; PID:G34412

R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A/Reference number: S15853; MUID:91264786; PMID:2049066

A/Accession: S15853

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 20-31 <STI>

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-28, 'X', 30-31 <ST2>

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
 Blood 70, 983-993, 1987
 A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
 A;Reference number: S07160; MUID:88001031; PMID:3477300
 A;Accession: S07160
 A;Molecule type: mRNA
 A;Residues: 436-487, 'A', 489-711 <RAD>
 A;Cross-references: EMBL:M18642; NID:G986855
 R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
 Cancer Res. 51, 3037-3043, 1991
 A;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
 A;Reference number: A61169; MUID:91235214; PMID:1674448
 A;Accession: A61169
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 3-701, 'SWKPVN' <PAN>
 A;Experimental source: normal breast tissue
 R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
 Eur. J. Biochem. 145, 659-666, 1984
 A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with other
 A;Reference number: A31000; MUID:85076667; PMID:6510420
 A;Accession: A31000
 A;Molecule type: protein
 A;Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4
 A;Note: this is the final paper in a series
 R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
 Eur. J. Biochem. 241, 303-308, 1996
 A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminoethyl affinity
 A;Reference number: S74119; MUID:97054624; PMID:8898921
 A;Accession: S74119
 A;Molecule type: protein
 A;Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>
 A;Experimental source: neutrophil granulocytes
 C;Genetics:
 A;Gene: GDB:LTF
 A;Cross-references: GDB:119368; OMIM:150210
 A;Map position: 3q21-3q23
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication; glycoprotein; iron binding; milk
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-711/Product: lactotransferrin #status experimental <MAT>
 F;21-356/Domain: transferrin repeat homology <TRH1>
 F;360-699/Domain: transferrin repeat homology <TRH2>
 F;29-65, 39-55, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status e
 F;1498/Binding site: carbohydrate (Asn) (covalent) #status experimental
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 DB 39 CFQWQNRNARKV 50
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 JC2323
 lactoferrin - goat
 C;Species: Capra aegagrus hircus (domestic goat)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 C;Accession: JC2323
 R;Le Provost, F.; Nocard, M.; Guerin, G.; Martin, P.
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
 A;Reference number: JC2323; MUID:94380047; PMID:8093048
 A;Accession: JC2323
 A;Molecule type: mRNA
 A;Residues: 1-708 cLEP>
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication; glycoprotein
 F;359-696/Domain: transferrin repeat homology <TRH2>
 F;252, 300, 387, 495, 564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.6%; Score 48; DB 2; Length 708;
 Best Local Similarity 63.8%; Pred. No. 1.5; Mismatches 2; Indels 0; Gaps 0;
 Matches 7; Conservative

QY 1 CFQWQNRNARKV 11
 DB 38 CFQWQNRNARKV 48

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 hypothetical protein F07C3.1 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T28820
 R;Favella, A.; Gattung, S.
 submitted to the EMBL Data Library, March 1996
 A;Description: The sequence of C. elegans cosmid F07C3.
 A;Reference number: Z20528
 A;Accession: T28820
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-932 <FAV>
 A;Cross-references: EMBL:U50308; PIDN:AAC48001.1; GSPDB:GN000023; CESP:F07C3.1
 A;Experimental source: strain Bristol N2; clone F07C3
 C;Genetics:
 A;Gene: CESP:F07C3.1
 A;Map position: 5
 A;Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 595/3;
 Query Match 65.7%; Score 46; DB 2; Length 932;
 Best Local Similarity 72.7%; Pred. No. 4.3; Mismatches 2; Indels 0; Gaps 0;
 Matches 8; Conservative

QY 2 FQWQNRNARKV 12
 DB 579 FQWQNRNARKV 589

RESULT 4
 S52107
 lactoferrin - sheep (fragment)
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
 C;Accession: S52107
 R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
 Biochim. Biophys. Acta 1243, 25-32, 1995
 A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet
 A;Reference number: S52107; MUID:95127729; PMID:7827104
 A;Accession: S52107
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-33 <QIA>
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication

Query Match 64.3%; Score 45; DB 2; Length 33;
 Best Local Similarity 54.5%; Pred. No. 0.27; Mismatches 3; Indels 0; Gaps 0;
 Matches 6; Conservative

QY 1 CFQWQNRNARKV 11
 DB 19 CFQWQNRNARKV 29

RESULT 5
 B85431
 trichohyalin like protein [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
 C;Accession: B85431
 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

QY 1 CFOWQNRNARKV 12
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 Db 1852 CFOWQSQLRYIQ 1863

RESULT 10

signal peptidase I [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
 C:Accession: E87515
 R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A>Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; PMID:12173698; PMID:11259647
 A:Accession: E87515
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-255 <STO>
 A:Cross-references: GB:AE005673; NID:gl3423643; PIDN:AAK24121.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC2150
 C:Superfamily: signal peptidase I

Query Match 57.1%; Score 40; DB 2; Length 255;
 Best Local Similarity 63.6%; Pred. No. 14;
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QY 2 FQWQNRNARKV 12
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 Db 245 FQWDFARPFR 255

RESULT 11

hypothetical protein C24H11.8 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T19429
 R.Lloyd, C.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19123
 A:Accession: T19429
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-681 <WIL>
 A:Cross-references: EMBL:Z81475; PIDN:CAB03914.1; GSPDB:GN00021; CESP:C24H11.8
 A:Experimental source: clone C24H11
 C:Genetics:
 A:Gene: CESP:C24H11.8
 A:Map position: 3
 A:Introns: 18/3; 65/3; 108/1; 138/1; 177/3; 256/2; 303/2; 343/1; 409/3; 484/3; 532/2; 56

Query Match 57.1%; Score 40; DB 2; Length 681;
 Best Local Similarity 60.0%; Pred. No. 36;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWQNRNARKV 12
 |||||
 Db 192 RWQKRRVR 201

RESULT 12

probable cytochrome P450 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana [mouse-ear cross]
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 23-Mar-2001
 C:Accession: B84514
 R.Liu, X.; Kaul, S.; Rounleay, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; PMID:20083487; PMID:10617197

A:Accession: B84514
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-518 <STO>
 A:Cross-references: GB:AE002093; NID:g4587680; PIDN:AAD25850.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g14100

A:Map position: 2
 C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C:Keywords: heme; iron; metalloprotein
 F:453/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 55.7%; Score 39; DB 2; Length 518;
 Best Local Similarity 54.5%; Pred. No. 42;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFOWQNRNARKV 11
 |||||
 Db 473 CFQWRTNGDKV 483

RESULT 13

T46261
 hypothetical protein DKFPZP761E1824.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
 C:Accession: T46261
 R.Bioecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000
 A:Reference number: Z23032
 A:Accession: T46261
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-570 <AAA>

A:Cross-references: EMBL:AL137432
 A:Experimental source: adult amygdala; clone DKFPZP761E1824
 C:Genetics:
 A:Note: DKFPZP761E1824.1

Query Match 55.7%; Score 39; DB 2; Length 570;
 Best Local Similarity 45.5%; Pred. No. 46;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFOWQNRNARKV 11
 |||||
 Db 134 CVRWQINSRRI 144

RESULT 14

A28438
 lactoferrin precursor - mouse
 N:Alternate names: lactotransferrin
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A28438; A41205
 R.Pentecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A>Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret
 A:Reference number: A92596; PMID:87280033; PMID:3611056
 A:Accession: A28438
 A:Molecule type: mRNA

A:Residues: 3-707 <PEN>
 A:Cross-references: EMBL:J03298
 R.Liu, Y.; Teng, C.T.

J. Biol. Chem. 266, 21880-21885, 1991

A>Title: Characterization of estrogen-responsive mouse lactoferrin promoter.

A:Reference number: A41205; PMID:92042099; PMID:1939212
 A:Accession: A41205
 A:Molecule type: DNA

A;Residues: 1-15 <LIU>
A;Cross-references: GB:M74778
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-707/Product: lactotransferrin #status predicted <MAT>
F;358-695/Domain: transferrin repeat homology <TRH2>
F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.7%; Score 39; DB 1; Length 707;
Best Local Similarity 54.5%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQNRKRV 11
| | | | |
Db 37 CLRWQNRKRV 47

RESULT 15
AH3147
hypothetical protein Atu4804 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AH3147
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AH3147
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-121 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL45598.1; PID:g17743317; GSPDB:GN00187
C;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu4804
A;Map position: linear chromosome

Query Match 54.3%; Score 38; DB 2; Length 121;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQNRKRV 11
| | | | |
Db 14 CLAWQNRKRV 24

Search completed: February 21, 2003, 07:47:47
Job time : 11.65 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds
(without alignments)
108.199 Million cell updates/sec

Title: US-09-743-107b-75
Perfect score: 70
Sequence: 1 CFQWQRNARKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	711	1	TREL_HUMAN
2	48	68.6	708	1	TREL_CAMDR
3	48	68.6	708	1	TREL_CAPHI
4	43	61.4	146	1	RPOB_LIBAF
5	41	58.6	458	1	DYHB_CHLRE
6	40	57.1	695	1	TREL_HORSE
7	39	55.7	707	1	TREL_MOUSE
8	38	54.3	365	1	LA34_HUMAN
9	38	54.3	749	1	VP4_ROTGA
10	38	54.3	783	1	YNR2_CAEEL
11	37	52.9	238	1	PELX_ERWCA
12	37	52.9	238	1	YBM9_SCHPO
13	37	52.9	287	1	LEP4_XANCP
14	37	52.9	292	1	NLA_DROME
15	37	52.9	374	1	PEL2_ERWCA
16	37	52.9	455	1	YQV1_CAEEL
17	37	52.9	480	1	YQ81_CAEEL
18	37	52.9	493	1	NURM_NEUCR
19	37	52.9	510	1	YAGF_SCHPO
20	36	51.4	85	1	PMRD_SALTY
21	36	51.4	211	1	LOLB_VIBCH
22	36	51.4	214	1	VIF_SIVS4
23	36	51.4	235	1	FL3L_HUMAN
24	36	51.4	241	1	AGL9_PETHY
25	36	51.4	374	1	PEL3_ERWCA
26	36	51.4	375	1	PELB_ERWCH
27	35	50.0	62	1	RL28_THETN
28	35	50.0	208	1	FGFA_HUMAN
29	35	50.0	209	1	FGFA_MOUSE
30	35	50.0	215	1	FGFA_RAT
31	35	50.0	275	1	IL2A_BOVIN
32	35	50.0	275	1	IL2A_SHEEP
33	35	50.0	288	1	LEP4_PSEPU

ALIGNMENTS

RESULT 1

ID	TREL_HUMAN	STANDARD;	PRT;	711 AA.
AC	P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9HI23; Q95KZ4;			
AC	Q96KZ5;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactoferrin precursor (Lactoferrin) [Contains: Lactoferrin A;			
DE	Lactoferrin B; Lactoferrin C]			
GN	LTF OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RC	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;			
RT	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RL	Nucleic Acids Res. 18:5288-5288(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cho Y.Y.;			
RL	Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Conneely O.M.;			
RT	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RT	"Molecular cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Rado T.A.;			
RT	"Human neutrophil lactoferrin coding and 5' flanking region DNA			
RL	sequences.";			
RN	[6]			
RP	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cheng H., Chen X., Huan L.;			
RT	"cDNA cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN	[8]			

34	35	50.0	306	1	BUB2 YEAST	R26448	saccharomyc
35	35	50.0	355	1	MURG_NEIMA	Q9J827	neisseria m
36	35	50.0	355	1	MURG_NEIMB	Q9K0V2	neisseria m
37	35	50.0	487	1	HEP_DROME	Q23977	drosofila
38	35	50.0	502	1	C91I_ARATH	Q9F65	arabidopsis
39	35	50.0	665	1	YLL4_CAEEL	Q11500	caenorhabdi
40	35	50.0	2671	1	IP3T_HUMAN	Q14573	homo sapien
41	34	48.6	160	1	RNH_SYNY3	Q55801	synecocyst
42	34	48.6	289	1	PA1_SALTY	P37442	salmonella
43	34	48.6	401	1	O88A_DROME	Q9VFN2	drosofila
44	34	48.6	467	1	DCEC_LISIN	Q928K4	listeria in
45	34	48.6	467	1	DCEC_LISMO	Q8Y4K4	listeria mo

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE-Mammary Gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ogden J.E.;
RT "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076567; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
RT "Human lactotransferrin: amino acid sequence and structural
RT comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1984).
RN [10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
Jolles P.;
RT "The present state of the human lactotransferrin sequence. Study and
RT alignment of the cyanogen bromide fragments and characterization of
RT N- and C-terminal domains.";
RL Biochim. Biophys. Acta 670:243-254(1981).
RN [11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
RT lactotransferrin";
RL FEBS Lett. 142:107-110(1982).
RN [12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
RN [13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
Sagripanti J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2385506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human diferric lactoferrin refined at 2.2-A
RT resolution.";
RL Acta Crystallogr. D 51:629-646(1995).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RT 253-->methionine mutant.";
RL Biochemistry 36:341-346(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in Aspergillus
RT awamori.";
RL Acta Crystallogr. D 55:403-407(1999).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
RT and analysis of ligand-induced conformational change.";
RL Acta Crystallogr. D 54:1319-1335(1998).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of opioid antagonist peptides derived
RT from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810(1990).
RN [20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
Sagar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
Hejtmancik J.F., Teng C.T.;
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RL Mol. Vision 4:31-32(1998).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; X53961; CAA37914.1; -
DR EMBL; U07643; AAB60324.1; -
DR EMBL; M93150; AAA36159.1; -
DR EMBL; M83202; AAA59511.1; -
DR EMBL; M83205; AAA58656.1; -
DR EMBL; M18642; AAA86665.1; -
DR EMBL; AF332168; AAG48753.1; -
DR EMBL; BC015822; AAH15822.1; -
DR EMBL; BC015823; AAH15823.1; -
DR EMBL; M73700; AAA59479.1; -
DR EMBL; X52941; CAA37116.1; -
DR EMBL; U95626; AAB57795.1; -
DR PIR; S11228; TFHUL; -
DR PDB; 1LCF; 31-AUG-94.
DR PDB; 1LCT; 31-OCT-93.
DR PDB; 1LEG; 31-JUL-94.
DR PDB; 1LFH; 31-OCT-93.
DR PDB; 1LFT; 31-OCT-93.
DR PDB; 1LGE; 31-AUG-94.
DR PDB; 1LGC; 31-AUG-94.
DR PDB; 1BKA; 08-NOV-96.
DR PDB; 1DSN; 08-MAR-96.
DR PDB; 1HSE; 12-MAR-97.
DR PDB; 1VFD; 21-APR-97.

Query Match 92.9%; Score 65; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.00035;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRNARKVR 12
 |||||
 Db 39 CFQWQRNARKVR 50

RESULT 2

TRFL_CAMDR STANDARD; PRT; 708 AA.
 AC Q9TUM0; Q9MZS5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;
 RA Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
 RL Int. Dairy J. 9:481-486(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION. USUALLY BICARBONATE (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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 CC -----

DR EMBL; AJ131674; CAB53387.1; -;
 DR EMBL; AF165879; AAF82241.1; -;
 DR HSP; O77811; 131X.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00034; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN 1; 2.
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.
 DR PROSITE; PS00207; TRANSFERRIN 3; 2.
 KW Transport; iron transport; Glycoprotein; Metal-binding; Repeat;
 Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 708
 FT REPEAT 20 363
 FT REPEAT 364 708
 FT REPEAT 1.
 FT BY SIMILARITY.
 FT DISULFID 28 64
 FT BY SIMILARITY.
 FT DISULFID 38 55
 FT BY SIMILARITY.
 FT DISULFID 134 217
 FT BY SIMILARITY.
 FT DISULFID 176 192
 FT BY SIMILARITY.
 FT DISULFID 189 200
 FT BY SIMILARITY.
 FT DISULFID 250 264
 FT BY SIMILARITY.
 FT DISULFID 367 399
 FT BY SIMILARITY.

FT DISULFID 377 390
 FT BY SIMILARITY.
 FT DISULFID 424 703
 FT BY SIMILARITY.
 FT DISULFID 444 666
 FT BY SIMILARITY.
 FT DISULFID 476 551
 FT BY SIMILARITY.
 FT DISULFID 500 694
 FT BY SIMILARITY.
 FT DISULFID 510 524
 FT BY SIMILARITY.
 FT DISULFID 521 534
 FT BY SIMILARITY.
 FT DISULFID 592 606
 FT BY SIMILARITY.
 FT DISULFID 644 649
 FT BY SIMILARITY.
 FT METAL 79 79
 FT METAL 111 111
 FT METAL 211 211
 FT METAL 272 272
 FT METAL 414 414
 FT METAL 452 452
 FT METAL 545 545
 FT METAL 614 614
 FT BINDING 140 140
 FT BINDING 482 482
 FT CARBOHYD 252 252
 FT CARBOHYD 385 385
 FT CARBOHYD 537 537
 FT CARBOHYD 594 594
 FT CONFLICT 261 261
 FT CONFLICT 304 304
 FT CONFLICT 330 330
 FT CONFLICT 492 494
 FT CONFLICT 506 506
 FT CONFLICT 609 609
 FT CONFLICT 642 642
 SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match 68.6%; Score 48; DB 1; Length 708;
 Best Local Similarity 66.7%; Pred. No. 0.4;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQRNARKVR 12
 |||||
 Db 38 CAQWQRNARKVR 49

RESULT 3

TRFL_CAPHI STANDARD; PRT; 708 AA.
 ID TRFL_CAPHI
 AC Q29477; Q29479;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=94380047; PubMed=8093048;
 RA le Provost F., Nocart M., Guerin G., Martin P.;
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the relevant locus to bovine U12 syntenic group."
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION. USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.


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RP SEQUENCE FROM N.A.
RC STRAIN=21gr;
RX MEDLINE=94274778; PubMed=8006077;
RA Mitchell D.R.; Brown K.S.;
RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
RL chain genes.";
RJ J. Cell Sci. 107:635-644(1994).
CC -J- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
CC FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC DYEIN HAS ATPASE ACTIVITY.
CC -I- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
CC GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
CC -I- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
CC
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CC
CC EMBL; U02963; AAA19956.1; -.
DR InterPro; IPR004273; Dynein_heavy;
DR Pfam; PF03028; Dynein_heavy; 1.
KW Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
KW Coiled coil.
FT DOMAIN 277 293 COILED COIL (POTENTIAL).
FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).
FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
FT DOMAIN 2017 2045 COILED COIL (POTENTIAL).
FT DOMAIN 2831 2848 MICROTUBULE-BINDING (POTENTIAL).
FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
FT DOMAIN 3339 3425 COILED COIL (POTENTIAL).
FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
FT NP_BIND 1919 1926 ATP (POTENTIAL).
FT NP_BIND 2202 2209 ATP (POTENTIAL).
FT NP_BIND 2530 2537 ATP (POTENTIAL).
FT NP_BIND 2879 2886 ATP (POTENTIAL).
SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;

Query Match 58.6%; Score 41; DB 1; Length 4568;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQNRVARKVR 12
Db 1852 CFQWQSLRVIQ 1863
|||||
:::

RESULT 6
ID TRPL HORSE STANDARD; PRT; 695 AA.
AC 077811;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUN-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin) (Fragment).
GN LTP.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
RT "cDNA sequence of mare lactoferrin.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RC TISSUE=Milk;

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RX MEDLINE=99296631; PubMed=10366507;
RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
RT "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
RL resolution.";
RJ J. Mol. Biol. 289:303-317(1999).
CC -J- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -I- SUBUNIT: MONOMER.
CC -I- SURCELLULAR LOCATION: Secreted.
CC -I- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -I- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC
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CC
CC EMBL; AJ010930; CAA09407.1; -.
DR PDB; 1B1X; 02-DEC-98.
DR PDB; 1B7U; 02-FEB-99.
DR PDB; 1B7Z; 02-FEB-99.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal; 3D-structure.
FT NON_TER 1 1
FT SIGNAL <1 6
FT CHAIN 7 695 LACTOTRANSFERRIN.
FT REPEAT 7 350 1.
FT REPEAT 351 695 2.
FT DISULFID 15 51
FT DISULFID 25 42
FT DISULFID 121 204
FT DISULFID 163 179
FT DISULFID 166 189
FT DISULFID 176 187
FT DISULFID 237 251
FT DISULFID 354 386
FT DISULFID 364 377
FT DISULFID 411 690
FT DISULFID 431 653
FT DISULFID 463 538
FT DISULFID 487 681
FT DISULFID 497 511
FT DISULFID 508 521
FT DISULFID 579 593
FT DISULFID 631 636
FT METAL 66 66 IRON 1 (BY SIMILARITY).
FT METAL 98 98 IRON 1 (BY SIMILARITY).
FT METAL 198 198 IRON 1 (BY SIMILARITY).
FT METAL 259 259 IRON 1 (BY SIMILARITY).
FT METAL 401 401 IRON 2 (BY SIMILARITY).
FT METAL 439 439 IRON 2 (BY SIMILARITY).
FT METAL 532 532 IRON 2 (BY SIMILARITY).
FT METAL 601 601 IRON 2 (BY SIMILARITY).
FT BINDING 127 127 ANION (BY SIMILARITY).
FT BINDING 143 143 ANION (BY SIMILARITY).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 482 482 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 695 AA; 75991 MW; 07BB84D50E1B165D CRC64;

Query Match 57.1%; Score 40; DB 1; Length 695;
Best Local Similarity 58.3%; Pred. No. 11;

```

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQNRKRV 12
| : ||| : |||
Db 25 CAXFQNRKRV 36

RESULT 7

ID TRFL MOUSE STANDARD; PRT; 707 AA.
AC P08071; P70690; Q61799; Q922P2;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN LTF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=87280033; PubMed=3611056;
RA Pentecost B.T.; Teng C.T.;
RT "Lactotransferrin is the major estrogen inducible protein of mouse uterine secretions.";
RL J. Biol. Chem. 262:10134-10139 (1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Morishita K.;
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=92042099; PubMed=1939212;
RA Liu Y.; Teng C.T.;
RT "Characterization of estrogen-responsive mouse lactoferrin promoter.";
RN J. Biol. Chem. 266:21880-21885 (1991).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC
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CC
CC EMBL; J03298; AAA40525.1; -
CC EMBL; D88510; BAAL3633.1; -
CC EMBL; BC006904; AAH06904.1; -
CC EMBL; M74778; AAA39427.1; -
CC PIR; A28438; A28438.
CC HSP; P02788; LCB8.
CC MGD; MG196837; Lcf.
CC InterPro; IPR001156; Transferrin.
CC Pfam; PF00405; transferrin; 2.
CC PRINTS; PR00422; TRANSFERRIN.
CC SMART; SM00094; TR FER; 2.
CC PROSITE; PS00205; TRANSFERRIN_1; 1.
CC PROSITE; PS00206; TRANSFERRIN_2; 2.
CC PROSITE; PS00207; TRANSFERRIN_3; 2.

KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;

Signal.
FT CHAIN 19 BY SIMILARITY.
FT REPEAT 20 707 LACTOTRANSFERRIN.
FT REPEAT 358 357 1.
FT REPEAT 707 2.
FT DISULFID 27 63 BY SIMILARITY.
FT DISULFID 37 54 BY SIMILARITY.
FT DISULFID 133 216 BY SIMILARITY.
FT DISULFID 175 191 BY SIMILARITY.
FT DISULFID 188 199 BY SIMILARITY.
FT DISULFID 249 263 BY SIMILARITY.
FT DISULFID 366 398 BY SIMILARITY.
FT DISULFID 376 389 BY SIMILARITY.
FT DISULFID 423 702 BY SIMILARITY.
FT DISULFID 443 665 BY SIMILARITY.
FT DISULFID 475 550 BY SIMILARITY.
FT DISULFID 499 693 BY SIMILARITY.
FT DISULFID 509 523 BY SIMILARITY.
FT DISULFID 520 533 BY SIMILARITY.
FT DISULFID 591 605 BY SIMILARITY.
FT DISULFID 643 648 BY SIMILARITY.
FT METAL 78 78 IRON 1 (BY SIMILARITY).
FT METAL 110 110 IRON 1 (BY SIMILARITY).
FT METAL 210 210 IRON 1 (BY SIMILARITY).
FT METAL 271 271 IRON 1 (BY SIMILARITY).
FT METAL 413 413 IRON 2 (BY SIMILARITY).
FT METAL 451 451 IRON 2 (BY SIMILARITY).
FT METAL 544 544 IRON 2 (BY SIMILARITY).
FT METAL 613 613 IRON 2 (BY SIMILARITY).
FT BINDING 139 139 ANION (POTENTIAL).
FT BINDING 481 481 ANION (POTENTIAL).
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 494 494 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 1 2 MR -> IQG (IN REF. 1).
FT CONFLICT 25 25 R -> Q (IN REF. 2).
FT CONFLICT 82 82 M -> L (IN REF. 2).
FT CONFLICT 359 359 S -> T (IN REF. 2).
FT CONFLICT 382 382 A -> D (IN REF. 1).
FT CONFLICT 449 449 E -> G (IN REF. 2).
FT CONFLICT 629 629 L -> V (IN REF. 1).
SQ SEQUENCE 707 AA; 77865 MW; F26AE0340A4C19A8 CRC64;

Query Match 55.7%; Score 39; DB 1; Length 707;

Best Local Similarity 54.5%; Pred.No. 17; Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQNRKRV 11
| : |||
Db 37 CLRQWQNRKRV 47

RESULT 8

ID 1A34 HUMAN STANDARD; PRT; 365 AA.
AC P30453; P30454;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, AW-34 (A-10) alpha chain precursor.
DE HLA-A OR HLA-A.
CN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (A*3401/A*3402).
RX MEDLINE=93056508; PubMed=1431115;
RA Madrigal J.A.; Belich M.P.; Hildebrand W.H.; Benjamin R.J.;
RA Little A.-M.; Zemmour J.; Ennis P.D.; Ward F.E.; Petzl-Erler M.L.;
RA Martell R.W.; du Toit E.D.; Parham P.;
RT "Distinctive HLA-A,B antigens of black populations formed by

interallelic conversion.";
 J. Immunol. 149:3411-3415 (1992).
 (2)
 SEQUENCE FROM N.A. (A*3401/A*3402).
 MEDLINE=92325211; PubMed=9475492.
 Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,
 Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
 du Toit E.D., Farham P.;
 "Structural diversity in the HLA-A10 family of alleles: correlations
 with serology.";
 Tissue Antigens 41:72-80 (1993).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
 CC -1- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401
 (AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
 A*3401.
 CC -----
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 CC -----
 DR EMBL; X61704; CAA43873.1; -;
 DR EMBL; X61705; CAA43874.1; -;
 DR PIR; S16767; S16767.
 DR PIR; S16771; S16771.
 DR HSP; O19673; IHSB.
 DR MM; 142800; -;
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig_1.
 DR Pfam; PF00129; MHC_I_1.
 DR ProDom; PD000050; MHC_I_1.
 DR SMART; SM00407; IGL1; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 365
 FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT AW-34 (A-10) ALPHA CHAIN.
 FT EXTRACELLULAR ALPHA-1.
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 365
 FT CYTOPLASMIC TAIL.
 FT N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT BY SIMILARITY.
 FT I -> V (IN A*3402).
 FT /FTID=VAR 004379.
 FT K -> N (IN A*3402).
 FT /FTID=VAR 004380.
 FT R -> I (IN A*3402).
 FT /FTID=VAR 004381.
 FT P -> S (IN A*3402).
 FT /FTID=VAR 004382.
 FT Q -> R (IN A*3402).
 FT /FTID=VAR 004383.
 FT W -> L (IN A*3402).
 FT /FTID=VAR 004384.
 FT L -> I (IN A*3402).
 FT /FTID=VAR 004385.
 FT SEQUENCE 365 AA; 41055 MW; 063BF63E656E01F6 CRC64;
 Query Match 54.3%; Score 38; DB 1; Length 365;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 WORNARKVR 12
 DB 84 WDRNTRKVK 92
 RESULT 9
 VP4_ROTGA
 ID VP4_ROTGA STANDARD; PRT; 749 AA.
 AC Q04316;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).
 GN S4.
 OS Rotavirus (Group B / strain ADRV) (Adult diarrhoea rotavirus).
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
 OX NCBI_TaxID=12705;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93233240; PubMed=8386274;
 RA Mackow E.R., Werner-Eckert R., Ray M.E., Tao H., Chen G.-M.;
 RT "Identification and baculovirus expression of the VP4 protein of the
 human group B rotavirus ADRV.";
 RL J. Virol. 67:2730-2738 (1993).
 CC -1- SUBCELLULAR LOCATION: Outer capsid.
 CC -1- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; M91434; AAA47338.1; -;
 DR InterPro; IPR000416; Cap_VP4.
 DR Pfam; PF00426; VP4; 1.
 DR Coat protein; Glycoprotein.
 FT CARBOHYD 29 29
 FT CARBOHYD 53 53
 FT CARBOHYD 109 109
 FT CARBOHYD 133 133
 FT CARBOHYD 407 407
 FT CARBOHYD 527 527
 FT CARBOHYD 568 568
 FT CARBOHYD 620 620
 FT CARBOHYD 681 681
 FT CARBOHYD 698 698
 FT SEQUENCE 749 AA; 84362 MW; D1223527DEAE0F21 CRC84;
 Query Match 54.3%; Score 38; DB 1; Length 749;
 Best Local Similarity 50.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CFQWQNRARKVR 12
 DB 195 CFTWDMNCANVR 206
 RESULT 10
 YNR2_CAEL
 ID YNR2_CAEL STANDARD; PRT; 783 AA.
 AC Q21988;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein R3G10.2 in chromosome III.
 GN R3G10.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.

```

OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RD Gardner A.E.;
RE Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RL (2)
RN REVISIONS.
RP
RA Durbin R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RC -1- COFACTOR: FAD (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
CC
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CC
CC EMBL: Z35602; CAA84671.2;
DR WormPep; R13G10.2; CR25088.
DR InterPro; IPR002937; Amino oxidase.
DR Pfam; PF01593; Amino oxidase; 1.
KW Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.
FT NP_BOND 311 366 FAD (ADP PART) (POTENTIAL).
SQ SEQUENCE 783 AA; 88799 MW; 8D087E96464DC908 CRC64;

Query Match 54.3%; Score 38; DB 1; Length 783;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 CFQWQNRKVR 12
DB 540 CIDWGRDRKVK 551

RESULT 11
ID PELX_EBWCA STANDARD; PRT; 238 AA.
AC P16530;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Putative pectate lyase X precursor (EC 4.2.2.2).
GN PEL X
OS Erwinia carotovora.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ER;
RA Ito K., Kobayashi R., Nikaide N., Izaki K.;
RT "DNA structure of pectate lyase I gene cloned from Erwinia
RT carotovora.";
RL Agric. Biol. Chem. 52:479-487(1988).
CC -1- FUNCTION: INVOLVED IN MACERATION AND SOFT-ROTTING OF PLANT TISSUE.
CC -1- CATALYTIC ACTIVITY: Eliminative cleavage of pectate to give
CC oligosaccharides with 4-deoxy-alpha-D-gluc-4-enuronosyl groups at
CC their non-reducing ends.
CC
CC -1- INDUCTION: BY PECTIN.
CC
CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
CC
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CC
EMBL: D00218; BAA00156.1;
DR HSSP; P11073; IAIK.
DR InterPro; IPR002022; Amb_allergen.
DR Pfam; PF00544; pec_lyase; 1.
KW Lyase; Multigene family; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 238 PUTATIVE PECTATE LYASE X.
SQ SEQUENCE 238 AA; 26094 MW; 46800EBA1CF41B64 CRC64;

Query Match 52.9%; Score 37; DB 1; Length 238;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 CFQWQNRKVR 12
DB 93 CGQWSKDRGVQ 104

RESULT 12
ID YEM9_SCHPO STANDARD; PRT; 238 AA.
AC Q10333;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein c582.09 in chromosome II.
GN SPC582.09.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RC MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Brooks J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Sgouros K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs W., Fritzc C., Holzer E., Mostl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Wambutt R., Purnelle B.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado I., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC
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CC
EMBL: AL096788; CAB46672.1;
KW Hypothetical protein.
```

SQ SEQUENCE 238 AA; 26479 MW; 58095AA8CD708180 CRC64;
Query Match 52.9%; Score 37; DB 1; Length 238;
Best Local Similarity 33.3%; Pred. No. 13;
Matches 4; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CFQWQARNKVR 12
|:|:|:|:|:
Db 155 CYELQNSKKIK 166
RESULT 13
LEP4_XANCP STANDARD; PRT; 287 AA.
ID LEP4_XANCP
AC Q56763;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Type 4 prelin-like protease leader peptide processing enzyme
DE [includes: leader peptidase (EC 3.4.99.-) (prelin peptidase); N-
DE methyltransferase (EC 2.1.1.-)].
GN XPSO OR PILD OR XCC3101.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Xci1701;
RX MEDLINE=96414476; PubMed=8817497;
RA Hu N.-T.T., Lee P.F., Chen C.;
RT "The type IV pre-pilin leader peptidase of Xanthomonas campestris pv.
RT campestris is functional without conserved cysteine residues";
RL Mol. Microbiol. 18:769-777(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Canarotte G., Cannavan F., Cardozo J., Chabergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463(2002).
CC -!- FUNCTION: CLEAVES TYPE-4 FIBRILLAR LEADER SEQUENCE AND METHYLATES
CC THE N-TERMINAL (GENERALLY PHE) RESIDUE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A24.
CC
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CC
CC EMBL: U12432; AAC43571.1;
CC ENBL: AE012425; AM42372.1;
CC MEROPS: A24.001; -.

DR InterPro; IPR000045; Peptidase C20.
DR Pfam; PF01478; Peptidase C20; I.
DR PRINTS; PR00864; PREPILPEPTASE;
KW Multifunctional enzyme; Hydrolase; Protease; Transferase;
KW Methyltransferase; Transmembrane; Inner membrane.
FT METHYLTRANSFERASE 10 30 POTENTIAL.
FT TRANSMEM 101 121 POTENTIAL.
FT TRANSMEM 125 145 POTENTIAL.
FT TRANSMEM 177 197 POTENTIAL.
FT TRANSMEM 226 246 POTENTIAL.
FT TRANSMEM 253 273 POTENTIAL.
SQ SEQUENCE 287 AA; 31843 MW; A58DDIA514F9ECC2 CRC64;
Query Match 52.9%; Score 37; DB 1; Length 287;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 2 FQWQARNKVR 11
|:|:|:|:|:
Db 39 WQWRDAREI 48
RESULT 14
NLA_DROME STANDARD; PRT; 292 AA.
ID NLA_DROME
AC Q9XZL8; Q9V391;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nebula protein.
GN NLA OR CG6072.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.Y.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Curtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke H., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA Foeller C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matti B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mervulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Furi V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Srapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
CC -1- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.
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DR EMBL; AF147700; AAD33987.1; -;
DR EMBL; AF003712; AAF55285.1; -;
DR FlyBase; FBgn026629; nla.
SQ SEQUENCE 292 AA; 31423 MW; 64F1BBF5F5EAC6F9 CRC64;
Query Match 52.9%; Score 37; DB 1; Length 292;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 FQWQNRKVR 12
DB 150 FQWLSFRRLR 160
RESULT 15
ID PEL2_ERWCA STANDARD; PRT; 374 AA.
AC P11431; Q06112; Q47469;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Pectate lyase II precursor (EC 4.2.2.2) (PEL II) (PEB).
GN PEL2 OR PELB.
OS Erwinia carotovora.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ER / IAM1068;
RX MEDLINE=93113068; PubMed=1369060;
RA Yoshida A., Matsuo Y., Kamio Y., Izaki K.;
RT "Molecular cloning and sequencing of the extracellular pectate lyase
RT II gene from *Erwinia carotovora* Er.";
RL Biosci. Biotechnol. Biochem. 56:1596-1600(1992).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=SP. atroseptica EC;
RX MEDLINE=87308030; PubMed=3040692;
RA Lei S.-P., Lin H.-C., Wang S.-S., Callaway J., Wilcox G.;
RT "Characterization of the *Erwinia carotovora* pelB gene and its product
RT pectate lyase.";
RL J. Bacteriol. 169:4379-4383(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SP. atroseptica C18;
RX MEDLINE=95291436; PubMed=7773390;
RA Bartling S., Wegener C., Olsen O.;
RT "Synergism between *Erwinia* pectate lyase isoenzymes that depolymerize
RT both pectate and pectin.";
RL Microbiology 141:873-881(1995).

CC -1- FUNCTION: INVOLVED IN MACERATION AND SOFT-ROTTING OF PLANT TISSUE.
CC -1- CATALYTIC ACTIVITY: Eliminative cleavage of pectate to give
CC oligosaccharides with 4-deoxy-alpha-D-gluc-4-enuronosyl groups at
CC their non-reducing ends.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1. PLADES
CC SUBFAMILY.
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CC -----
DR EMBL; S51475; AAC60422.1; -;
DR EMBL; M17364; AAA24848.1; -;
DR EMBL; X81847; CAA57440.1; -;
DR HSSP; P11073; IAIR.
DR InterPro; IPR002022; Amb allergen.
DR Pfam; PF00544; pec lyase; 1.
DR Lyase; Multigene family; Signal.
FT SIGNAL 1 22
FT CHAIN 23 374 PECTATE LYASE II.
FT DISULFID 93 176 BY SIMILARITY.
FT DISULFID 350 373 BY SIMILARITY.
FT ACT SITE 239 239 POTENTIAL.
FT VARIANT 35 35 E -> D (IN STRAIN EC).
FT VARIANT 47 48 MK -> LQ (IN STRAIN EC).
FT VARIANT 58 58 Q -> K (IN STRAIN EC).
FT VARIANT 78 78 S -> N (IN STRAIN EC).
FT VARIANT 136 136 V -> L (IN STRAIN C18).
FT VARIANT 139 139 M -> I (IN STRAIN C18).
FT VARIANT 144 144 M -> I (IN STRAIN C18).
FT VARIANT 150 150 D -> H (IN STRAIN C18).
FT VARIANT 156 156 I -> V (IN STRAIN EC).
FT VARIANT 168 168 E -> K (IN STRAIN EC).
FT VARIANT 172 173 KN -> QS (IN STRAIN EC).
FT VARIANT 234 234 R -> S (IN STRAIN C18).
FT VARIANT 252 252 N -> T (IN STRAIN EC).
FT VARIANT 280 280 N -> I (IN STRAIN EC).
FT VARIANT 306 311 SPSEFA -> KPDEF (IN STRAINS C18 AND EC).
FT VARIANT 314 314 K -> N (IN STRAIN EC).
FT VARIANT 319 319 K -> R (IN STRAIN EC).
FT VARIANT 322 322 S -> T (IN STRAIN EC).
FT VARIANT 325 325 I -> V (IN STRAIN EC).
FT VARIANT 329 329 N -> D (IN STRAINS C18 AND EC).
FT VARIANT 338 339 SI -> AV (IN STRAIN C18).
SQ SEQUENCE 374 AA; 40380 MW; FAE3FD00ACD29ED5 CRC64;
Query Match 52.9%; Score 37; DB 1; Length 374;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFQWQNRKVR 12
DB 93 CQWSKDARGVQ 104

Search completed: February 21, 2003, 07:27:49
Job time : 5.6 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds
(without alignments)
118.873 Million cell updates/sec

Title: US-09-743-107b-75
Perfect score: 70
Sequence: 1 CFQWQNRKRV 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	85.7	711	4 Q8TCD2	Q8TCD2 homo sapien
2	56	80.0	38	4 Q9UCY5	Q9UCY5 homo sapien
3	46	65.7	932	5 Q19153	Q19153 caenorhabdi
4	45	64.3	33	6 Q9TR80	Q9TR80 ovine aries
5	43	61.4	1432	10 Q23230	Q23230 arabidopsis
6	43	61.4	2186	5 Q9N906	Q9N906 trypanosoma
7	42	60.0	105	10 Q9KFD5	Q9KFD5 oryza sativ
8	42	60.0	289	10 Q9C6N2	Q9C6N2 arabidopsis
9	42	60.0	511	16 Q8Z462	Q8Z462 salmonella
10	41	58.6	279	16 Q8XSE2	Q8XSE2 raietonia s
11	41	58.6	298	16 Q8YP77	Q8YP77 anabaena sp
12	40	57.1	255	16 Q9A6EA	Q9A6EA caulobacter
13	40	57.1	372	10 Q81653	Q81653 hemerocalli
14	40	57.1	397	9 Q38229	Q38229 lactococcus
15	40	57.1	514	5 Q9VI18	Q9VI18 drosophila
16	40	57.1	543	5 Q9XZ30	Q9XZ30 drosophila

17	40	57.1	681	5 Q9XVD1	Q9XVD1 caenorhabdi
18	40	57.1	1376	3 Q8X1P2	Q8X1P2 podospira a
19	39	55.7	253	12 Q68541	Q68541 horseadish
20	39	55.7	349	5 Q9VII2	Q9VII2 drosophila
21	39	55.7	355	5 Q9SUS1	Q9SUS1 drosophila
22	39	55.7	513	10 Q9LJY8	Q9LJY8 arabidopsis
23	39	55.7	518	10 Q9SI49	Q9SI49 arabidopsis
24	39	55.7	570	4 Q9NTA7	Q9NTA7 homo sapien
25	39	55.7	570	4 Q96DM9	Q96DM9 homo sapien
26	39	55.7	620	4 Q8WX60	Q8WX60 homo sapien
27	38	54.3	121	16 Q8U6K3	Q8U6K3 agrobacteri
28	38	54.3	137	10 Q9FYI2	Q9FYI2 oryza sativ
29	38	54.3	148	11 Q9CFX3	Q9CFX3 mus musculu
30	38	54.3	274	4 Q96M21	Q96M21 homo sapien
31	38	54.3	283	16 Q9WYQ1	Q9WYQ1 thermotoga
32	38	54.3	314	5 Q9WIG8	Q9WIG8 drosophila
33	38	54.3	339	10 Q8RWE0	Q8RWE0 arabidopsis
34	38	54.3	340	10 Q9LPS1	Q9LPS1 arabidopsis
35	38	54.3	514	10 Q9SP27	Q9SP27 callistephu
36	38	54.3	515	10 Q22185	Q22185 arabidopsis
37	38	54.3	543	10 Q22188	Q22188 arabidopsis
38	38	54.3	553	4 Q9NZL7	Q9NZL7 homo sapien
39	38	54.3	554	4 Q9NV67	Q9NV67 homo sapien
40	38	54.3	558	4 Q9URK6	Q9URK6 homo sapien
41	38	54.3	1778	5 Q9NE6S	Q9NE6S leishmania
42	38	54.3	5636	4 Q96RW7	Q96RW7 homo sapien
43	38	54.3	6632	5 Q17362	Q17362 caenorhabdi
44	38	54.3	6632	5 Q01761	Q01761 caenorhabdi
45	37	52.9	89	16 Q8U5P6	Q8U5P6 agrobacteri

ALIGNMENTS

RESULT 1

Q8TCD2 PRELIMINARY; PRT; 711 AA.
 ID Q8TCD2 PRELIMINARY; PRT; 711 AA.
 AC Q8TCD2, 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Lactotransferrin.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PROSTATE;
 RA Strausberg R.;
 EL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC022347; AAH22347.1; -. 1B9C7EB097C45FAF CRC64;
 SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EB097C45FAF CRC64;

Query Match 85.7%; Score 60; DB 4; Length 711;
 Best Local Similarity 90.9%; Pred. No. 0.0087;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRKRV 11
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 Db 39 CFQWQNRKRV 49

RESULT 2

Q9UCY5 PRELIMINARY; PRT; 38 AA.
 ID Q9UCY5 PRELIMINARY; PRT; 38 AA.
 AC Q9UCY5
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Lactoferrin homolog (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DE Conserved hypothetical protein CHRI.67.
GN CHRI.67.
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OC NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU927;
RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,
RA Leonard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,
RA Gerrard C., Rajandream M.A., Barrell B.G.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL359782; CAB95377.1; -;
DR InterPro; IPR002035; VNF_A.
DR SMART; SM00327; VNF; 1.
DR PROSITE; PSS0234; VNF; 1.
KW Hypothetical protein.
SQ SEQUENCE 2186 AA; 245737 MW; 78BB75505012005A CRC64;
Query Match 61.4%; Score 43; DB 5; Length 2186;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWQARNK 10
Db 588 CYEWERNASR 597
RESULT 7
Q9XFD5 PRELIMINARY; PRT; 105 AA.
AC Q9XFD5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome P450 (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OC NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PANICLE;
RA Liu J., Yang J.;
RT "Suppression subtractive hybridization (SSH) identified candidate
RT genes that are differentially expressed at rice young panicle."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL: AF140486; AAD29699.1; -;
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PSS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
FT NON TER 1
SQ SEQUENCE 105 AA; 11912 MW; B0EEFCDD487E19F9 CRC64;
Query Match 60.0%; Score 42; DB 10; Length 105;
Best Local Similarity 60.0%; Pred. No. 2.4;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CFQWQARNK 10
Db 61 CFQWRLGKK 70
RESULT 8
Q9C6N2 PRELIMINARY; PRT; 289 AA.
ID Q9C6N2
AC Q9C6N2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Hypothetical 33.3 kDa protein.
GN F28U5.13
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Btgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysocka V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana";
RL Nature 408:816-820(2000).
DR EMBL; AC079280; AAG50577.1; -;
SQ SEQUENCE 289 AA; 33338 MW; 753AA27BED0F840C CRC64;
Query Match 60.0%; Score 42; DB 10; Length 289;
Best Local Similarity 58.3%; Pred. No. 7.4;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 CFQWQARNKVR 12
Db 8 CFTWBEYARHVR 19
RESULT 9
Q8Z462 PRELIMINARY; PRT; 511 AA.
ID Q8Z462
AC Q8Z462;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein STY3070.
GN STY3070.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OC NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagers K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18";
RL Nature 413:848-852(2001).
DR EMBL; AL627276; CAD06049.1; -;

```

KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 511 AA; 58126 MW; E2DDDD124E0D178B CRC64;

Query Match 60.0%; Score 42; DB 16; Length 511;
Best Local Similarity 58.3%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12
   |||
   |||
Db 350 CFQWQNRKVR 361

RESULT 10
Q8XSE2 PRELIMINARY; PRT; 279 AA.
AC Q8XSE2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative ICC protein homolog.
GN ICC OR RSP0534 OR RS00414.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000.
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave P., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choine N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissbach J.B., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646079; CAD17685.1; -.
DR InterPro; IPR004843; M-peptidase.
DR TrEMBL; IPR004844; S/T phosphatase.
DR Pfam; PF00149; Metallophos. 1.
KW Plasmid; Complete proteome.
SQ SEQUENCE 279 AA; 31541 MW; AB338818004B2EDA CRC64;

Query Match 58.6%; Score 41; DB 16; Length 279;
Best Local Similarity 41.7%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12
   |||
   |||
Db 244 CFQWQNRKVR 255

RESULT 11
Q8YP77 PRELIMINARY; PRT; 298 AA.
AC Q8YP77;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Alr4323.
GN ALR4323.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2159285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003596; BAB76022.1; -.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 298 AA; 34513 MW; 64036E6B52299A9F CRC64;

Query Match 58.6%; Score 41; DB 16; Length 298;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNRKVR 10
   |||
   |||
Db 163 FQWQNRKVR 171

RESULT 12
Q9A6E4 PRELIMINARY; PRT; 255 AA.
AC Q9A6E4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Signal peptidase I.
GN CC2150.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nieman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005887; AAK24121.1; -.
DR HSP; P00803; IB12.
DR TrEMBL; CC2150; -.
DR InterPro; IPR000508; SigPase.
DR TrEMBL; IPR000223; SigPase_S26A.
DR Pfam; PF00461; Peptidase_S26; 1.
DR PRINTS; PR00727; LEADERPTASE.
DR PROSITE; PS00501; SPASE_I_1; UNKNOWN_1.
DR PROSITE; PS00760; SPASE_I_2; 1.
DR PROSITE; PS00761; SPASE_I_3; 1.
KW Complete proteome.
SQ SEQUENCE 255 AA; 28041 MW; 0D1D2A11781A9DEE CRC64;

Query Match 57.1%; Score 40; DB 16; Length 255;
Best Local Similarity 63.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FQWQNRKVR 12
   |||
   |||
Db 245 FQWQNRKVR 255

RESULT 13
Q81653 PRELIMINARY; PRT; 372 AA.
AC Q81653;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Senescence-associated protein 3 (Fragment).

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GN SA3.
 OS Hemerocallis hybrid cultivar.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
 OC Hemerocallidaceae; Hemerocallis.
 OX NCBI_TaxID=80862;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. STELLA D'ORO; TISSUE=SENESCING PETALS;
 RX MEDLINE=99339248; PubMed=10412903;
 RA Panavas T., Pikula A., Reid P.D., Rubinstein B., Walker E.L.;
 RT "Identification of senescence-associated genes from daylily petals."
 RL Plant Mol. Biol. 40:237-248(1999).
 CC -i- SMILARIY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR EMBL; AF082028; AAC34853.1; -
 DR InterPro; IPR001128; Cytochrome_P450.
 DR Pfam; PF00067; P450; 1.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN_1.
 DR Heme; Monooxygenase; Oxidoreductase.
 FT NON_TER
 SQ SEQUENCE 372 AA; 41909 MW; 55FB3EAF9699595E CRC64;
 Query Match 57.1%; Score 40; DB 10; Length 372;
 Best Local Similarity 50.0%; Pred. No. 23;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWQARNARK 10
 ||: ||:
 Db 328 CPWMDRNGEE 337
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 RESULT 14
 Q38229 PRELIMINARY; PRT; 397 AA.
 ID Q38229;
 AC Q38229;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Unidentified ORF36.
 OS Lactococcus phage bIL67.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC c2-like viruses.
 OX NCBI_TaxID=36343;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95111629; PubMed=7812447;
 RA Schouler C., Ehrlich S.D., Chopin M.C.;
 RT "Sequence and organization of the lactococcal prolate-headed bIL67
 RT phage genome."
 RL Microbiology 140:3061-3069(1994).
 DR EMBL; L33769; AAA74323.1; -
 SQ SEQUENCE 397 AA; 45956 MW; 09BCE9281EC0DA6E CRC64;
 Query Match 57.1%; Score 40; DB 9; Length 397;
 Best Local Similarity 54.5%; Pred. No. 25;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 FQWQARNARKVR 12
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 Db 128 YTWQFNARKIK 138
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 RESULT 15
 Q9V118 PRELIMINARY; PRT; 514 AA.
 ID Q9V118;
 AC Q9V118;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE BCDNA.LD21969 protein.
 GN BCDNA.LD21969 OR C31024.
 OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Bencos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
 RA Fester C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003675; AAF54126.1; -
 DR FlyBase; FBgn0027514; BcDNA:LD21969.
 DR InterPro; IPR000822; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2_1.
 DR SMART; SM00355; Znf_C2H2_4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 2.
 KW DNA-binding; Metal-binding; Zinc-finger.
 SQ SEQUENCE 514 AA; 59192 MW; 43C7DD7D9FEB86B9 CRC64;

Query Match 57.1%; Score 40; DB 5; Length 514;
 Best Local Similarity 60.0%; Pred. No. 33;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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 Db 47 CFKQWENARK 56
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Search completed: February 21, 2003, 07:44:29
 Job time : 22.8 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds
(without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	65	92.9	12	21	AA1981
3	65	92.9	12	21	AA1982
4	65	92.9	12	21	AA1983
5	65	92.9	12	21	AA1984
6	65	92.9	12	21	AA1985
7	65	92.9	12	21	AA1986
8	65	92.9	12	21	AA1987
9	65	92.9	12	21	AA1988
10	65	92.9	12	21	AA1989

11	65	92.9	14	21	AA1980	Human lactoferrin
12	65	92.9	15	17	AA1985	Peptide for anti-u
13	65	92.9	15	21	AA1983	Human lactoferrin
14	65	92.9	15	21	AA1986	Human lactoferrin
15	65	92.9	15	21	AA1980	Human lactoferrin
16	65	92.9	16	21	AA1983	Human lactoferrin
17	65	92.9	16	21	AA1986	Human lactoferrin
18	65	92.9	16	21	AA1980	Human lactoferrin
19	65	92.9	17	21	AA1983	Human lactoferrin
20	65	92.9	17	21	AA1986	Human lactoferrin
21	65	92.9	17	21	AA1980	Human lactoferrin
22	65	92.9	18	15	AA1985	Human lactoferrin
23	65	92.9	18	17	AA1983	Advanced glycosyla
24	65	92.9	18	21	AA1980	Human lactoferrin
25	65	92.9	19	21	AA1986	Amino acid sequenc
26	65	92.9	19	21	AA1980	Human lactoferrin
27	65	92.9	19	21	AA1983	Anti microbial pep
28	65	92.9	20	14	AA1984	Lactoferrin-relate
29	65	92.9	20	15	AA1985	Lactoferrin derive
30	65	92.9	20	15	AA1986	Lactoferrin derive
31	65	92.9	20	15	AA1980	Lactoferrin derive
32	65	92.9	20	15	AA1983	Lactoferrin derive
33	65	92.9	20	16	AA1984	Bovine lactoferrin
34	65	92.9	20	16	AA1986	Bovine lactoferrin
35	65	92.9	20	16	AA1980	Anti-parasitic lac
36	65	92.9	20	16	AA1983	Peptide for anti-u
37	65	92.9	20	17	AA1986	Lactoferrin-derive
38	65	92.9	20	17	AA1980	Lactoferrin-derive
39	65	92.9	20	17	AA1983	Lactoferrin derive
40	65	92.9	20	17	AA1986	Lactoferrin derive
41	65	92.9	20	17	AA1980	Lactoferrin-derive
42	65	92.9	20	17	AA1983	Lactoferrin derive
43	65	92.9	20	18	AA1986	Lactoferrin deriva
44	65	92.9	20	18	AA1980	Anti-parasitic pep
45	65	92.9	20	19	AA1983	Thrombus formation

ALIGNMENTS

RESULT 1
AA1980
ID AA1980 standard; Peptide; 12 AA.
XX AA198076;
AC AA198076;
XX AA198076;
DT 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:76.

DE Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.

OS Homo sapiens.
OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Matthey-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;
 Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 4.5e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNNKVR 12
 DB 1 CFQWQRNNKVR 12
 |||||

RESULT 4
 AAY78047
 ID AAY78047 standard; Peptide; 12 AA.
 AC AAY78047;
 DT 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:47.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 PN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1999; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 23-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PA Hanson LA, Mattesby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 18; Page 73; 102pp; English.

CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;
 Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 4.5e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNNKVR 12
 DB 1 CFQWQRNNKVR 12
 |||||

RESULT 5
 AAY78083
 ID AAY78083 standard; Peptide; 12 AA.
 AC AAY78083;
 DT 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:83.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 PN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1999; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PA Hanson LA, Mattesby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 22; Page 36; 102pp; English.

CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;
 Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 4.5e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNNAKVR 12
 |||||
 Db 1 CFQWQRNNAKVR 12

RESULT 6
 AAY78037
 ID AAY78037 standard; Peptide; 13 AA.

AC AAY78037;
 XX
 DT 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:37.
 DE
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 PF 06-JUL-1999; 99WO-SB01230.
 XX
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 XX (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 XX Claim 12; Page 70; 102pp; English.
 XX
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 XX Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 4.9e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRNNAKVR 12
 |||||
 Db 2 CFQWQRNNAKVR 13

RESULT 7
 AAY78048

ID AAY78048 standard; Peptide; 13 AA.

XX
 AC AAY78048;

XX
 DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:48.

DE
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 PF 06-JUL-1999; 99WO-SB01230.
 XX
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 XX (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 XX Claim 15; Page 74; 102pp; English.
 XX
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 XX Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 4.9e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRNNAKVR 12
 |||||
 Db 2 CFQWQRNNAKVR 13

RESULT 8
 AAY78049

ID AAY78049 standard; Peptide; 13 AA.

XX
 AC AAY78049;

XX
 DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:49.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SB01230.
 XX
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 XX (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX
 DR WPI; 2000-147388/13.
 XX
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 PS Claim 18; Page 74; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 13 AA;
 Query Match 92.9%; Score 65; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 4.9e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRNNAKVR 12
 Db 2 CFQWQRNNAKVR 13
 XX
 RESULT 9
 ID AAY78036
 AC AAY78036; Peptide; 14 AA.
 XX
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:36.
 DE
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.

OS Synthetic.
 XX WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SB01230.
 XX
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 XX (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX
 DR WPI; 2000-147388/13.
 XX
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 PS Claim 12; Page 69; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 14 AA;
 Query Match 92.9%; Score 65; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 5.3e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRNNAKVR 12
 Db 3 CFQWQRNNAKVR 14
 XX
 RESULT 10
 ID AAY78050 standard; Peptide; 14 AA.
 XX
 AC AAY78050;
 XX
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:50.
 DE
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SB01230.
 PF

XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 75; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations, and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 14 AA;
 SQ Query Match 92.9%; Score 65; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 5.3e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 CFQWQRMNAKVR 12
 Db |||||
 3 CFQWQRMNAKVR 14
 RESULT 11
 AAY78051
 ID AAY78051 standard; Peptide; 14 AA.
 AC AAY78051;
 DT 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:51.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 PN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 75; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations, and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 18; Page 75; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 14 AA;
 SQ Query Match 92.9%; Score 65; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 5.3e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 CFQWQRMNAKVR 12
 Db |||||
 3 CFQWQRMNAKVR 14
 RESULT 12
 AAR98554
 ID AAR98554 standard; Peptide; 15 AA.
 XX AAR98554;
 AC AAR98554;
 DT 12-NOV-1996 (first entry)
 XX Peptide for anti-ulcer agent.
 DE anti-ulcer agent; low toxicity; stable; heat-resistant.
 KW Synthetic.
 OS JP08143468-A.
 PN 04-JUN-1996.
 PD 17-NOV-1994; 94JP-0283869.
 PF 17-NOV-1994; 94JP-0283869.
 PR (MORG) MORINAGA MILK IND CO LTD.
 XX WPI; 1996-318857/32.
 XX Anti-ulcer agent contg. peptide - has low toxicity, is
 PT heat-resistant and water-soluble
 XX Claim 1; Page 11; 11pp; Japanese.
 XX AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
 CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be
 CC administered orally and be produced in large amounts.
 XX Sequence 15 AA;
 SQ

Query Match 92.9%; Score 65; DB 17; Length 15;
 Best Local Similarity 91.7%; Pred. No. 5.7e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQNRMAKVR 12
 DB 2 CFQWQNRMAKVR 13

RESULT 13
 AAY78035
 ID AAY78035 standard; Peptide, 15 AA.
 XX AC AAY78035;
 XX DT 25-APR-2000 (first entry)
 XX DE Human lactoferrin derived peptide SEQ ID NO:35.
 XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200001730-A1.
 XX PD 13-JAN-2000.
 XX PF 06-JUL-1999; 99WO-SE01230.
 XX PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX PA (ASCII-) A+ SCI INVEST AB.
 XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PS Claim 12; Page 69; 102pp; English.
 XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 15 AA;
 SQ

Query Match 92.9%; Score 65; DB 21; Length 15;
 Best Local Similarity 91.7%; Pred. No. 5.7e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQNRMAKVR 12
 DB 4 CFQWQNRMAKVR 15

RESULT 15
 AAY78063
 ID AAY78063 standard; Peptide, 15 AA.
 XX AC AAY78063;

RESULT 14
 AAY78062
 ID AAY78062 standard; Peptide, 15 AA.
 XX AC AAY78062;
 XX DT 25-APR-2000 (first entry)
 XX DE Human lactoferrin derived peptide SEQ ID NO:62.
 XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200001730-A1.
 XX PD 13-JAN-2000.
 XX PF 06-JUL-1999; 99WO-SE01230.
 XX PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX PA (ASCII-) A+ SCI INVEST AB.
 XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PS Claim 15; Page 81; 102pp; English.
 XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 15 AA;
 SQ

Query Match 92.9%; Score 65; DB 21; Length 15;
 Best Local Similarity 91.7%; Pred. No. 5.7e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQNRMAKVR 12
 DB 4 CFQWQNRMAKVR 15

RESULT 15
 AAY78063
 ID AAY78063 standard; Peptide, 15 AA.
 XX AC AAY78063;

XX 25-APR-2000 (first entry)
DT Human lactoferrin derived peptide SEQ ID NO:63.
XX
DE Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX WO200001730-A1.
PN 13-JAN-2000.
XX
PD 06-JUL-1999; 99WO-SE01230.
XX
PF 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
PA
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
PI WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 18; Page 81; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX Sequence 15 AA;
SQ

Query Match 92.9%; Score 65; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 5.7e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNNAKVR 12
| | | | | | | | | |
DB 4 CFQWQNRNNAKVR 15

Search completed: February 21, 2003, 07:37:12
Job time : 28.35 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 Seconds
(without alignments)
40.818 Million cell updates/sec

Title: US-09-743-107B-76

Perfect score: 70

Sequence: 1 CFQWRNMAKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PGTUS COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	18	1	US-08-204-487-3
2	65	92.9	18	2	US-08-485-948-8
3	65	92.9	18	2	US-08-628-380-8
4	65	92.9	18	2	US-08-475-055-8
5	65	92.9	20	1	US-07-755-161A-3
6	65	92.9	20	1	US-07-891-174-3
7	65	92.9	20	1	US-08-204-487-1
8	65	92.9	20	1	US-08-256-771-24
9	65	92.9	20	1	US-08-256-771-25
10	65	92.9	20	1	US-08-381-984-24
11	65	92.9	20	1	US-08-381-984-25
12	65	92.9	22	4	US-09-308-734-4
13	65	92.9	24	4	US-09-508-734-6
14	65	92.9	25	1	US-07-755-161A-10
15	65	92.9	25	1	US-07-891-174-10
16	65	92.9	25	1	US-08-204-487-7
17	65	92.9	29	4	US-09-508-734-8
18	65	92.9	36	1	US-07-755-161A-8
19	65	92.9	36	1	US-07-891-174-8
20	65	92.9	36	1	US-08-386-771-30
21	65	92.9	36	1	US-08-381-984-29
22	65	92.9	47	2	US-08-464-182A-6
23	65	92.9	47	2	US-08-406-271-6
24	65	92.9	50	2	US-08-693-274A-7
25	65	92.9	52	4	US-09-017-043A-3
26	65	92.9	53	2	US-08-464-182A-5
27	65	92.9	53	2	US-08-406-271-5

28	65	92.9	54	2	US-08-464-182A-2	Sequence 2, Appli
29	65	92.9	54	2	US-08-406-271-2	Sequence 2, Appli
30	65	92.9	594	3	US-08-721-586-2	Sequence 2, Appli
31	65	92.9	594	4	US-09-421-632-2	Sequence 2, Appli
32	65	92.9	694	4	US-09-932-190-2	Sequence 2, Appli
33	65	92.9	705	2	US-08-655-640-2	Sequence 2, Appli
34	65	92.9	708	2	US-08-655-640-4	Sequence 4, Appli
35	65	92.9	711	1	US-08-154-019-4	Sequence 4, Appli
36	65	92.9	711	1	US-08-461-333-4	Sequence 4, Appli
37	65	92.9	711	3	US-08-464-187-4	Sequence 4, Appli
38	65	92.9	711	3	US-09-158-313-4	Sequence 4, Appli
39	65	92.9	711	4	US-08-476-798-4	Sequence 4, Appli
40	62	88.6	711	1	US-08-145-681-2	Sequence 2, Appli
41	62	88.6	711	1	US-08-250-308-2	Sequence 2, Appli
42	62	88.6	711	1	US-08-453-703-2	Sequence 2, Appli
43	62	88.6	711	2	US-08-456-106-2	Sequence 2, Appli
44	62	88.6	711	3	US-08-456-108-2	Sequence 2, Appli
45	62	88.6	711	4	US-09-265-577-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESS: THIBEAULT
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: F0N-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37) "
US-08-204-487-3

Query Match 92.9%; Score 65; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMKVR 12
|||||
Db 1 CFQWQRNMKVR 12

RESULT 2
US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,948
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,217
; FILING DATE: JUNE 7, 1995
; APPLICATION NUMBER: 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-485-948-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMKVR 12
|||||
Db 1 CFQWQRNMKVR 12

RESULT 3
US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341
; GENERAL INFORMATION:
; APPLICANT: LI, YONG MING
; APPLICANT: VLASSARA, HELEN
; APPLICANT: CERAMI, ANTHONY
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,380
; FILING DATE: April 4, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-628-380-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMKVR 12
|||||
Db 1 CFQWQRNMKVR 12

RESULT 4
US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Klauber & Jackson
;; STREET: 411 Hackensack Avenue
;; CITY: Hackensack
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07601
;;
;; COMPUTER READABLE FORM: disk
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA: US/08/475,055
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/485,948
;; FILING DATE:
;; APPLICATION NUMBER: 08/488,217
;; FILING DATE: JUNE 7, 1995
;; APPLICATION NUMBER: 08/418,642
;; FILING DATE: APRIL 7, 1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Reg., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 947-1-008A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 343-1684
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;;
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; DESCRIPTION: LF-CL, 8-25
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
;;
US-08-475-055-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKVR 12
| | | | | | | | | | | | | | | | | |
Db 1 CFQWQRMNAKVR 12

RESULT 5
US-07-755-161A-3
; Sequence 3, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible

;;
;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: DisplayWrite
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/755,161A
;; FILING DATE: 19910905
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX: 202-371-8856
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE:
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; CELL LINE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY: modified site
;; LOCATION: 2
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 19"
;; FEATURE:
;; NAME/KEY: modified site
;; LOCATION: 19
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 2"
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

Query Match 92.9%; Score 65; DB 1; Length 20;

Best Local Similarity 91.7%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRNMAKVR 12
Db 2 CFQWQRNMAKVR 13

RESULT 6

US-07-891-174-3
; Sequence 3, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb

COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/755,161

FILING DATE: 05-SEP-1991

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELEPHONE: 202-371-8850

TELEFAX: 202-371-8856

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE:

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM:

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE:

CELL LINE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY: modified site

LOCATION: 2
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 19"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 19
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 2"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-07-891-174-3

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRNMAKVR 12

Db 2 CFQWQRNMAKVR 13

RESULT 7

US-08-204-487-1

; Sequence 1, Application US/08204487

; Patent No. 5565425

; GENERAL INFORMATION:

APPLICANT: YAMAMOTO, NAOKI

APPLICANT: NAKASHIMA, HIDEKI

APPLICANT: MOSUCHI, WATARU

APPLICANT: TANAKA, SHIGEAKI

APPLICANT: DOSAKO, SHUN'ICHI

APPLICANT: KAWASAKI, YOSHIHIRO

APPLICANT: UCHIDA, TOSHIKI

TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION

TITLE OF INVENTION: INHIBITORS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &

ADDRESSEE: THIBEAULT

STREET: 53 STATE STREET

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/204,487

FILING DATE: 02-MAR-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: CAMPBELL, PAULA A.

REGISTRATION NUMBER: 32,503

REFERENCE/DOCKET NUMBER: FUN-019

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
US-08-204-487-1

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKVR 12
DB 2 CFQWQRMNAKVR 13

RESULT 8
US-08-256-771-24
Sequence 24, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKVR 12
DB 2 CFQWQRMNAKVR 13

RESULT 10
US-08-381-984-24

US-08-256-771-24

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKVR 12
DB 2 CFQWQRMNAKVR 13

RESULT 9
US-08-256-771-25
Sequence 25, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are protected to
OTHER INFORMATION: prevent disulfide bond"

US-08-256-771-25
Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKVR 12
DB 2 CFQWQRMNAKVR 13

RESULT 10
US-08-381-984-24

; Sequence 24, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: April 11, 1995
; APPLICATION NUMBER: 252
; PRIOR APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at positions 2
; OTHER INFORMATION: and 19 are bonded by disulfide linkage"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
; US-08-381-984-24

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRNNAKVR 12
Db 2 CFQWRNNAKVR 13

RESULT 11
US-08-381-984-25
; Sequence 25, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: April 11, 1995
; APPLICATION NUMBER: 252
; PRIOR APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at positions 2
; OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
; US-08-381-984-25

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRNNAKVR 12
Db 2 CFQWRNNAKVR 13

RESULT 12
US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; TITLE OF INVENTION: useful microorganism thereof
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 4

LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
US-09-508-734-4

Query Match 92.9%; Score 65; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 2.5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNMKVR 12
Db 2 CFQWQNNMKVR 13

RESULT 13

US-09-508-734-6
Sequence 6, Application US/09508734
Patent No. 6423509

GENERAL INFORMATION:

APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 6
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
US-09-508-734-6

Query Match 92.9%; Score 65; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 2.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNMKVR 12
Db 3 CFQWQNNMKVR 14

RESULT 14

US-07-755-161A-10
Sequence 10, Application US/07755161A
Patent No. 5304633

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:

ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:

CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:

FEATURE:
NAME/KEY: modified site

LOCATION: 4

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of

OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"

FEATURE:

NAME/KEY: modified site

LOCATION: 21

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of

OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUES:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10

Query Match 92.9%; Score 65; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 2.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNMKVR 12

Db 4 CFQWQNNMKVR 15

RESULT 15

US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21

; IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
Query Match 92.9%; Score 65; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 2.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWQRNNAKVR 12
||| ||| |||
Db 4 CFQWQRNNAKVR 15
Search completed: February 21, 2003, 07:50:34
Job time : 8.7 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds
(without alignments)
35.508 Million cell updates/sec

Title: US-09-743-107b-76
Perfect score: 70
Sequence: 1 CFQWQRNNAKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications AA.*
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14: /cgn2_6/prodata/2/pubpaa/US60 PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	15	9	US-09-798-869-2
2	65	92.9	25	9	US-09-798-869-20
3	65	92.9	694	9	US-10-023-096-2
4	57	81.4	15	9	US-09-798-869-6
5	48	68.6	15	9	US-09-798-869-3
6	48	68.6	25	9	US-09-798-869-23
7	40	57.1	15	9	US-09-798-869-7
8	39	55.7	15	9	US-09-798-869-4
9	39	55.7	15	9	US-09-798-869-29
10	39	55.7	15	9	US-09-798-869-30
11	39	55.7	25	9	US-09-798-869-22
12	39	55.7	1617	9	US-10-090-453A-2
13	37	52.9	21	10	US-09-864-761-47985
14	36	51.4	15	9	US-09-798-869-8
15	35	50.0	846	9	US-10-051-409-4
16	34	48.6	95	10	US-09-764-864-1031
17	34	48.6	312	10	US-09-935-428A-4
18	34	48.6	1564	10	US-09-801-368-244
19	33	47.1	26	10	US-09-864-761-46809

20	33	47.1	77	10	US-09-864-761-41002	Sequence 41002, A
21	33	47.1	78	10	US-09-820-893-136	Sequence 136, App
22	33	47.1	199	9	US-09-764-868-963	Sequence 963, App
23	33	47.1	331	9	US-10-093-275-2	Sequence 2, Appli
24	33	47.1	331	10	US-09-953-956-8	Sequence 8, Appli
25	33	47.1	331	12	US-10-114-464-8	Sequence 8, Appli
26	33	47.1	332	9	US-09-738-626-5674	Sequence 5674, Ap
27	33	47.1	333	9	US-09-796-753-26	Sequence 119, App
28	33	47.1	338	9	US-09-978-295A-119	Sequence 119, App
29	33	47.1	338	9	US-09-978-697-119	Sequence 119, App
30	33	47.1	338	9	US-09-978-192A-119	Sequence 119, App
31	33	47.1	338	9	US-09-999-832A-119	Sequence 119, App
32	33	47.1	338	9	US-09-978-189-119	Sequence 119, App
33	33	47.1	553	9	US-09-796-753-14	Sequence 14, Appli
34	33	47.1	553	10	US-09-981-649A-6	Sequence 6, Appli
35	33	47.1	553	10	US-09-981-649A-24	Sequence 24, Appli
36	33	47.1	554	10	US-09-981-649A-30	Sequence 30, Appli
37	33	47.1	554	10	US-09-981-649A-32	Sequence 32, Appli
38	33	47.1	559	10	US-09-981-649A-28	Sequence 28, Appli
39	33	47.1	782	10	US-09-841-739-9	Sequence 9, Appli
40	33	47.1	1403	8	US-08-913-322-22	Sequence 22, Appli
41	33	47.1	1403	8	US-08-913-322-24	Sequence 24, Appli
42	33	47.1	1579	10	US-09-801-368-368	Sequence 368, App
43	33	47.1	2273	10	US-09-995-542-12	Sequence 12, Appli
44	33	47.1	2310	10	US-09-995-542-10	Sequence 10, Appli
45	32	45.7	56	10	US-09-864-761-44710	Sequence 44710, A

ALIGNMENTS

RESULT 1
US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ/RNNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GS99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2

Query Match 92.9%; Score 65; DB 9; Length 15;
Best Local Similarity 91.7%; Pred. NO. 2.7e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRNNAKVR 12
| | | | | | | | | | | | | |
Db 3 CFQWQRNNAKVR 14

RESULT 2
US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ/RNNSON

```

; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798.869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: G39818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-798-869-20

```

```
Query Match      92.9%; Score 65; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
```

QY	1	CFQWQRNMAKVR	12
Db	3	CFQWRNRKVR	14

RESULT 3
US-10-023-096-2
/ Sequence 2, Application US/10023096
/ Patent No. US20020160941A1
/ GENERAL INFORMATION:
/ APPLICANT: Kruzel, Marian L.
/ APPLICANT: Kurecki, Tomasz
/ APPLICANT: Gollnick, Paul D.
/ APPLICANT: Doyle, Darrell J.
/ TITLE OF INVENTION: Cloning, Expression, and Uses of Human
/ TITLE OF INVENTION: Lactoferrin
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Jacobson, Price, Holman & Stern
/ STREET: 400 Seventh St. N.W.
/ CITY: Washington D.C.
/ COUNTRY: U.S.A.

```
Query Match      92.9%; Score 65; DB 9; Length 694;
Best Local Similarity 91.7%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 1; Indels
```

Qy 1 CFQQRNMAKVR 12
Dp 22 CFQQRNMRKVR 33

```

RESULT 4
US-09-798-869-6
; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ(RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-6

```

Query Match 81.4%; Score 57; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.00064;
Matches 10; Conservative 0; Mismatches 2; Indels

Qy 1 CFQWQRNMAKVR 12
|||
Db 3 CFQWQWNMRKVR 14
|||

```

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US2003022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBU (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/G899/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: G89818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-3

```

Query Match 68.6%; Score 48; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.022;

US-10-023-096-2

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11
|:|||||:
Db 3 CYQWQWRMKL 13

RESULT 6
US-09-798-869-23
; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ(RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23

Query Match 68.8%; Score 48; DB 9; Length 25;
Best Local Similarity 63.6%; Pred. No. 0.037;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11
|:|||||:
Db 3 CYQWQWRMKL 13

RESULT 7
US-09-798-869-7
; Sequence 7, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ(RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-7

Query Match 57.1%; Score 40; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.53;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11
|:|||||:
Db 3 CYQWQWRMKL 13

RESULT 8
US-09-798-869-4
; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ(RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4

Query Match 55.7%; Score 39; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.78;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11
|:|||||:
Db 3 CLRWQWRMKV 13

RESULT 9
US-09-798-869-29
; Sequence 29, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ(RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29

Query Match 55.7%; Score 39; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.78;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11
|:|||||:
Db 3 CFRWQWRMKL 13

RESULT 10

US-09-798-869-30
; Sequence 30, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-30

Query Match 55.7%; Score 39; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.78;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11
|:|:|:|:|:
DB 3 CFQWQRMNAKV 13

RESULT 11

US-09-798-869-22
; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-22

Query Match 55.7%; Score 39; DB 9; Length 25;
Best Local Similarity 54.5%; Pred. No. 1.3;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11
|:|:|:|:|:
DB 3 CFQWQRMNAKV 13

RESULT 12

US-10-090-453A-2
; Sequence 2, Application US/10090453A
; Patent No. US20020173004A1
; GENERAL INFORMATION:

; APPLICANT: Chen, Hongyun
; APPLICANT: Le Bihan, Stephane
; APPLICANT: Kulhanek, Barbara
; TITLE OF INVENTION: NOVEL ABCA6 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: 100103.404
; CURRENT APPLICATION NUMBER: US/10/090,453A
; CURRENT FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1617
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-453A-2

Query Match 55.7%; Score 39; DB 9; Length 1617;
Best Local Similarity 72.7%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11
|:|:|:|:|:
DB 440 CFQWQRMNAKV 450

RESULT 13

US-09-864-761-47985
; Sequence 47985, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anicomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47985
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL096701.14
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EST_HUMAN HIT: AW294800.1, EVALUATE 1.00e-06
US-09-864-761-47985

Query Match 52.9%; Score 37; DB 10; Length 21;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQR 6
Db 16 CFQWRR 21

RESULT 14

US-09-798-869-8
; Sequence 8, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJARNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine
; OTHER INFORMATION: sequence)
US-09-798-863-8

Query Match 51.4%; Score 36; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 2.6;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMAKV 11
Db 3 CLRQWQEMRKV 13

RESULT 15

US-10-051-409-4
; Sequence 4, Application US/10051409
; Publication No. US20030027171A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Chu-Wen
; APPLICANT: Tsou, Ann-Ping
; APPLICANT: Chi, Chin-Wen
; APPLICANT: Fann, Ming-Ji
; APPLICANT: Chou, Chen-Kung
; TITLE OF INVENTION: CELL CYCLE REGULATOR PROTEIN
; FILE REFERENCE: 12005-003001

; CURRENT APPLICATION NUMBER: US/10/051,409
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/262,885
; PRIOR FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 846
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-051-409-4

Query Match 50.0%; Score 35; DB 9; Length 846;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRNM 8
Db 448 CFQWDRKL 455

Search completed: February 21, 2003, 08:08:05
Job time : 10.55 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 seconds
(without alignments)
120.168 Million cell updates/sec

Title: US-09-743-107B-76

Perfect score: 70

Sequence: 1 CFQWQNNMAKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73.*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	711	1 TFHUL	lactotransferrin p
2	48	68.6	708	2 J2323	lactoferrin - goat
3	47	67.1	511	2 AB0858	hypothetical prote
4	45	64.3	33	2 S52107	lactoferrin - shee
5	42	60.0	749	2 A45687	outer capsid prote
6	40	57.1	205	2 E90094	26S proteasome SU
7	40	57.1	317	2 T47233	cysteine synthase
8	39	55.7	707	1 A28438	lactoferrin precu
9	38	54.3	515	2 T00510	probable cytochrom
10	38	54.3	543	2 T00513	cytochrome P450 ho
11	38	54.3	584	2 C84325	hypothetical prote
12	38	54.3	4568	2 T09030	dyein beta heavy
13	37	52.9	742	2 T25415	hypothetical prote
14	37	52.9	2517	2 S5380	probable RNA-direc
15	36.5	52.1	290	2 C97414	hypothetical prote
16	36	51.4	57	2 D81949	hypothetical prote
17	36	51.4	298	2 AD2346	hypothetical prote
18	36	51.4	405	2 AB1461	B. subtilis YabE p
19	36	51.4	408	2 AC1098	B. subtilis YabE p
20	36	51.4	435	2 S52784	ornithine decarbox
21	36	51.4	496	2 T50146	probable era/thd
22	36	51.4	501	2 T39801	hypothetical sh3-c
23	36	51.4	518	2 B84514	probable cytochrom
24	36	51.4	628	2 S77374	cell division prot
25	36	51.4	710	2 T49516	Atu related protei
26	36	51.4	717	2 T33295	hypothetical prote
27	36	51.4	820	2 G82168	trimethylamine-N-o
28	36	51.4	1274	2 T04018	hypothetical prote
29	36	51.4	1767	2 T00458	hypothetical prote

30 35.5 50.7 451 2 AB2296
31 35 50.0 145 2 F84496
32 35 50.0 275 2 T22597
33 35 50.0 282 2 F90580
34 35 50.0 283 2 D72378
35 50.0 447 2 S53309
36 35 50.0 481 2 B96691
37 35 50.0 492 2 B85441
38 35 50.0 499 2 T04730
39 35 50.0 500 2 C85441
40 35 50.0 500 2 T52174
41 35 50.0 649 2 AB2154
42 35 50.0 665 2 T34079
43 35 50.0 668 2 C71868
44 35 50.0 708 2 B84950
45 35 50.0 728 2 S71467

ALIGNMENTS

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000

C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S741

R:Cho, Y.

submitted to the EMBL Data Library, March 1994

A:Reference number: G06820

A:Accession: G01394

A:Status: preliminary; translated from GE/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-711 <CHO>

A:Cross-references: EMBL:U07643; NID:G467236; PIDN:AA560324.1; PID:G467237

R:Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A:Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A:Reference number: S11228; MUID:90384839; PMID:2402455

A:Accession: S11228

A:Molecule type: mRNA

A:Residues: 1-148 'T', 150-422 'C', 424-711 <REY>

A:Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R:Teng, C.T.; Liu, Y.; Kang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A:Title: Differential molecular mechanism of the estrogen action that regulates lactofer

A:Reference number: A45401; MUID:93125571; PMID:1480183

A:Accession: A45401

A:Molecule type: DNA

A:Residues: 1-15 <TEN>

A:Cross-references: GB:S52559; NID:G263311; PIDN:AAB24877.1; PID:G263312

A:Experimental source: placenta

A>Note: sequence extracted from NCBI backbone (NCBIIP:122202)

R:Powell, M.J.; Oden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A:Title: Nucleotide sequence of human lactoferrin cDNA.

A:Reference number: S10324; MUID:90326545; PMID:2374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <POW>

A:Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A:Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A:Reference number: S15853; MUID:91264786; PMID:2049066

A:Accession: S15853

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 20-31 <ST1>

A:Accession: S20841

A:Molecule type: protein

A:Residues: 20-28 'X', 30-31 <ST2>

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
 Blood 70, 989-993, 1987
 A>Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
 A/Reference number: S07160; MUID:88001031; PMID:3477300
 A/Accession: S07160
 A/Molecule type: mRNA
 A/Residues: 436-487, 'A', 489-711 <RAD>
 A/Cross-references: EMBL:M18642; NID:9186815; PIDN:AAA86665.1; PID:9386855
 R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
 Cancer Res. 51, 3037-3043, 1991
 A>Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
 A/Reference number: A61169; MUID:91235214; PMID:1674448
 A/Accession: A61169
 A>Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 3701, 'SWKPVN' <PAN>
 A/Experimental source: normal breast tissue
 R;Mets-Butigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
 Eur. J. Biochem. 145, 659-666, 1984
 A>Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
 A/Reference number: A31000; MUID:85076667; PMID:6510420
 A/Accession: A31000
 A/Molecule type: protein
 A/Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
 A>Note: this is the final paper in a series
 R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
 Eur. J. Biochem. 241, 303-308, 1996
 A>Title: Lactoferrin: similarity to diamine oxidase and purification by aminoethyl affini
 A/Reference number: S74119; MUID:97054624; PMID:8898921
 A/Accession: S74119
 A/Molecule type: protein
 A/Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
 A/Experimental source: neutrophil granulocytes
 C/Genetics:
 A/Gene: GDB:LTF
 A/Cross-references: GDB:119368; OMIM:150210
 A/Map position: 3q21-3q23
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication; glycoprotein; iron binding; milk
 F.1-19/Domain: signal sequence #status predicted <SIG>
 F.20-711/Product: lactotransferrin #status experimental <MAT>
 F.21-356/Domain: transferrin repeat homology <TRH1>
 F.360-699/Domain: transferrin repeat homology <TRH2>
 F.729-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
 F.157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F.368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
 Query Match 92.9%; Score 65; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.00068;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRNNAKVR 12
 Db 39 CFQWQRNNAKVR 50
 RESULT 2
 JC2323
 lactoferrin - goat
 C/Species: Capra aegagrus hircus (domestic goat)
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 C/Accession: JC2323
 R;Le Provost, F.; Nocard, M.; Guerin, G.; Martin, P.
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A>Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
 A/Reference number: JC2323; MUID:94380047; PMID:8093048
 A/Accession: JC2323
 A/Molecule type: mRNA
 A/Residues: 1-708 <LEP>
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication; glycoprotein
 F.359-696/Domain: transferrin repeat homology <TRH2>
 F.252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.6%; Score 48; DB 2; Length 708;
 Best Local Similarity 53.8%; Pred. No. 0.87;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRNNAKVR 11
 Db 38 CYQWQRNNAKVR 48

RESULT 3
 AB0858
 hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Ty
 C/Species: Salmonella enterica subsp. enterica serovar Typhi
 A/Note: this species has also been called Salmonella typhi
 C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
 C/Accession: AB0858
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A/Reference number: AB0502; PMID:11677608
 A/Accession: AB0858
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-511 <PAR>
 A/Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:G16504016; GSPDB:GN00176
 C/Genetics:
 A/Gene: STY3070

Query Match 67.1%; Score 47; DB 2; Length 511;
 Best Local Similarity 66.7%; Pred. No. 0.96;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRNNAKVR 12
 Db 350 CFQWQRNNAKVR 361

RESULT 4
 S52107
 lactoferrin - sheep (fragment)
 C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C/Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
 C/Accession: S52107
 R;Qian, Z.Y.; Jolles, P.; Migliore-Samouri, D.; Fiat, A.M.
 Biochim. Biophys. Acta 1243, 25-32, 1995
 A/Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet a
 A/Reference number: S52107; MUID:95127729; PMID:7827104
 A/Accession: S52107
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-33 <QIA>
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication

Query Match 64.3%; Score 45; DB 2; Length 33;
 Best Local Similarity 54.5%; Pred. No. 0.14;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRNNAKVR 11
 Db 19 CYQWQRNNAKVR 29

RESULT 5
 A45687
 outer capsid protein VP4 - human rotavirus B
 C/Species: human rotavirus B
 C/Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 19-Feb-1999
 C/Accession: A45687

R.Mackow, E.R.; Werner-Eckert, R.; Fay, M.E.; Tao, H.; Chen, G.
 J. Virol. 67, 2730-2738, 1993
 A:Title: Identification and baculovirus expression of the VP4 protein of the human group
 A:Reference number: A45687; MUID:93233240; PMID:8386274
 A:Accession: A45687
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-749 <MAC>
 A>Note: sequence inconsistent with the nucleotide translation
 A>Note: sequence extracted from NCBI backbone (NCBIN:130353, NCBI:130355)
 C:Superfamily: rotavirus core protein

Query Match 60.0%; Score 42; DB 2; Length 749;
 Best Local Similarity 58.3%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CFQWQNMAYR 12
 |||:|:|:
 Db 195 CFTWDMNCANVR 206

RESULT 6
 E90094
 26S proteasome SU B5 [imported] - Guillardia theta nucleomorph
 C:Species: nucleomorph Guillardia theta
 A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
 C:Accession: E90094
 R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reil
 Nature 410, 1091-1096, 2001
 A:Title: The highly reduced genome of an enslaved algal nucleus.
 A:Reference number: A99082; MUID:11323671; PMID:11323671
 A:Accession: E90094
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-205 <DOU>
 A:Cross-references: GB:AF165818; NID:G13794510; PIDN:AAK39885.1; GSPDB:GN00150
 C:Genetics:
 A:Gene: prSB5
 A:Map position: 1
 A:Genome: nucleomorph
 C:Keywords: nucleomorph

Query Match 57.1%; Score 40; DB 2; Length 205;
 Best Local Similarity 45.5%; Pred. No. 7.3;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQNMAYR 11
 |||:|:|:
 Db 63 CFTWERNLSSL 73

RESULT 7
 T47233
 cysteine synthase (EC 4.2.99.8) cysK - Lactococcus lactis subsp. cremoris
 N:Alternate names: O-acetylserine sulfhydrylase
 C:Species: Lactococcus lactis subsp. cremoris
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 03-Nov-2000
 C:Accession: T47233
 R:Fernandez, M.; van Doesburg, W.; Rutten, G.A.M.; Marugg, J.D.; Altling, A.C.; van Kran
 Appl. Environ. Microbiol. 66, 42-48, 2000
 A:Title: Molecular and functional analysis of the metC gene of Lactococcus lactis, encod
 A:Reference number: Z24409; MUID:20087515; PMID:10618201
 A:Accession: T47233
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-317 <PER>
 A:Cross-references: EMBL:AF131880; NID:G6513594; PIDN:AAF14694.1; PID:G6513596
 A:Experimental source: strain MG1363; asp. cremoris
 C:Genetics:
 A:Gene: cysK
 C:Superfamily: threonine dehydratase
 C:Keywords: carbon-oxygen lyase; phosphoprotein; pyridoxal phosphate

F:44/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted
 Query Match 57.1%; Score 40; DB 2; Length 317;
 Best Local Similarity 55.6%; Pred. No. 11;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WQNNMAKVR 12
 |||:|:|:
 Db 277 WQNNMAKVR 285

RESULT 8
 A28438
 lactoferrin precursor - mouse
 N:Alternate names: lactotransferrin
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A28438; A41205
 R:Pentecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A:Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret
 A:Reference number: A92596; MUID:87280033; PMID:3611056
 A:Accession: A28438
 A:Molecule type: mRNA
 A:Residues: 3-707 <PEN>
 A:Cross-references: EMBL:J03298
 R:Liu, Y.; Teng, C.T.
 J. Biol. Chem. 266, 21880-21885, 1991
 A:Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
 A:Reference number: A41205; MUID:92042099; PMID:1939212
 A:Accession: A41205
 A:Molecule type: DNA
 A:Residues: 1-15 <LIU>
 A:Cross-references: GB:M74778
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-707/Product: lactotransferrin #status predicted <MAR>
 F:358-695/Domain: transferrin repeat homology <TRH2>
 F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.7%; Score 39; DB 1; Length 707;
 Best Local Similarity 54.5%; Pred. No. 38;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQNMAYR 11
 |||:|:|:
 Db 37 CLRQWQNMAYR 47

RESULT 9
 T00510
 probable cytochrome P450 At2g23220 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
 C:Accession: T00510; A84622
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
 submitted to the EMBL Data Library, November 1997
 A:Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.
 A:Reference number: Z14164
 A:Accession: T00510
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-515 <ROU>
 A:Cross-references: EMBL:AC002391; NID:G2642427; PID:G2642441
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: A84622

A>Status: preliminary
A:Molecule type: DNA

A:Residues: 1-515 <STO>

A:Cross-references: GB:AE002093; NID:G2642441; PIDN:AA887109.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g23220; T20D16.15

A:Map position: 2

A:Introns: 182/3; 310/3

C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C:Keywords: heme; iron; metalloprotein

F:312-471/Domain: cytochrome P450 homology <P45>

F:449/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 54.3%; Score 38; DB 2; Length 515;

Best Local Similarity 83.3%; Pred. No. 43;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQR 6

DB 469 CFEWQR 474

RESULT 10

T00513

Cytochrome P450 homolog At2g23190 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001

C:Accession: T00513; F84621

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

submitted to the EMBL Data Library, November 1997

A:Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.

A:Reference number: Z14164

A:Accession: T00513

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-543 <STO>

A:Cross-references: EMBL:AC002391; NID:G2642427; PID:G2642444

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10637197

A:Accession: F84621

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-543 <STO>

A:Cross-references: GB:AE002093; NID:G2642444; PIDN:AA887112.1; GSPDB:GN00139

C:Genetics:

A:Gene: T20D16.18; At2g23190

A:Map position: 2

A:Introns: 211/3; 339/3

C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C:Keywords: heme; iron; metalloprotein

F:341-500/Domain: cytochrome P450 homology <P45>

F:478/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 54.3%; Score 38; DB 2; Length 543;

Best Local Similarity 83.3%; Pred. No. 45;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQR 6

DB 498 CFEWQR 503

RESULT 11

C84325

hypothetical protein Vng1732c [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: C84325

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S

; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.F.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: C84325

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-584 <STO>

A:Cross-references: GB:AE004437; NID:G10581192; PIDN:AAG19967.1; GSPDB:GN00138

C:Genetics:

A:Gene: VNG1732C

Query Match 54.3%; Score 38; DB 2; Length 584;

Best Local Similarity 41.7%; Pred. No. 48;

Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRNAKVR 12

DB 445 CFTWRKDMERK 456

RESULT 12

T08030

dyslin beta heavy chain - Chlamydomonas reinhardtii

C:Species: Chlamydomonas reinhardtii

C>Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001

C:Accession: T08030

R:Mitchell, D.R.; Brown, K.S.

J. Cell Sci. 107, 635-644, 1994

A:Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.

A:Reference number: Z16302; MUID:94274778; PMID:8006077

A:Accession: T08030

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-4568 <MIT>

A:Cross-references: EMBL:U02963; NID:G409965; PIDN:AAA19956.1; PID:G514215

A:Experimental source: strain 21gr

C:Genetics:

A:Gene: ODA4

A:Map position: IX

A:Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;

3334/3; 3686/3; 3882/3; 4240/3

C:Superfamily: dynein heavy chain, ciliary

C:Keywords: nucleotide binding; P-loop

F:1919-1926/Region: nucleotide-binding motif A (P-loop)

F:2202-2209/Region: nucleotide-binding motif A (P-loop)

F:2530-2537/Region: nucleotide-binding motif A (P-loop)

Query Match 54.3%; Score 38; DB 2; Length 4569;

Best Local Similarity 41.7%; Pred. No. 3.8e+02;

Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRNAKVR 12

DB 1852 CFQWQSOLRYIQ 1863

RESULT 13

T25415

hypothetical protein T28D6.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

C:Accession: T25415

R:Wilkinson, J.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z20031

A:Accession: T25415

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-742 <WIL>

A;Cross-references: EMBL:Z81134; PIDN:CAB03450.1; GSPDB:GN00021; CESP:T28D6.5

A;Experimental source: clone T28D6

C;Genetics:

A;Gene: CESP:T28D6.5

A;Map position: 3

A;Introns: 9/3; 36/3; 70/3; 112/3; 258/3; 319/3; 468/2; 586/1; 638/3; 671/1

C;Superfamily: Caenorhabditis elegans hypothetical protein T28D6.5

Query Match

Best Local Similarity 52.9%; Score 37; DB 2; Length 742;

Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 CFQWQRMNAKVR 12

||| :|:

Db 193 CFWRVRKSKAK 204

||| :|:

RESULT 14

S58380

probable RNA-directed DNA polymerase (EC 2.7.7.49) - Crithidia fasciculata retrotransposon

N;Alternate names: probable reverse transcriptase

C;Species: Crithidia fasciculata

C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Sep-1997

C;Accession: S58380; S58381

R;Gabriel, A.

submitted to the EMBL Data Library, December 1994

A;Reference number: S58380

A;Accession: S58380

A;Molecule type: DNA

A;Residues: 1-2517 <GAB>

A;Cross-references: EMBL:U19151; NID:G624680; PID:G624681

R;Teng, S.-C.; Wang, S.-X.; Gabriel, A.

Nucleic Acids Res. 23, 2929-2936, 1995

A;Title: A new non-LTR retrotransposon provides evidence for multiple distinct site-spec

A;Reference number: S58381; MUID:95388509; PMID:7659515

A;Accession: S58381

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1825-2116 <TEN>

A;Cross-references: EMBL:U19151

A;Experimental source: retrotransposon CRE2

C;Genetics:

A;Mobile element: retrotransposon CRE2

C;Keywords: nucleotidyltransferase

Query Match

Best Local Similarity 52.9%; Score 37; DB 2; Length 2517;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 FQWQRMNAKVR 12

||| :|:

Db 2457 FQWRRLAGYK 2467

||| :|:

RESULT 15

C97414

hypothetical protein AGR_C 800 [imported] - Agrobacterium tumefaciens (strain C58, Cere

C;Species: Agrobacterium tumefaciens

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002

C;Accession: C97414

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A;Reference number: A97359; PMID:11743194

A;Accession: C97414

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-230 <KUR>

A;Cross-references: GB:AB007869; PIDN:AAK86268.1; PID:gl5155378; GSPDB:GN00169

C;Genetics:

A;Gene: AGR_C 800

A;Map position: circular chromosome

Query Match

Best Local Similarity 52.1%; Score 36.5; DB 2; Length 290;

Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 2 FQWQRMNAK 10

||| :|:

Db 40 FQWRRNQNAK 49

||| :|:

Search completed: February 21, 2003, 07:47:48

Job time : 10.65 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds
(without alignments)
108.199 Million cell updates/sec

Title: US-09-743-107B-76
Perfect score: 70
Sequence: 1 CFQWQRMNAKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	65	92.9	711	1 TRFL_HUMAN	P02788 homo sapien
2	51	72.9	708	1 TRFL_CAMDR	Q9tumo camelus dro
3	48	68.6	708	1 TRFL_CAPHI	Q29477 capra hircu
4	43	61.4	695	1 TRFL_HORSE	Q07811 equus caball
5	42	60.0	749	1 VP4_ROTGA	Q04916 rotavirus (
6	39	55.7	707	1 TRFL_MOUSE	P08071 mus musculu
7	38	54.3	4568	1 DYHE_CHIRE	Q39565 chlamydomon
8	36	51.4	435	1 DCOR_PANRE	P49725 panagrellus
9	36	51.4	496	1 MSS1_SCHPO	Q9ute7 schizosacch
10	36	51.4	628	1 FTH3_SYNY3	P73437 synectocyt
11	36	51.4	663	1 PDII_HUMAN	Q9ulc6 homo sapien
12	35	50.0	447	1 PD6C_SPIOL	P48629 spinacia ol
13	35	50.0	502	1 C911_ARATH	Q9f965 arabidopsis
14	35	50.0	665	1 YL14_CABEL	Q11100 caenorhabdi
15	35	50.0	708	1 FTA_EUCAI	P57273 buchnera ap
16	35	50.0	728	1 KDGI_ARATH	Q39017 arabidopsis
17	35	50.0	765	1 Y008_HUMAN	P27314 seoul virus
18	35	50.0	2151	1 RRPL_SEOUB	Q15398 homo sapien
19	34	48.6	137	1 YEDD_ECOLI	P31063 escherichia
20	34	48.6	141	1 YEDD_SALTY	Q06399 salmonella
21	34	48.6	172	1 Y703_METJA	Q58118 methanococc
22	34	48.6	238	1 RNPH_AGRT5	Q8u198 agrobacteri
23	34	48.6	246	1 Y495_SYNY3	Q55185 synectocyt
24	34	48.6	275	1 IL2A_BOVIN	P12342 bos taurus
25	34	48.6	275	1 IL2A_SHEEP	P26898 ovine aries
26	34	48.6	324	1 RADA_SULSO	Q55075 sulfolobus
27	34	48.6	401	1 O88A_DROME	Q90fz2 drosophila
28	34	48.6	422	1 PAPA_CHICK	Q90678 g platelet-
29	34	48.6	552	1 PYRG_SYNY3	P74208 synectocyt
30	34	48.6	566	1 YJ19_SYNY3	P73121 synectocyt
31	34	48.6	1135	1 PHYC_SORBI	P93528 sorghum bic
32	34	48.6	1564	1 PDRA_YEAST	P51533 saccharomyc
33	34	48.6	3680	1 DMD_CANFA	O97592 canis famli

34 33 47.1 128 1 YQ82_CABEL Q09237 caenorhabdi
35 33 47.1 154 1 YSCO_YERPS P40294 yersinia ps
36 33 47.1 164 1 DNAT_BUCAI P57135 buchnera ap
37 33 47.1 211 1 LOLE_VIBCH P57070 vibrio chol
38 33 47.1 274 1 APAH_BUCAI P57242 buchnera ap
39 33 47.1 285 1 YX47_STRCO Q9x8h0 streptomyce
40 33 47.1 292 1 NLA_DROME Q9xzl8 drosophila
41 33 47.1 303 1 UL24_HSVSA Q01005 herpesvirus
42 33 47.1 312 1 CCSA_ODOSI P49523 odontella s
43 33 47.1 331 1 CATS_HUMAN P25774 homo sapien
44 33 47.1 399 1 XYLR_CALSR P40981 caldicellul
45 33 47.1 407 1 YKAD_CABEL P34263 caenorhabdi

ALIGNMENTS

RESULT 1
TRFL_HUMAN STANDARD; PRJ: 711 AA.
AC P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96KZ4;
AC Q96KZ5;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin A;
DE Lactoferrin B; Lactoferrin C].
GN LTF OR LF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90384839; PubMed=2402455;
RA Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";
RL Nucleic Acids Res. 18:5288-5288(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cho Y.Y.;
RL Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
RN [3]
RP SEQUENCE FROM N.A.
RA Connely O.M.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Liang O., Jimenez-Flores R., Richardson T.;
RL "Molecular cloning and sequence analysis of human lactoferrin.";
RT Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Wei X., Han J., Rado T.A.;
RL "Human neutrophil lactoferrin coding and 5' flanking region DNA
sequences";
RT Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cheng H., Chen X., Huan L.;
RL "cDNA cloning and sequence analysis of human lactoferrin.";
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [8]

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE=Mammary Gland.
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ogden J.E.;
RT "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
RA Legrand D., Spik G., Montreuil J., Jolles P.;
RT "Human lactotransferrin: amino acid sequence and structural
RT comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1984).
RN [10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RA Jolles P.;
RT "The present state of the human lactotransferrin sequence. Study and
RT alignment of the cyanogen bromide fragments and characterization of
RT N- and C-terminal domains.";
RL Biochim. Biophys. Acta 670:243-254(1981).
RN [11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
RA Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
RT lactotransferrin.";
RL FEBS Lett. 142:107-110(1982).
RN [12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
RN [13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Chao L., la Bastide M., Kaplan N., Greco T., Touchman J., Mazny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sagripanti J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human diferric lactoferrin refined at 2.2-A
RT resolution.";
RL Acta Crystallogr. D 51:629-646(1995).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
RA Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RT 253->methionine mutant.";
RL Biochemistry 36:341-346(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in Aspergillus
RT awamori.";
RL Acta Crystallogr. D 55:403-407(1999).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
RT and analysis of ligand-induced conformational change.";
RL Acta Crystallogr. D 54:1319-1335(1998).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of opioic antagonist peptides derived
RT from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810(1990).
RN [20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
RA Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
RA El Matiri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
RA Hejtmandik J.F., Teng C.T.;
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RL Mol. Vision 4:31-32(1998).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPTOID ANTAGONIST
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X53961; CAA37914.1; -
CC EMBL; U07643; AAB60324.1; -
CC EMBL; M93150; AAA36159.1; -
CC EMBL; M83202; AAA59511.1; -
CC EMBL; M83205; AAA58656.1; -
CC EMBL; M18642; AAA86665.1; -
CC EMBL; AE332168; AAG48753.1; -
CC EMBL; BC015822; AAH15822.1; -
CC EMBL; BC015823; AAH15823.1; -
CC EMBL; M73700; AAA59479.1; -
CC EMBL; X52941; CAA37116.1; -
CC EMBL; U95626; AAB57795.1; -
CC PIR; S11228; TFFUL.
CC PDB; 1LCE; 31-AUG-94.
CC PDB; 1LCT; 31-OCT-93.
CC PDB; 1LFG; 31-JUL-94.
CC PDB; 1LPH; 31-OCT-93.
CC PDB; 1LPI; 31-OCT-93.
CC PDB; 1LGB; 31-AUG-94.
CC PDB; 1LGC; 31-AUG-94.
CC PDB; 1LKA; 08-NOV-96.
CC PDB; 1DSN; 08-MAR-96.
CC PDB; 1HSE; 12-MAR-97.
CC PDB; 1VFD; 21-APR-97.

Query Match 92.9%; Score 65; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.00048;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
 DB 39 CFQWQRMKVR 50

RESULT 2
 ID TRFL CAMDR STANDARD; PRT; 708 AA.

AC O9TU0; Q9WZ55;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (lactoferrin).
 GN LTF.

OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;
 RA Kappeler S.R.; Ackermann M.; Farah Z.; Puhon Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
 RL Int. Dairy J. 9:481-486(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M.; Srinivasan A.; Singh R.; Sahani M.S.; Singh T.P.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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CC -----
 DR EMBL; AJ131674; CAB53387.1; -;
 DR EMBL; AF165879; AAF82241.1; -;
 DR HSP; O77811; 1B1X.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN 1; 2.
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.
 DR PROSITE; PS00207; TRANSFERRIN 3; 2.
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal.
 FT SIGNAL. 1 19 BY SIMILARITY.
 FT CHAIN 20 708 LACTOTRANSFERRIN.
 FT REPEAT 20 363 1.
 FT REPEAT 364 708 2.
 FT DISULFID 28 64 BY SIMILARITY.
 FT DISULFID 38 55 BY SIMILARITY.
 FT DISULFID 134 217 BY SIMILARITY.
 FT DISULFID 176 192 BY SIMILARITY.
 FT DISULFID 189 200 BY SIMILARITY.
 FT DISULFID 250 264 BY SIMILARITY.
 FT DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.
 FT DISULFID 424 703 BY SIMILARITY.
 FT DISULFID 444 666 BY SIMILARITY.
 FT DISULFID 476 551 BY SIMILARITY.
 FT DISULFID 500 694 BY SIMILARITY.
 FT DISULFID 510 524 BY SIMILARITY.
 FT DISULFID 521 534 BY SIMILARITY.
 FT DISULFID 592 606 BY SIMILARITY.
 FT DISULFID 644 649 BY SIMILARITY.
 FT METAL 79 79 IRON 1 (BY SIMILARITY).
 FT METAL 111 111 IRON 1 (BY SIMILARITY).
 FT METAL 211 211 IRON 1 (BY SIMILARITY).
 FT METAL 272 272 IRON 1 (BY SIMILARITY).
 FT METAL 414 414 IRON 2 (BY SIMILARITY).
 FT METAL 452 452 IRON 2 (BY SIMILARITY).
 FT METAL 545 545 IRON 2 (BY SIMILARITY).
 FT METAL 614 614 IRON 2 (BY SIMILARITY).
 FT BINDING 140 140 ANION (BY SIMILARITY).
 FT BINDING 482 482 ANION (BY SIMILARITY).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .)
 FT CONFLICT 261 261 F -> S (IN REF. 2).
 FT CONFLICT 304 304 G -> A (IN REF. 2).
 FT CONFLICT 330 330 S -> P (IN REF. 2).
 FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).
 FT CONFLICT 506 506 L -> F (IN REF. 2).
 FT CONFLICT 609 609 A -> P (IN REF. 2).
 FT CONFLICT 642 642 R -> Q (IN REF. 2).
 SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match 72.9%; Score 51; DB 1; Length 708;
 Best Local Similarity 75.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
 DB 38 CAQWQRMKVR 49

RESULT 3
 ID TRFL CAPHI STANDARD; PRT; 708 AA.

AC Q29477; Q29479;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.

OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA MEDLINE=9438004; PubMed=8093048;
 RA le Provost F.; Nocart M.; Guerin G.; Martin P.;
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the
 RT relevant locus to bovine U12 syntenic group.";
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.

FT DISULFID 463 538
 FT DISULFID 487 681
 FT DISULFID 497 511
 FT DISULFID 508 521
 FT DISULFID 579 593
 FT DISULFID 631 636
 FT METAL 66 66
 FT METAL 98 98
 FT METAL 138 198
 FT METAL 239 259
 FT METAL 401 401
 FT METAL 439 439
 FT METAL 532 532
 FT METAL 601 601
 FT BINDING 127 127
 FT BINDING 469 469
 FT CARBOHYD 143 143
 FT CARBOHYD 287 287
 FT CARBOHYD 482 482
 SQ SEQUENCE 695 AA; 75991 MW; 07B884D50E1B165D CRC64;
 Query Match 61.4%; Score 43; DB 1; Length 695;
 Best Local Similarity 66.7%; Pred. No. 3.7; Indels 2; Mismatches 2; Gaps 0;
 Matches 8; Conservative 2; Indels 2; Gaps 0;
 QY 1 CFQWQRMNAKVR 12
 DB 25 CAKFQRMNAKVR 36
 RESULT 5
 VP4_ROTGA STANDARD; PRT; 749 AA.
 ID VP4_ROTGA
 AC Q04916;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DE 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).
 GN S4.
 OS Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).
 OC Viruses; deRNA viruses; Reoviridae; Rotavirus.
 OX NCBI_TaxID=12705;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93233240; PubMed=8386274;
 RA Mackow E.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M.;
 RT "Identification and baculovirus expression of the VP4 protein of the
 human group B rotavirus ADRV";
 RL J. Virol. 67:2730-2738(1993).
 CC -!- SUBCELLULAR LOCATION: Outer capsid.
 CC -!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
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 DR EMBL; M51434; AAA47338.1; -;
 DR InterPro; IPR000416; Cap_VP4.
 DR Pfam; PF00426; VP4; 1.
 KW Coat protein; Glycoprotein.
 FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 527 527 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 568 568 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 681 681 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 598 598 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 749 AA; 84362 MW; D1223527DEAE0F21 CRC64;
 Query Match 60.0%; Score 42; DB 1; Length 749;
 Best Local Similarity 58.3%; Pred. No. 6;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CFQWQRMNAKVR 12
 DB 195 CFTWDMNCANVR 206
 RESULT 6
 TRPL_MOUSE STANDARD; PRT; 707 AA.
 ID TRPL_MOUSE
 AC P08071; P70690; Q61799; Q922P2;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Uterus;
 RX MEDLINE=87280033; PubMed=3611056;
 RA Pentecost B.T., Teng C.T.;
 RT "Lactotransferrin is the major estrogen inducible protein of mouse
 uterine secretions";
 RL J. Biol. Chem. 262:10134-10139(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Uterus;
 RA Morishita K.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-14 FROM N.A.
 RX MEDLINE=92042099; PubMed=1939212;
 RA Liu Y., Teng C.T.;
 RT "Characterization of estrogen-responsive mouse lactoferrin promoter";
 RL J. Biol. Chem. 266:21880-21885(1991).
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 OF AN ANION, USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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 or send an email to license@isb-sib.ch).
 DR EMBL; J03298; AAA40525.1; -;
 DR EMBL; D88510; BAA13633.1; -;
 DR EMBL; BC006904; AAH06904.1; -;
 DR EMBL; M74778; AAA39427.1; -;
 DR PIR; A28438; A28438.
 DR HSP; P02788; 1CB6.
 DR MGD; MGI:96837; Ltf.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.


```

FT CHAIN 66 447 OMEGA-6 FATTY ACID DESATURASE.
FT DOMAIN 171 175 HISTIDINE BOX-1.
FT DOMAIN 207 211 HISTIDINE BOX-2.
FT DOMAIN 367 371 HISTIDINE BOX-3.
SQ SEQUENCE 447 AA; 51306 MW; 2BA7C87FF9F5350E CRC64;

Query Match 50.0%; Score 35; DB 1; Length 447;
Best Local Similarity 43.8%; Pred. No. 62;
Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 1 CFQWQ----RNNAKVR 12
Db 33 CIKQKPCRLNLGHVR 48

RESULT 13
C911 ARATH STANDARD; PRT; 502 AA.
AC Q9FG65; O65789;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Cytochrome P450 91A1 (EC 1.14.14.1).
GN CYP91A1 OR AT5G36220 OR T3066.3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016721; PubMed=11130714;
RA Tabata S., Kaneo T., Nakamura Y., Kotani H., Kato T., Asamizu E.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Habermann K., Murray J., Johnson D., Rohlfing J., Nelson J.,
RA Stoneking T., Pepin K., Speth J., Sekhon M., Armstrong J., Becker M.,
RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,
RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,
RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strommatt C.,
RA Wagner-McPherson C., Wollam A., Yeakum M., Bell M., Dedhia N.,
RA Parnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Martensen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
RA Volckaert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,
RA Entian K.-D., Terry N., Hartley N., Bent E., Johnson S.,
RA Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,
RA Ramperger U., Wedler H., Balke K., Wedler E., Peters S.,
RA van Staveren M., Dirkse W., Mooijman P., Klein Lankhorst R.,
RA Weizsaecker T., Bothe G., Rose M., Hauf J., Berner S., Hempel S.,
RA Feldpausch M., Lamberth S., Villarreal R., Giesen J., Ardiles W.,
RA Bents O., Lemcke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H.,
RA Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Franz P.F.,
RT "Sequence and analysis of chromosome 5 of the plant Arabidopsis
thaliana."
RL Nature 408:823-826(2000).
RN [2]
RP SEQUENCE OF 3-502 FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=98281573; PubMed=9620263;
RA Mizutani M., Ward E., Ohta D.,
RT "Cytochrome P450 superfamily in Arabidopsis thaliana: isolation of
cDNAs, differential expression, and RFLP mapping of multiple
cytochromes P450."
RL Plant Mol. Biol. 37:39-52(1998).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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QY 4 WORNMAKVR 12
 DB 380 WORNDRKLR 388

RESULT 15
 ID_PTA_BUCAI STANDARD; PRT; 708 AA.
 AC P57273;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Phosphate acetyltransferase (EC 2.3.1.8) (Phosphotransacetylase).
 GN PTA OR BUL76;
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 ON NCBI TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tokyo 1998;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 Buchnera sp. APS.";
 RL Nature 407:81-86(2000).
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + phosphate = CoA + acetyl
 phosphate
 CC -!- PATHWAY: LAST OF TWO STEPS IN THE CONVERSION OF ACETATE TO
 ACETYL-COA.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; CONTAINS A DOMAIN WITH SOME
 SIMILARITIES WITH COBQ/BIOD.
 CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE PHOSPHATE
 ACETYLTRANSFERASE AND BUTYRYLTRANSFERASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF001118; BAB12893.1; -.
 DR InterPro; IPR002505; PTA_PTB.
 DR InterPro; IPR004614; Pta_
 DR Pfam; PF01515; PTA_PTB; 1.
 DR TIGRFAMs; TIGR00651; pta; 1.
 KW Transferase; Acyltransferase; Complete proteome.
 FT DOMAIN 388 708 PHOSPHATE ACETYLTRANSFERASE.
 SQ SEQUENCE 708 AA; 80770 MW; 1EDC4394824ED89A CRC64;

Query Match 50.0%; Score 35; DB 1; Length 708;
 Best Local Similarity 41.7%; Pred No. 98;
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CFQWORNMAKVR 12
 DB 217 CIPWNRNIVTR 228

Search completed: February 21, 2003, 07:27:51
 Job time : 6.6 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds
(without alignments)
118.873 Million cell updates/sec

Title: US-09-743-107B-76
Perfect score: 70
Sequence: 1 CFQWQRNMAKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL 21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_protist.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archesp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	85.7	711	4 Q8TCD2	Q8TCD2 homo sapien
2	56	80.0	38	4 Q9UCY5	Q9UCY5 homo sapien
3	47	67.1	511	16 Q82462	Q82462 salmonella
4	45	64.3	33	6 Q9TR80	Q9TR80 ovis aries
5	41	58.6	469	9 Q38115	Q38115 bacterioph
6	40	57.1	205	8 Q98RR2	Q98RR2 guillardia
7	40	57.1	1376	3 Q8X1P2	Q8X1P2 podospora a
8	40	57.1	2186	5 Q9N906	Q9N906 trypanosoma
9	39	55.7	372	10 Q81653	Q81653 hemerocalli
10	39	55.7	1617	4 Q8WRZ6	Q8WRZ6 homo sapien
11	38	54.3	105	10 Q9XFD5	Q9XFD5 oryza sativ
12	38	54.3	515	10 Q22185	Q22185 arabidopsis
13	38	54.3	543	10 Q22188	Q22188 arabidopsis
14	38	54.3	584	17 Q9HPA3	Q9HPA3 halobacteri
15	38	54.3	750	12 Q9E8I8	Q9E8I8 human rotav
16	37	52.9	212	5 Q9BID5	Q9BID5 heterodera

17	52.9	212	5	Q967G4	Q967G4 heterodera
18	37	52.9	444	10 Q9AX10	Q9AX10 oryza sativ
19	37	52.9	730	12 Q83343	Q83343 murid herpe
20	37	52.9	742	5 Q18151	Q18151 caenorhabdi
21	36.5	52.1	290	16 Q8U5K9	Q8U5K9 agrobacteri
22	36	51.4	57	16 Q9JV34	Q9JV34 neisseria m
23	36	51.4	91	15 Q77855	Q77855 human immun
24	36	51.4	91	15 Q77856	Q77856 human immun
25	36	51.4	119	15 Q8Q454	Q8Q454 human immun
26	36	51.4	148	10 Q9XHP1	Q9XHP1 sesamum ind
27	36	51.4	298	16 Q8YP77	Q8YP77 anabaena sp
28	36	51.4	341	11 Q8R2A4	Q8R2A4 mus musculu
29	36	51.4	405	16 Q92F81	Q92F81 listeria in
30	36	51.4	408	16 Q9YAE4	Q9YAE4 listeria mo
31	36	51.4	501	3 Q9UUD0	Q9UUD0 schistosacch
32	36	51.4	518	10 Q9SI49	Q9SI49 arabidopsis
33	36	51.4	602	10 Q8S013	Q8S013 oryza sativ
34	36	51.4	753	5 Q9NDT2	Q9NDT2 plasmodium
35	36	51.4	820	16 Q9KEF0	Q9KEF0 vibrio chol
36	36	51.4	1049	10 Q9FUG3	Q9FUG3 arabidopsis
37	36	51.4	1055	10 Q9LIV9	Q9LIV9 oryza sativ
38	36	51.4	1137	5 Q9VSA6	Q9VSA6 drosophila
39	36	51.4	1274	10 Q9S287	Q9S287 arabidopsis
40	36	51.4	1767	10 Q80663	Q80663 arabidopsis
41	35.5	50.7	451	16 Q8YQB2	Q8YQB2 anabaena sp
42	35	50.0	99	15 Q8Q2M7	Q8Q2M7 human immun
43	35	50.0	145	10 Q9ZQM4	Q9ZQM4 arabidopsis
44	35	50.0	160	5 Q9VII2	Q9VII2 drosophila
45	35	50.0	185	10 Q9SW68	Q9SW68 arabidopsis

ALIGNMENTS

RESULT 1

Q8TCD2 PRELIMINARY, PRT; 711 AA.
ID Q8TCD2;
AC Q8TCD2;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Lactotransferrin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022347; AAH22347.1; -- 1B9CTEE097C45PAP CRC64;
SQ SEQUENCE 711 AA; 78327 MW; 1B9CTEE097C45PAP CRC64;

Query Match 85.7%; Score 60; DB 4; Length 711;
Best Local Similarity 90.9%; Pred. No. 0.0052;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMAKV 11
DB 39 CFQWQRNMAKV 49

RESULT 2

Q9UCY5 PRELIMINARY, PRT; 38 AA.
ID Q9UCY5;
AC Q9UCY5;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE Lactoferrin homolog (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 ON NCBI_TaxID=9606;
 RX SEQUENCE FROM N.A.
 RP MEDLINE=96081613; PubMed=8551695;
 RA Sato I.;
 RT "Characterization of the 84-kDa protein with ABH activity in human
 RT seminal plasma.";
 RL Jpn. J. Legal Med. 49:281-293(1995).
 DR HSP; P02788; 1BKA.
 DR InterPro: IPR001156; Transferrin.
 DR Pfam: PF00405; transferrin; 1.
 SQ SEQUENCE 38 AA; 4459 MW; 0402P490B5EBDBES CRC64;

Query Match 80.0%; Score 56; DB 4; Length 38;
 Best Local Similarity 90.9%; Pred. No. 0.0012;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQWQNRKVR 12
 Db 21 FQWQNRKVR 31
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 |||||

RESULT 3
 Q82462
 ID Q82462 PRELIMINARY; PRT; 511 AA.
 AC Q82462;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein ST3070.
 GN STY3070.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18.
 RX MEDLINE=21534947; PubMed=11577608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Fellwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagers K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrall B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 DR EMBL; AL622276; CAD06049.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 511 AA; 58126 MW; E2DD124E10D178B CRC64;

Query Match 67.1%; Score 47; DB 16; Length 511;
 Best Local Similarity 66.7%; Pred. No. 1.1;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12
 Db 350 CFQWQNRKVR 361
 |||||
 |||||

RESULT 4
 Q9TR80
 ID Q9TR80 PRELIMINARY; PRT; 33 AA.
 AC Q9TR80;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Lactoferrin (Fragment).
 OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=95127729; PubMed=7827104;
 RA Qian Z.Y., Jolles P., Migliore-Samouri D., Fiat A.M.;
 RL Biochim. Biophys. Acta 1243:25-32(1995).
 DR HSP; O77698; ICE2.
 DR InterPro: IPR001156; Transferrin.
 DR Pfam: PF00405; transferrin; 1.
 SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 64.3%; Score 45; DB 6; Length 33;
 Best Local Similarity 54.5%; Pred. No. 0.13;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 11
 Db 19 CYQWQNRKVR 29
 |||||
 |||||

RESULT 5
 Q38115
 ID Q38115 PRELIMINARY; PRT; 469 AA.
 AC Q38115;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE ORF29.
 OS Bacteriophage rit.
 OC Viruses.
 OX NCBI_TaxID=43695;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96332668; PubMed=8730874;
 RA Nauta A., Van Sinderen D., Karsens H., Smit E., Venema G., Kok J.;
 RT "Inducible gene expression mediated by a repressor-operator system
 RT isolated from Lactococcus lactis bacteriophage rit.";
 RL Mol. Microbiol. 19:1331-1341(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96332669; PubMed=8730875;
 RA Van Sinderen D., Karsens H., Kok J., Terpstra P., Ruiters M.H.,
 RA Venema G., Nauta A.;
 RT "Sequence analysis and molecular characterization of the temperate
 RT lactococcal bacteriophage rit.";
 RL Mol. Microbiol. 19:1343-1355(1996).
 DR EMBL; U38906; AAB18704.1; -.
 SQ SEQUENCE 469 AA; 53160 MW; 1F8E02D4325C6BB9 CRC64;

Query Match 58.6%; Score 41; DB 9; Length 469;
 Best Local Similarity 50.0%; Pred. No. 14;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 10
 Db 39 CYPWQNRKVR 48
 |||||
 |||||

RESULT 6
 Q98RR2
 ID Q98RR2 PRELIMINARY; PRT; 205 AA.
 AC Q98RR2;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE 2S proteasome SU B5.
 GN PRS5.
 OS Guillardia theta (Cryptomonas phi).
 OC Nucleomorph.
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.

```

OX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2123349; PubMed=11323671;
RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,
RT Wu X., Reich M., Cavalier-Smith T., Maier U.G.;
RL "The highly reduced genome of an enslaved algal nucleus.";
DR EMBL; AF165818; AAK39885.1; -.
DR InterPro; IPR000243; Proteasome_B.
DR Pfam; PF00227; proteasome_1.
DR PRINTS; PR00141; PROTEASOME.
KW Proteasome.
SQ SEQUENCE 205 AA; 22691 MW; D30F5289C8C85049 CRC64;

Query Match 57.1%; Score 40; DB 8; Length 205;
Best Local Similarity 45.5%; Pred. No. 9;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNNMAKV 11
|||:|:|:|
DB 63 CFFWERNLSSL 73

RESULT 7
Q8X1P2 PRELIMINARY; PRT; 1376 AA.
AC Q8X1P2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta transducin-like protein HET-D2Y.
GN HET-D.
OS Podosporea anserina.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Lasiosphaeriaceae; Podospora.
OX NCBI_TaxID=5145;
RN [1]
RP SEQUENCE FROM N.A.
RA Espagne E., Balhadere P., Begueret J., Turcq B.;
RT "A new family of WD40 proteins implicated in vegetative
RT incompatibility; evidence for a major role of WD40 repeat domain in
RT the specificity of het-e and het-d genes.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF225585; AAL37301.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 12.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 9.
DR SMART; SM00320; WD40; 12.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_11.
DR PROSITE; PS0082; WD_REPEATS_2; 11.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
SQ SEQUENCE 1376 AA; 152068 MW; 2191826AA5C62D97 CRC64;

Query Match 57.1%; Score 40; DB 3; Length 1376;
Best Local Similarity 77.8%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWYRNAAK 10
|||:|:|:|
DB 95 FQWYRNAAK 103

RESULT 8
Q9N906 PRELIMINARY; PRT; 2186 AA.
AC Q9N906;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Conserved hypothetical protein CHRI.67.

GN NCBI_TaxID=55529;
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=5691;
RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,
RA Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,
RA Gerrard C., Rajandream M.A., Barrell B.G.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL359782; CAB95377.1; -.
DR InterPro; IPR002035; VWF_A.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00234; VWF; 1.
KW Hypothetical protein.
SQ SEQUENCE 2186 AA; 245737 MW; 78BB75505012005A CRC64;

Query Match 57.1%; Score 40; DB 5; Length 2186;
Best Local Similarity 40.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNMAK 10
|||:|:|:|
DB 588 CYWERNASR 597

RESULT 9
Q81653 PRELIMINARY; PRT; 372 AA.
AC Q81653;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Senescence-associated protein 3 (Fragment).
GN SA3.
OS Hemerocallis hybrid cultivar.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
OC Hemerocallidaceae; Hemerocallis.
OX NCBI_TaxID=80862;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CV. STELLA D'ORO; TISSUE=SENESCING PETALS;
RX MEDLINE=99339249; PubMed=10412903;
RA Panavas T., Pikula A., Reid P.D., Rubinstein B., Walker E.L.;
RL Plant Mol. Biol. 40:237-248(1999).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AF082028; AAC34853.1; -.
DR InterPro; IPR01128; Cytochrome_P450.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
DR Heme; Monooxygenase; Oxidoreductase.
FT NON TER 1
SQ SEQUENCE 372 AA; 41909 MW; 55FB3EAF9699595E CRC64;

Query Match 55.7%; Score 39; DB 10; Length 372;
Best Local Similarity 71.4%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNN 7
|||:|:|:|
DB 328 CFQWQNN 334

RESULT 10
Q8WWZ6 PRELIMINARY; PRT; 1617 AA.
AC Q8WWZ6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

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DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE ATP-binding cassette A6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Schriber L.M., Arnould I., Prades C., Lachtermacher-Rocha M.,
RA Schneider T., Maitoux C., Lemoine C., Debono D., Devaud C.,
RA Naudin L., Bauche S., Annat M., Alimets R., Deneffe P., Rosier M.,
RA Dean M.;
RT "Identification and characterization of a cluster of five new ATP-
RT binding cassette transporter genes on human chromosome 17q24: a novel
RT sub-group within the ABCA sub-family.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY028898; AAK30023.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR004881; DUF258.
DR Pfam; PF00005; ABC_tran; 2.
DR Pfam; PF03193; DUF258; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SMC0382; AAA; 2.
KW ATP-binding.
SQ SEQUENCE 1617 AA; 184254 MW; E7A9641621045DC1 CRC64;
Query Match 55.7%; Score 39; DB 4; Length 1617;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNRVAKV 11
DB 440 CFQHQRTNAKV 450
|||||

RESULT 11
Q9XFD5 PRELIMINARY; PRT; 105 AA.
AC Q9XFD5;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Cytochrome P450 (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA LIU J., Yang J.;
RT "Suppression subtractive hybridization (SSH) identified candidate
RT genes that are differentially expressed at rice young panicle.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AF140486; RAD29699.1; -.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
FT NON_TER
SQ SEQUENCE 105 AA; 11912 MW; BOEEFCD487819F9 CRC64;
Query Match 54.3%; Score 38; DB 10; Length 105;
Best Local Similarity 83.3%; Pred. No. 10;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQR 6
DB 61 CFQWR 66
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RESULT 12
O22185 PRELIMINARY; PRT; 515 AA.
AC O22185;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Putative cytochrome P450.
GN AT2G23220.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Gruell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Cressy T.H., Goodman H.M., Somerville C.R.,
RA Coppenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AC002391; BAB87109.1; -.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 515 AA; 59089 MW; 3177CC439269D15B CRC64;
Query Match 54.3%; Score 38; DB 10; Length 515;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQR 6
DB 469 CFQWR 474
|||||

RESULT 13
O22188 PRELIMINARY; PRT; 543 AA.
AC O22188;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Putative cytochrome P450.
GN AT2G23190.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

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RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Cressy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhagen G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana";
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR EMBL; AC002391; AAB87112.1; -.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR Pfam; PF00067; P450.1.
 DR PRINTS; PF00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 KW Heme; Monooxygenase; Oxidoreductase.
 SQ SEQUENCE 543 AA; 62777 MW; 06332D6C090FDB12 CRC64;

Query Match 54.3%; Score 38; DB 10; Length 543;

Best Local Similarity 83.3%; Pred. No. 63;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWQR 6

Db 498 CFQWQR 503

RESULT 14

ID Q9HPA3 PRELIMINARY; PRT; 584 AA.
 AC Q9HPA3;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Vng1732c.
 GN VNG1732C.
 OS Halobacterium sp. (strain NRC-1).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorason V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 RA Leithauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlischer M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
 RT "Genome sequence of Halobacterium species NRC-1";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL; AE005078; AAG19967.1; -.
 DR InterPro; IPR001646; Septicide_repeat.
 DR InterPro; IPR001622; K-channel_pore.
 DR Pfam; PF00805; Pentapeptide; 2.
 KW Complete proteome.
 SQ SEQUENCE 584 AA; 65151 MW; 21BF5D5F0486CC06 CRC64;

Query Match 54.3%; Score 38; DB 17; Length 584;

Best Local Similarity 41.7%; Pred. No. 68;

Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQRMAKVR 12

Db 445 CFQWQRMAKVR 456

RESULT 15

Q9B818 PRELIMINARY; PRT; 750 AA.
 ID Q9B818;
 AC Q9B818;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Outer capsid protein VP4.
 OS Human rotavirus B.
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
 OX NCBI_TaxID=10942;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CAL;
 RX MEDLINE=21080727; PubMed=11213100;
 RA Sen A., Kobayashi N., Das S., Krishnan T., Bhattacharya S.K.,
 RA Naik T.N.;
 RT "The evolution of human group B rotaviruses";
 RL Lancet 357:198-199(2001).
 DR EMBL; AF184084; AAG16961.1; -.
 DR InterPro; IPR000416; Cap_VP4.
 DR Pfam; PF00426; VP4; 1.
 SQ SEQUENCE 750 AA; 84727 MW; AF2F7BADE93BF9E8 CRC64;

Query Match 54.3%; Score 38; DB 12; Length 750;

Best Local Similarity 50.0%; Pred. No. 89;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CFQWQRMAKVR 12

Db 196 CFQWQRMAKVR 207

Search completed: February 21, 2003, 07:44:30

Job time : 21.8 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds
(without alignments)
56,502 Million cell updates/sec

Title: US-09-743-107b-77
Perfect score: 70
Sequence: 1 CFQWQNNRAVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	70	100.0	12	21	AAV78077 Human lactoferrin
2	65	92.9	12	21	AAV78038 Human lactoferrin
3	65	92.9	12	21	AAV78046 Human lactoferrin
4	65	92.9	12	21	AAV78047 Human lactoferrin
5	65	92.9	13	21	AAV78037 Human lactoferrin
6	65	92.9	13	21	AAV78048 Human lactoferrin
7	65	92.9	13	21	AAV78049 Human lactoferrin
8	65	92.9	14	21	AAV78036 Human lactoferrin
9	65	92.9	14	21	AAV78050 Human lactoferrin
10	65	92.9	14	21	AAV78051 Human lactoferrin

11	65	92.9	15	17	AAV98854	Peptide for anti-u
12	65	92.9	15	21	AAV78035	Human lactoferrin
13	65	92.9	15	21	AAV78052	Human lactoferrin
14	65	92.9	15	21	AAV78063	Human lactoferrin
15	65	92.9	16	21	AAV78031	Human lactoferrin
16	65	92.9	16	21	AAV78064	Human lactoferrin
17	65	92.9	16	21	AAV78065	Human lactoferrin
18	65	92.9	17	21	AAV78034	Human lactoferrin
19	65	92.9	17	21	AAV78066	Human lactoferrin
20	65	92.9	17	21	AAV78067	Human lactoferrin
21	65	92.9	18	15	AAV69352	Human lactoferrin
22	65	92.9	18	17	AAV13397	Advanced glycosyla
23	65	92.9	18	21	AAV78033	Human lactoferrin
24	65	92.9	19	21	AAV68867	Amino acid sequenc
25	65	92.9	19	21	AAV78032	Human lactoferrin
26	65	92.9	20	13	AAV21810	Anti microbial pep
27	65	92.9	20	14	AAV44841	Lactoferrin-relate
28	65	92.9	20	15	AAV48530	Lactoferrin derive
29	65	92.9	20	15	AAV48531	Lactoferrin derive
30	65	92.9	20	15	AAV57461	Lactoferrin derive
31	65	92.9	20	15	AAV57462	Lactoferrin derive
32	65	92.9	20	16	AAV84698	Bovine lactoferrin
33	65	92.9	20	16	AAV84699	Bovine lactoferrin
34	65	92.9	20	16	AAV80283	Anti-parasitic lac
35	65	92.9	20	16	AAV80284	Anti-parasitic lac
36	65	92.9	20	17	AAV98553	Peptide for anti-u
37	65	92.9	20	17	AAV91852	Lactoferrin-derive
38	65	92.9	20	17	AAV03045	Lactoferrin-derive
39	65	92.9	20	17	AAV90607	Lactoferrin-derive
40	65	92.9	20	17	AAV87621	Lactoferrin-derive
41	65	92.9	20	17	AAV87622	Lactoferrin-derive
42	65	92.9	20	18	AAV26150	Lactoferrin-derive
43	65	92.9	20	18	AAV14036	Anti-parasitic pep
44	65	92.9	20	19	AAV70310	Thrombus formation
45	65	92.9	20	19	AAV53224	Lactoferrin hydrol

ALIGNMENTS

RESULT 1

AAV78077
ID AAV78077 standard; Peptide; 12 AA.
XX AC AAV78077;
XX DT 25-APR-2000 (first entry)
XX DE Human lactoferrin derived peptide SEQ ID NO:77.
XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.
XX OS Homo sapiens.
OS Synthetic.
XX WO200001730-A1.
XX PD 13-JAN-2000.
XX PF 06-JUL-1999; 99WO-SE01230.
XX PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX PA (ASCI-) A+ SCI INVEST AB.
XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX Claim 22; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides are also
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX SQ Sequence 12 AA;
Query Match 100.0%; Score 70; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNRAVR 12
DB |||||

RESULT 2
AAY78038
ID AAY78038 standard; Peptide; 12 AA.
XX AC AAY78038;
XX DT 25-APR-2000 (first entry)
XX DE Human lactoferrin derived peptide SEQ ID NO:38.
XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX KW urinary tract infection; colitis; Candida infection; fungicidal;
XX KW bactericidal; preservative.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200001730-A1.
XX PD 13-JAN-2000.
XX PF 06-JUL-1999; 99WO-SE01230.
XX PR 06-JUL-1998; 98SE-0002441.
XX PR 17-JUL-1998; 98SE-0002562.
XX PR 29-DEC-1998; 98SE-0004614.
XX PA (ASCI-) A+ SCI INVEST AB.
XX PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides are also
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX SQ Sequence 12 AA;
Query Match 92.9%; Score 65; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNRAVR 12
DB |||||

RESULT 3
AAY78046
ID AAY78046 standard; Peptide; 12 AA.
XX AC AAY78046;
XX DT 25-APR-2000 (first entry)
XX DE Human lactoferrin derived peptide SEQ ID NO:46.
XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX KW urinary tract infection; colitis; Candida infection; fungicidal;
XX KW bactericidal; preservative.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200001730-A1.
XX PD 13-JAN-2000.
XX PF 06-JUL-1999; 99WO-SE01230.
XX PR 06-JUL-1998; 98SE-0002441.
XX PR 17-JUL-1998; 98SE-0002562.
XX PR 29-DEC-1998; 98SE-0004614.
XX PA (ASCI-) A+ SCI INVEST AB.
XX PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX Claim 15; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides are also
CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 9.6e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNNRVR 12
 |||||
 Db 1 CFQWQNNRVR 12

RESULT 4

AAAY78047
 ID AAY78047 standard; Peptide; 12 AA.

XX AC AAY78047;

DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:47.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX OS Homo sapiens.
 OS Synthetic.

XX PN WO200001730-A1.

XX DT 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 18; Page 73; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 9.6e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNNRVR 12
 |||||
 Db 1 CFQWQNNRVR 12

RESULT 5

AAAY78037
 ID AAY78037 standard; Peptide; 13 AA.

XX AC AAY78037;

DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:37.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX OS Homo sapiens.
 OS Synthetic.

XX PN WO200001730-A1.

XX DT 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 0.0001;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNRAVR 12
 |||||
 Db 2 CFQWQNRNRAVR 13

RESULT 6

ID AAY78048
 AAY78048 standard; Peptide; 13 AA.

XX AC AAY78048;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:48.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;
 XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX XX WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
 XX PT inflammations and tumors and for use in infant formula food -
 XX PS Claim 15; Page 74; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. No. 0.0001; 1; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Mismatches 0; Gaps 0;

QY 1 CFQWQNRNRAVR 12

|||

Db 2 CFQWQNRNRAVR 13

RESULT 7

AAY78049

ID AAY78049 standard; Peptide; 13 AA.

XX AC AAY78049;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:49.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;
 XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX XX WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
 XX PT inflammations and tumors and for use in infant formula food -
 XX PS Claim 18; Page 74; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. No. 0.0001;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNRAVR 12

|||

Db 2 CFQWQNRNRAVR 13

RESULT 8

AAY78036

ID AAY78036 standard; Peptide; 14 AA.

XX AC AAY78036;

XX AC AAY78036;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:36.

XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 18; Page 75; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 XX SQ Sequence 14 AA;
 Query Match 92.9%; Score 65; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00011;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRNRAVR 12
 DB 3 CFQWQRNRAVR 14
 RESULT 11
 AAR98554
 ID AAR98554 standard; Peptide; 15 AA.
 AC AAR98554;
 XX 12-NOV-1996 (first entry)
 DT Peptide for anti-ulcer agent.
 DE anti-ulcer agent; low toxicity; stable; heat-resistant.
 XX Synthetic.
 XX JP08143468-A.
 PN 04-JUN-1996.
 XX 17-NOV-1994; 94JP-0283869.
 PR 17-NOV-1994; 94JP-0283869.
 XX (MORG) MORINAGA MILK IND CO LTD.
 PA WPI; 1996-318857/32.
 XX Anti-ulcer agent contg. peptide - has low toxicity, is
 PT heat-resistant and water-soluble
 XX Claim 1; Page 11; 11pp; Japanese.

XX AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
 CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be
 CC administered orally and be produced in large amounts.
 XX SQ Sequence 15 AA;
 Query Match 92.9%; Score 65; DB 17; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.00012;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRNRAVR 12
 DB 2 CFQWQRNRAVR 13
 RESULT 12
 AAY78035
 ID AAY78035 standard; Peptide; 15 AA.
 AC AAY78035;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:35.
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 12; Page 69; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 XX SQ Sequence 15 AA;

Query Match 92.9%; Score 65; DB 21; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.00012;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRAVR 12
 DB 4 CFQWQNNRAVR 15

RESULT 13
 AAY78062
 ID AAY78062 standard; Peptide; 15 AA.
 AC AAY78062;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:62.
 DE Human, lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 OS WO200001730-A1.
 PN 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PT Claim 15; Page 81; 102pp; English.
 PS AAY78001 to AAY78100 represent peptides having sequences based on human
 XX lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 15 AA;
 SQ Query Match 92.9%; Score 65; DB 21; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.00012;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRAVR 12
 DB 4 CFQWQNNRAVR 15

RESULT 15
 AAY78031
 ID AAY78031 standard; Peptide; 16 AA.
 XX AC AAY78031;

XX 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:31.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147398/13.
 XX New peptides used for treatment and prevention of infections.
 PT inflammations and tumors and for use in infant formula food.
 XX Claim 11; Page 68; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 16 AA;
 Query Match 92.9%; Score 65; DB 21; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.00013;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQNNRAVR 12
 |||||
 Db 5 CFQWQNNRAVR 16

Search completed: February 21, 2003, 07:37:13
 Job time : 29.35 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 Seconds
(without alignments)
40.818 Million cell updates/sec

Title: US-09-743-107B-77

Perfect score: 70

Sequence: 1 CFQWRNRAVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	18	1	US-08-204-487-3
2	65	92.9	18	2	US-08-485-948-8
3	65	92.9	18	2	US-08-628-380-8
4	65	92.9	18	2	US-08-475-055-8
5	65	92.9	20	1	US-07-755-161A-3
6	65	92.9	20	1	US-07-891-174-3
7	65	92.9	20	1	US-08-204-487-1
8	65	92.9	20	1	US-08-256-771-24
9	65	92.9	20	1	US-08-256-771-25
10	65	92.9	20	1	US-08-381-984-24
11	65	92.9	20	1	US-08-381-984-25
12	65	92.9	22	4	US-03-508-734-4
13	65	92.9	24	4	US-03-508-734-6
14	65	92.9	25	1	US-07-755-161A-10
15	65	92.9	25	1	US-07-891-174-10
16	65	92.9	25	1	US-08-204-487-7
17	65	92.9	29	4	US-09-508-734-8
18	65	92.9	36	1	US-07-755-161A-8
19	65	92.9	36	1	US-07-891-174-8
20	65	92.9	36	1	US-08-256-771-30
21	65	92.9	36	1	US-08-381-984-29
22	65	92.9	47	2	US-08-464-182A-6
23	65	92.9	47	2	US-08-406-271-6
24	65	92.9	50	2	US-08-693-274A-7
25	65	92.9	52	4	US-09-017-043A-3
26	65	92.9	53	2	US-08-464-182A-5
27	65	92.9	53	2	US-08-406-271-5

28	65	92.9	54	2	US-08-464-182A-2	Sequence 2, Appli
29	65	92.9	54	2	US-08-406-271-2	Sequence 2, Appli
30	65	92.9	594	3	US-08-724-586-2	Sequence 2, Appli
31	65	92.9	594	4	US-09-421-632-2	Sequence 2, Appli
32	65	92.9	694	4	US-09-932-190-2	Sequence 2, Appli
33	65	92.9	705	2	US-08-655-640-2	Sequence 2, Appli
34	65	92.9	708	2	US-08-655-640-4	Sequence 4, Appli
35	65	92.9	711	1	US-08-145-681-2	Sequence 2, Appli
36	65	92.9	711	1	US-08-250-308-2	Sequence 2, Appli
37	65	92.9	711	1	US-08-154-013-4	Sequence 4, Appli
38	65	92.9	711	1	US-08-461-333-4	Sequence 4, Appli
39	65	92.9	711	1	US-08-453-703-2	Sequence 2, Appli
40	65	92.9	711	2	US-08-456-106-2	Sequence 2, Appli
41	65	92.9	711	3	US-08-464-167-4	Sequence 4, Appli
42	65	92.9	711	3	US-09-158-313-4	Sequence 4, Appli
43	65	92.9	711	3	US-08-456-108-2	Sequence 2, Appli
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45	65	92.9	711	4	US-09-263-577-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOIKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEAKI
; APPLICANT: DOSAKO, SHUN/ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIAKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FJN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO. 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37)"
US-08-204-487-3

Query Match 92.9%; Score 65; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 6.4e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRRAVR 12
| | | | | | | | | | | | | | | | | |
Db 1 CFQWQNNRKRVR 12

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VIASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
FILING DATE:
CLASSIFICATION: 436

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

US-08-485-948-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 6.4e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRRAVR 12
| | | | | | | | | | | | | | | | | |
Db 1 CFQWQNNRKRVR 12

RESULT 3

US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341
; GENERAL INFORMATION:
; APPLICANT: LI, YONG MING
; APPLICANT: VIASSARA, HELEN
; APPLICANT: CERAMI, ANTHONY
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,380
FILING DATE: April 4, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

US-08-628-380-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 6.4e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRRAVR 12
| | | | | | | | | | | | | | | | | |
Db 1 CFQWQNNRKRVR 12

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VIASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1664
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 6.4e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRKVR 12
Db 1 CFQWQNRKVR 12

RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KB
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

Query Match 92.9%; Score 65; DB 1; Length 20;
```


Best Local Similarity 91.7%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNRAVR 12
| | | | | | | | | |
Db 2 CFQWQNRNRAVR 13

RESULT 6

US-07-891-174-3
; Sequence 3, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids

TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE:

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM:

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY: modified site

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNRAVR 12

Db 2 CFQWQNRNRAVR 13

RESULT 7

US-06-204-487-1
; Sequence 1, Application US/06204487
; Patent No. 5563425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000

RESULT 10
US-08-381-984-24

Sequence 24, Application US/08381984
 Patent No. 5804555
 GENERAL INFORMATION:
 APPLICANT: Mamoru TOMITA et al.
 TITLE OF INVENTION: ANTIOXIDANT
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wenderoth, Lind & Ponack
 CITY: 805 Fifteenth Street, N.W., #700
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/381,984
 FILING DATE: April 11, 1995
 CLASSIFICATION: 252
 PRIOR APPLICATION NUMBER:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-8850
 TELEFAX:

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: /note= "cysteine residues at positions 2
 and 19 are bonded by disulfide linkage"
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: /note= "the specified peptide as well as
 peptides including the specified peptide as a fragment thereof"

US-08-381-984-24

Query Match 92.9%; Score 65; DB 1; Length 20;
 Best Local Similarity 91.7%; Pred. No. 7.2e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRNRAVR 12
 Db 2 CFQWQRNRAVR 13

RESULT 11

US-08-381-984-25
 Sequence 25, Application US/08381984
 Patent No. 5804555
 GENERAL INFORMATION:
 APPLICANT: Mamoru TOMITA et al.
 TITLE OF INVENTION: ANTIOXIDANT
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/381,984
 FILING DATE: April 11, 1995
 CLASSIFICATION: 252
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-8850
 TELEFAX:

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: /note= "the specified peptide as well as
 peptides including the specified peptide as a fragment thereof"

US-08-381-984-25

Query Match 92.9%; Score 65; DB 1; Length 20;
 Best Local Similarity 91.7%; Pred. No. 7.2e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRNRAVR 12
 Db 2 CFQWQRNRAVR 13

RESULT 12

US-09-508-734-4
 Sequence 4, Application US/09508734
 Patent No. 6423509
 GENERAL INFORMATION:
 APPLICANT: Samyang Genex Corporation
 TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
 useful microorganism thereof
 FILE REFERENCE: PA/SYG/00139
 CURRENT APPLICATION NUMBER: US/09/508,734
 CURRENT FILING DATE: 2000-06-01
 PRIOR APPLICATION NUMBER: PCT/KR99/00373
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: KR1998-29351
 PRIOR FILING DATE: 1998-07-13
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: KopatentIn 1.71
 SEQ ID NO 4

LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
US-09-508-734-4

Query Match 92.9%; Score 65; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRVR 12
DB 2 CFQWQNNRKR 13

RESULT 13

US-09-508-734-6
Sequence 6, Application US/09508734
Patent No. 6423509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 6
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
US-09-508-734-6

Query Match 92.9%; Score 65; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 8.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRVR 12
DB 3 CFQWQNNRKR 14

RESULT 14

US-07-755-161A-10
Sequence 10, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755.161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLSCULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
LOCATION: 21
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
Query Match 92.9%; Score 65; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWQNNRVR 12
DB 4 CFQWQNNRKR 15

RESULT 15
US-07-891-174-10
Sequence 10, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
LOCATION: 21

IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
Query Match 92.9%; Score 65; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CFQWRNMEAVR 12
Db 4 CFQWRNMEAVR 15
Search completed: February 21, 2003, 07:50:34
Job time : 8.7 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 seconds
(without alignments)
35.508 Million cell updates/sec

Title: US-09-743-107b-77
Perfect score: 70
Sequence: 1 CFQWQNMRAVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	15	9	US-09-798-869-2
2	65	92.9	25	9	US-09-798-869-20
3	65	92.9	694	9	US-10-023-096-2
4	57	81.4	15	9	US-09-798-869-6
5	48	68.6	15	9	US-09-798-869-3
6	48	68.6	25	9	US-09-798-869-23
7	40	57.1	15	9	US-09-798-869-7
8	39	55.7	15	9	US-09-798-869-4
9	39	55.7	25	9	US-09-798-869-22
10	38	54.3	338	9	US-09-798-869-119
11	38	54.3	338	9	US-09-798-869-119
12	38	54.3	338	9	US-09-798-869-119
13	38	54.3	338	9	US-09-798-869-119
14	38	54.3	338	9	US-09-798-869-119
15	38	54.3	553	9	US-09-796-753-14
16	38	54.3	553	10	US-09-981-649A-6
17	38	54.3	553	10	US-09-981-649A-24
18	38	54.3	554	10	US-09-981-649A-30
19	38	54.3	554	10	US-09-981-649A-32

20	38	54.3	559	10	US-09-981-649A-28	Sequence 28, Appl
21	37	52.9	21	10	US-09-864-761-47985	Sequence 47985, A
22	37	52.9	333	9	US-09-796-753-26	Sequence 26, Appl
23	36	51.4	15	9	US-09-798-869-8	Sequence 8, Appl
24	36	51.4	15	9	US-09-798-869-29	Sequence 29, Appl
25	36	51.4	15	9	US-09-798-869-30	Sequence 30, Appl
26	36	51.4	46	10	US-09-864-761-48879	Sequence 48879, A
27	36	51.4	351	10	US-09-853-625B-16	Sequence 16, Appl
28	36	51.4	2273	10	US-09-995-542-12	Sequence 12, Appl
29	36	51.4	2310	10	US-09-995-542-10	Sequence 10, Appl
30	35	50.0	607	9	US-09-881-579-10	Sequence 10, Appl
31	35	50.0	688	9	US-09-881-579-15	Sequence 15, Appl
32	35	50.0	846	9	US-10-051-409-4	Sequence 4, Appl
33	34	48.6	40	10	US-09-864-761-46393	Sequence 46393, A
34	34	48.6	95	10	US-09-764-864-1031	Sequence 1031, Ap
35	34	48.6	209	10	US-09-904-536-8	Sequence 8, Appl
36	34	48.6	209	10	US-09-904-536-9	Sequence 9, Appl
37	34	48.6	209	10	US-09-904-536-11	Sequence 11, Appl
38	34	48.6	209	10	US-09-904-536-12	Sequence 12, Appl
39	34	48.6	209	10	US-09-904-536-13	Sequence 13, Appl
40	34	48.6	209	10	US-09-904-536-14	Sequence 14, Appl
41	34	48.6	209	10	US-09-904-536-15	Sequence 15, Appl
42	34	48.6	209	10	US-09-904-536-16	Sequence 16, Appl
43	34	48.6	209	10	US-09-904-536-17	Sequence 17, Appl
44	34	48.6	209	10	US-09-904-536-18	Sequence 18, Appl
45	34	48.6	212	10	US-09-904-536-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBU (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2

Query Match 92.9%; Score 65; DB 9; Length 15;
Best local Similarity 91.7%; Pred. No. 4e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNMRAVR 12
DB 3 CFQWQNMRAVR 14

RESULT 2
US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBU (RNSON

```
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-798-869-20

Query Match          92.9%; Score 65; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 6.4e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWRNMRVAVR 12
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Db 3 CFQWRNMRVAVR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020150941A1
; GENERAL INFORMATION:
; APPLICANT: Krugel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human.
; TITLE OF INVENTION: Lactoferrin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,566
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-10-023-096-2

; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-798-869-20

Query Match          92.9%; Score 65; DB 9; Length 694;
Best Local Similarity 91.7%; Pred. No. 0.0015;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWRNMRVAVR 12
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Db 22 CFQWRNMRVAVR 33

RESULT 4
US-09-798-869-6
; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL) RINSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens)
; OTHER INFORMATION: sequence)
; US-09-798-869-6

Query Match          81.4%; Score 57; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.00089;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWRNMRVAVR 12
   |||||
Db 3 CFQWRNMRVAVR 14

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL) RINSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
; US-09-798-869-3

Query Match          68.6%; Score 48; DB 9; Length 15;
Best Local Similarity 77.8%; Pred. No. 0.029;
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Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMNR 9
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Db 3 CYQWQRMNR 11

RESULT 6
US-09-798-869-23
; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23

Query Match 68.6%; Score 48; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 0.047;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMNR 9
|:|||||
Db 3 CYQWQRMNR 11

RESULT 7
US-09-798-869-7
; Sequence 7, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-7

Query Match 57.1%; Score 40; DB 9; Length 15;
Best Local Similarity 66.7%; Pred. No. 0.65;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQRMNR 9
|:|||||
Db 3 CYQWQRMNR 11

RESULT 8
US-09-798-869-4
; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4

Query Match 55.7%; Score 39; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.96;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQRMNR 11
|:|||||
Db 3 CLRWQNMERKV 13

RESULT 9
US-09-798-869-22
; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-22

Query Match 55.7%; Score 39; DB 9; Length 25;
Best Local Similarity 54.5%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQRMNR 11
|:|||||
Db 3 CLRWQNMERKV 13

RESULT 10

US-09-978-295A-119
Sequence 119, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
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PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-27
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PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
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PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR APPLICATION NUMBER: 60/079786

Query Match 54.3%; Score 38; DB 9; Length 338;
Best Local Similarity 45.5%; Pred. No. 27;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQRMNRAV 11
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Db 50 CYGWRNSKGV 60

RESULT 11
us-09-978-697-119
; Sequence 119, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.

;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079920
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 54.3%; Score 38; DB 9; Length 338;
Best Local Similarity 45.5%; Pred. No. 27;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQRNMRAV 11
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Db 50 CYGWRNSKGV 60

RESULT 12
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; Sequence 119, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Klavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James
Paoni, Nicholas P.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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/ Publication No. US20020192706A1		
/ GENERAL INFORMATION:		
/ APPLICANT: Ashkenazi, Avi		
/ APPLICANT: Baker Kevin P.		
/ APPLICANT: Botstein, David		
/ APPLICANT: Deenoyers, Luc		
/ APPLICANT: Eaton, Dan		
/ APPLICANT: Ferrara, Napoleon		
/ APPLICANT: Filvaroff, Ellen		
/ APPLICANT: Fong, Sherman		
/ APPLICANT: Gao, Wei-Qiang		
/ APPLICANT: Gerber, Hanspeter		
/ APPLICANT: Gerritsen, Wary E.		
/ APPLICANT: Goddard, Audrey		
/ APPLICANT: Godowski, Paul J.		
/ APPLICANT: Grimaldi, J. Christophe		
/ APPLICANT: Gurney, Austin L.		
/ APPLICANT: Hillan, Kenneth J.		

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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 54.3%; Score 38; DB 9; Length 338;
Best Local Similarity 45.5%; Pred. No. 27;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Db 50 CYGWRNRSGV 60

RESULT 14
US-09-978-189-119
; Sequence 119, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/084598

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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 54.3%; Score 38; DB 9; Length 338;
Best Local Similarity 45.5%; Pred. No. 27;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQNRNAV 11
Db 50 CYGWRNSKGV 60

RESULT 15

US-09-796-753-14
; Sequence 14, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634

; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 14
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-14

Query Match 54.3%; Score 38; DB 9; Length 553;
Best Local Similarity 45.5%; Pred. No. 42;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQNRNAV 11
Db 50 CYGWRNSKGV 60

Search completed: February 21, 2003, 08:08:06
Job time : 11.55 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 seconds
(without alignments)
120.168 Million cell updates/sec

Title: US-09-743-107B-77

Perfect score: 70

Sequence: 1 CFQQRNRAVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 73.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	92.9	711	1 TFHUL	lactotransferrin p
2	48	68.6	708	2 JC2323	lactoferrin - goat
3	45	64.3	33	2 S52107	lactoferrin - sheep
4	44	62.9	4568	2 T08030	dynain beta heavy
5	42	60.0	932	2 T28820	hypothetical prote
6	39	55.7	205	2 E90094	26S proteasome SU
7	39	55.7	367	2 G97449	glutamine syntheta
8	39	55.7	707	1 A28438	lactoferrin precur
9	38	54.3	515	2 T00510	probable cytochrom
10	38	54.3	543	2 T00513	cytochrome P450 ho
11	38	54.3	558	2 T17324	hypothetical prote
12	37	52.9	222	2 H70978	hypothetical prote
13	37	52.9	298	2 AD2346	hypothetical prote
14	37	52.9	357	2 T01607	probable triacylgl
15	37	52.9	568	1 A55377	CPE-binding protei
16	37	52.9	681	2 T19429	hypothetical prote
17	37	52.9	758	1 A39343	calpain (EC 3.4.22
18	37	52.9	2671	1 A49873	inositol 1,4,5-tri
19	36	51.4	144	1 F46335	trans-regulatory s
20	36	51.4	289	2 G86403	33.3K hypothetical
21	36	51.4	290	2 C97414	hypothetical prote
22	36	51.4	344	2 C95884	probable oxidoredu
23	36	51.4	351	2 S20078	NOV protein - chic
24	36	51.4	511	2 AB0858	hypothetical prote
25	36	51.4	560	2 T29586	hypothetical prote
26	36	51.4	594	2 C84325	hypothetical prote
27	36	51.4	614	2 S42526	finger protein unk
28	36	51.4	820	2 G82168	trimethylamine-N-o
29	36	51.4	846	2 S52418	GTP-binding regula

ALIGNMENTS

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text change 08-Dec-2000

C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74:

R:Cho, Y.

submitted to the EMBL Data Library, March 1994

A:Reference number: G06820

A:Accession: G01394

A>Status: preliminary; translated from GE/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-711 <CHO>

A:Cross-references: EMBL:U07643; NID:9467236; PIDN:AAB60324.1; PID:9467237

R:REV, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, P.R.

Nucleic Acids Res. 18, 5288, 1990

A>Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A:Reference number: S11228; MUID:90384839; PMID:2402455

A:Accession: S11228

A:Molecule type: mRNA

A:Residues: 1-148, 'T', 150-422, 'C', 424-711 <REV>

A:Cross-references: EMBL:X53961; NID:934415; PIDN:CAA37914.1; PID:934416

R:Feng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A>Title: Differential molecular mechanism of the estrogen action that regulates lactoferrin

A:Reference number: A45401; MUID:93125571; PMID:1480183

A:Accession: A45401

A:Molecule type: DNA

A:Residues: 1-15 <POW>

A:Cross-references: GB:S52659; NID:9263311; PIDN:AAB24877.1; PID:9263312

A:Experimental source: placenta

A>Note: sequence extracted from NCBI backbone (NCBI:P:122202)

R:Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A>Title: Nucleotide sequence of human lactoferrin cDNA.

A:Reference number: S10324; MUID:90326549; PMID:2374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <POW>

A:Cross-references: EMBL:X52941; NID:934411; PIDN:CAA37116.1; PID:934412

R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A>Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A:Reference number: S15853; MUID:91264786; PMID:2049066

A:Accession: S15853

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 20-31 <STI>

A:Accession: S20841

A:Molecule type: protein

A:Residues: 20-28, 'X', 30-31 <ST2>

RNA la protein - b
sag polyprotein -
hypothetical prote
pyridoxamine 5'-ph
pyridoxamine 5'-ph
probable pyridoxam
signal peptidase I
hypothetical prote
hypothetical prote
hypothetical prote
threonine synthase
histidyl-tRNA synt
conserved hypothet
probable cytochrom
cytochrome P450-li

```

Query Match          68.6%; Score 48; DB 2; Length 708
Best Local Similarity 77.8%; Pred. No. 1,2; Mismatches 1; Indels
Matches 7; Conservative
QY 1 CFQWRNMR 9
   | | | | |
DB 38 CYQWRNMR 46

RESULT 3
S52107
lactoferrin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic shah)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change
C;Accession: S52107
E;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
A;Title: Isolation and characterization of sheep lactoferrin, a
A;Reference number: S52107; MUID:95127729; PMID:7827104
A;Accession: S52107
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-33 <QIA>
C;Superfamily: transferin; transferin repeat homology
C;Keywords: duplication

Query Match          64.3%; Score 45; DB 2; Length 33;
Best Local Similarity 66.7%; Pred. No. 0,2;
Matches 6; Conservative 2; Mismatches 1; Indels
QY 1 CFQWRNMR 9
   | | | | |
DB 19 CYQWRNMR 27

RESULT 4
T08030
dyslin beta heavy chain - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change
C;Accession: T08030
R;Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta
A;Reference number: Z16302; MUID:94274778; PMID:8006077
A;Accession: T08030
A;Status: translated from GE/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-4568 <MIT>
A;Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1;
A;Experimental source: strain 21gr
C;Genetics:
A;Gene: ODA4
A;Map position: IX
A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2/2/2
334/3; 3686/3; 3862/3; 4240/3
C;Superfamily: dynein heavy chain, ciliary
C;Keywords: nucleotide binding; P-loop
F;1919-1926/Region: nucleotide-binding motif A (P-loop)
F;2202-2209/Region: nucleotide-binding motif A (P-loop)
F;2330-2537/Region: nucleotide-binding motif A (P-loop)

Query Match          62.9%; Score 44; DB 2; Length 4568
Best Local Similarity 50.0%; Pred. No. 40;
Matches 6; Conservative 3; Mismatches 3; Indels
QY 1 CFQWRNMR 12
   | | | | |
DB 1852 CFQWQSRIRIQ 1863

RESULT 5

```

T28820
 hypothetical protein F07C3.1 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C/Accession: T28820
 R/Pavello, A.; Gattung, S.
 submitted to the EMBL Data Library, March 1996
 A/Description: The sequence of C. elegans cosmid F07C3.
 A/Reference number: Z20528
 A/Accession: T28820
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-932 <FAV>
 A/Cross-references: EMBL:U50308; PIDN:AAK48001.1; GSPDB:GN00023; CESP:F07C3.1
 A/Experimental source: strain Bristol N2; clone F07C3
 C/Genetics:
 A/Map position: 5
 A/Gene: CESP:F07C3.1
 A/Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 599/3
 Query Match 50.0%; Score 42; DB 2; Length 932;
 Best Local Similarity 63.6%; Pred. No. 19;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 FQWQRMRAVR 12
 |||:|:|:
 Db 579 FQWQSRRLVK 589
 |||:|:|:
 RESULT 6
 E90094
 26S proteasome SU B5 [imported] - Guillardia theta nucleomorph
 C/Species: nucleomorph Guillardia theta
 A/Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
 C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
 C/Accession: E90094
 R/Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reif
 Nature 410, 1091-1096, 2001
 A/Title: The highly reduced genome of an enclaved algal nucleus.
 A/Reference number: A99082; MUID:11323671; PMID:11323671
 A/Accession: E90094
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-205 <DOU>
 A/Cross-references: GB:AF165818; NID:gl3794510; PIDN:AAK39885.1; GSPDB:GN00150
 C/Genetics:
 A/Gene: prsB5
 A/Map position: 1
 A/Genome: nucleomorph
 C/Keywords: nucleomorph
 Query Match 55.7%; Score 39; DB 2; Length 205;
 Best Local Similarity 45.5%; Pred. No. 14;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CFQWQRMRAVR 11
 |||:|:|:
 Db 63 CFFWERNLSSL 73
 |||:|:|:
 RESULT 7
 G97649
 glutamine synthetase II (glutamate-ammonia ligase II) (gsII) [imported] - Agrobacterium
 C/Species: Agrobacterium tumefaciens
 C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
 C/Accession: G97649
 R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A/Reference number: A97359; PMID:11743194
 A/Accession: G97649
 A/Status: preliminary

A/Molecule type: DNA
 A/Residues: 1-367 <KUR>
 A/Cross-references: GB:AE007869; PIDN:AAK88152.1; PID:gl515157592; GSPDB:GN00169
 C/Genetics:
 A/Gene: AGR_C_4385
 A/Map position: circular chromosome
 C/Superfamily: glutamate-ammonia ligase

Query Match 55.7%; Score 39; DB 2; Length 367;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMRAVR 12
 |||:|:|:
 Db 2 CFFWQKPRQASR 13
 |||:|:|:

RESULT 8

A28438
 lactoferrin precursor - mouse
 N/Alternate names: lactotransferrin
 C/Species: Mus musculus (house mouse)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: A28438; A41205
 R/Pentecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A/Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret
 A/Reference number: A92596; MUID:87280033; PMID:3611056
 A/Accession: A28438
 A/Molecule type: mRNA
 A/Residues: 3-707 <PEN>
 A/Cross-references: EMBL:J03298
 R/Liu, Y.; Teng, C.T.
 J. Biol. Chem. 266, 21880-21885, 1991
 A/Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
 A/Reference number: A41205; MUID:92042099; PMID:1939212
 A/Accession: A41205
 A/Molecule type: DNA
 A/Residues: 1-15 <LIU>
 A/Cross-references: GB:M74778
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication; glycoprotein
 F/1-19/Domain: signal sequence #status predicted <SIG>
 F/20-707/Product: lactotransferrin #status predicted <MAT>
 F/358-695/Domain: transferrin repeat homology <TRH2>
 F/494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.7%; Score 39; DB 1; Length 707;
 Best Local Similarity 54.5%; Pred. No. 48;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMRAVR 11
 |||:|:|:
 Db 37 CUFQWQNMKV 47
 |||:|:|:

RESULT 9

T00510
 probable cytochrome P450 At2g32320 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
 C/Accession: T00510; A84622
 R/Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
 submitted to the EMBL Data Library, November 1997
 A/Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.
 A/Reference number: Z14164
 A/Accession: T00510
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-515 <ROU>
 A/Cross-references: EMBL:AC002391; NID:g2642427; PID:g2642441
 A/Experimental source: cultivar Columbia
 R/Liu, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001

C:Accession: T00513; F84621

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

A:Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.

A:Reference number: Z14164

A:Accession: T00513

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-543 <ROU>

A:Cross-references: EMBL:AC002391; NID:g2642427; PID:g2642444

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: F84621

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-543 <STO>

A:Cross-references: GB:AE002093; NID:g2642444; PIDN:AAB87112.1; GSPDB:GN00139

C:Genetics:

A:Gene: T20D16.18; At2g23190

A:Map position: 2

A:Introns: 211/3; 339/3

C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C:Keywords: heme; iron; metalloprotein

F:341-500/Domain: cytochrome P450 homology <P45>

F:478/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 54.3%; Score 38; DB 2; Length 543;

Best Local Similarity 83.3%; Pred. No. 56;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQR 6

DB 469 CFQWQR 474

RESULT 10

T00513

Cytochrome P450 homolog At2g23190 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001

C:Accession: T00513; F84621

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

A:Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.

A:Reference number: Z14164

A:Accession: T00513

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-543 <ROU>

A:Cross-references: EMBL:AC002391; NID:g2642427; PID:g2642444

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: F84621

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-543 <STO>

A:Cross-references: GB:AE002093; NID:g2642444; PIDN:AAB87112.1; GSPDB:GN00139

C:Genetics:

A:Gene: T20D16.18; At2g23190

A:Map position: 2

A:Introns: 211/3; 339/3

C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C:Keywords: heme; iron; metalloprotein

F:341-500/Domain: cytochrome P450 homology <P45>

F:478/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 54.3%; Score 38; DB 2; Length 543;

Best Local Similarity 83.3%; Pred. No. 56;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQR 6

DB 498 CFQWQR 503

RESULT 13

AD2346

hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C:Accession: AD2346

R:Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759940

A:Accession: AD2346

A:Status: preliminary

RESULT 11

T17324

hypothetical protein DKFZp564P2063.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T17324

R:Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, September 1999

A:Reference number: Z18727

A:Accession: T17324

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-558 <DUE>

A:Cross-references: EMBL:AL117610

A:Experimental source: fetal brain; clone DKFZp564P2063

C:Genetics:

A:Note: DKFZp564P2063.1

Query Match 54.3%; Score 38; DB 2; Length 558;

Best Local Similarity 45.5%; Pred. No. 58;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRNRAV 11

DB 55 CYGWRNRSGV 65

RESULT 12

H70978

hypothetical protein Rv3271c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2000

C:Accession: H70978

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: H70978

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-222 <COL>

A:Cross-references: GB:Z92771; GB:AL123456; NID:g3242259; PIDN:CAB07084.1; PID:g306655;

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: Rv3271c

C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv3271c

Query Match 52.9%; Score 37; DB 2; Length 222;

Best Local Similarity 60.0%; Pred. No. 35;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 QWQRNRAVR 12

DB 24 EWQRNVRWAR 33

A:Molecule type: DNA
A:Residues: 1-298 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA076022.1; PID:g17133459; GSPDB:GN00179
A:Experimental source: strain FCC 7120
C:Genetics:
A:Gene: alr4323

Query Match 52.9%; Score 37; DB 2; Length 298;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CFQWQNNR 9
| | | | |
Db 163 FHWQNNR 170

RESULT 14
T01607
Probable triacylglycerol lipase At2g44810 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F16B22.30; hypothetical protein T13E15.18
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 02-Feb-2001
C:Accession: T00412; T01607; A84883
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masc
submitted to the EMBL Data Library, July 1997
A:Description: Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence.
A:Reference number: Z14146
A:Accession: T00412
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-357 <ROU>
A:Cross-references: EMBL:AC002388; NID:g3420042; PID:g23344903
A:Experimental source: cultivar Columbia
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, July 1998
A:Description: Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence.
A:Reference number: Z14284
A:Accession: T01607
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-357 <ROW>
A:Cross-references: EMBL:AC003672; NID:g3341671; PID:g3341700
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
cuse, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84883
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STO>
A:Cross-references: GB:AE002093; NID:g2344903; PIDN:AAC31843.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g44810; T13E15.18; F16B22.30
A:Map position: 2

Query Match 52.9%; Score 37; DB 2; Length 357;
Best Local Similarity 50.0%; Pred. No. 56;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNNR 10
| | | | |
Db 130 CLEWLENR 139

RESULT 15
A55377
CPE-binding protein - African clawed frog
N:Alternate names: cytoplasmic polyadenylation element-binding protein
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C:Accession: A55377
R:Hake, L.E.; Richter, J.D.
Cell 79, 617-627, 1994
A:Title: CPB is a specificity factor that mediates cytoplasmic polyadenylation during X;
A:Reference number: A55377; MUID:95042759; PMID:7954828
A:Accession: A55377
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-568 <HAK>
A:Cross-references: GB:U14169; NID:g987224; PIDN:AAA80483.1; PID:g624634
C:Superfamily: African clawed frog CPB-binding protein; ribonucleoprotein repeat homology;
F:314-388/Domain: ribonucleoprotein repeat homology <RRM1>

Query Match 52.9%; Score 37; DB 1; Length 568;
Best Local Similarity 41.7%; Pred. No. 88;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNNR 12
| | | | |
Db 542 CWHQHSMEILR 553

Search completed: February 21, 2003, 07:47:49
Job time : 10.65 secs

GenCore version 5.1.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds
(without alignments)
108.199 Million cell updates/sec

Title: US-09-743-107B-77

Perfect score: 70

Sequence: 1 CFQWQRMRAVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	711	1	TRFL_HUMAN
2	48	68.6	708	1	TRFL_CAMDR
3	48	68.6	708	1	TRFL_CAPHI
4	44	62.9	4568	1	DYHE_CHLRE
5	40	57.1	695	1	TRFL_HORSE
6	39	55.7	707	1	TRFL_MOUSE
7	37	52.9	758	1	CAN_SCHMA
8	37	52.9	2671	1	IP3T_HUMAN
9	36	51.4	144	1	REV_OMVVS
10	36	51.4	292	1	NLA_DROME
11	36	51.4	351	1	NOV_CHICK
12	36	51.4	522	1	SOA2_HUMAN
13	36	51.4	525	1	SOA2_MOUSE
14	36	51.4	961	1	VIA_BMV
15	36	51.4	2273	1	ABCR_HUMAN
16	35.5	50.7	441	1	GAG_CAEVC
17	35	50.0	428	1	SVH_CHLMU
18	35	50.0	455	1	YKII_CABEL
19	35	50.0	502	1	C9II_ARATH
20	35	50.0	728	1	KDGI_ARATH
21	35	50.0	749	1	VP4_ROTGA
22	35	50.0	765	1	Y008_HUMAN
23	35	50.0	857	1	EF2_CHICK
24	35	50.0	857	1	EF2_CRIGR
25	35	50.0	857	1	EF2_HUMAN
26	35	50.0	857	1	EF2_MESAU
27	35	50.0	857	1	EF2_MOUSE
28	35	50.0	857	1	EF2_RAT
29	35	50.0	958	1	VIA_CCMV
30	35	50.0	966	1	VIA_BBMV
31	35	50.0	1203	1	SDCI_CABEL
32	34	48.6	235	1	FL3I_HUMAN
33	34	48.6	238	1	PELX_ERWCA

RESULT 1

ID	TRFL_HUMAN	STANDARD;	PRT;	711 AA.
AC	P02788; Q16780; Q16785; Q16789; Q00756; Q9H1Z3; Q96KZ4;			
AC	Q96KZ5;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactoferrin precursor (lactoferrin) [Contains: Lactoferrin A;			
DE	Lactoferrin B; Lactoferrin C]			
GN	LTF OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	[1] SEQUENCE FROM N.A.			
RP	TISSUE=Mammary gland;			
RX	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;			
RA	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RL	Nucleic Acids Res. 18:5288-5288(1990).			
RN	[2] SEQUENCE FROM N.A.			
RP	TISSUE=Mammary gland;			
RC	Cho Y.Y.;			
RA	Thesis (1994), Genetic Engineering Research Institute / Taejeon, Korea.			
RL	[3] SEQUENCE FROM N.A.			
RN	Conneely O.M.;			
RA	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RP	[4] SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RL	"Molecular cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
[5]	SEQUENCE FROM N.A.			
RP	TISSUE=Bone marrow;			
RC	Wei X., Han J., Rado T.A.;			
RA	"Human neutrophil lactoferrin coding and 5' flanking region DNA			
RT	sequences.";			
RL	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
[6]	SEQUENCE FROM N.A.			
RP	TISSUE=Mammary gland;			
RC	Cheng H., Chen X., Huan L.;			
RA	"cDNA cloning and sequence analysis of human lactoferrin.";			
RT	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
[7]	SEQUENCE FROM N.A.			
RP	TISSUE=Prostate;			
RC	Strausberg R.;			
RA	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RL	[8]			

34	34	48.6	246	1	Y495_SYNY3
35	34	48.6	306	1	BUB2_YEAST
36	34	48.6	316	1	NORC_CHLTR
37	34	48.6	318	1	VG17_BPMD2
38	34	48.6	325	1	VG17_BPMLS
39	34	48.6	334	1	CATL_MOUSE
40	34	48.6	334	1	CATL_RAT
41	34	48.6	360	1	HIS8_LACIA
42	34	48.6	374	1	PEL2_ERWCA
43	34	48.6	401	1	Q88A_DROME
44	34	48.6	487	1	VGLI_HCMVA
45	34	48.6	566	1	YJ19_SYNY3

ALIGNMENTS

Q55185	synecocyst
P26448	saccharomyc
O84281	chlamydia t
O64210	mycobacteri
Q05223	mycobacteri
P06797	mus musculus
P07154	rattus norv
Q02135	lactococcus
P11431	erwinia car
Q9vfn2	drosophila
P16778	human cytom
P73121	synecocyst

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE-Mammary Gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Oden J.E.;
RT "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
RA Legrand D., Spik G., Montreuil J., Jolles P.;
RT "Human lactoferrin: amino acid sequence and structural
RT comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1984).
RN [10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RA Jolles P.;
RT "The present state of the human lactotransferrin sequence. Study and
RT alignment of the cyanogen bromide fragments and characterization of
RT N- and C-terminal domains.";
RL Biochim. Biophys. Acta 670:243-254(1981).
RN [11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
RA Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
RT lactotransferrin.";
RL FEBS Lett. 142:1107-110(1982).
RN [12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
RN [13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., La Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sagripanti J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human diferric lactoferrin refined at 2.2-A
RT resolution.";
RL Acta Crystallogr. D 51:629-646(1995).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
RA Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RT 253-->methionine mutant.";
RL Biochemistry 36:341-346(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
"Structure of recombinant human lactoferrin expressed in *Aspergillus*
awamori.";
Acta Crystallogr. D 55:403-407(1999).
[18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
RT and analysis of ligand-induced conformational change.";
RL Acta Crystallogr. D 54:1319-1335(1998).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of oploid antagonist peptides derived
RT from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810(1990).
RN [20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
RA Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
RA El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
RA Hejmancik J.F., Teng C.T.;
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RL Mol. Vision 4:31-32(1998).
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -!- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X53961; CAA37914.1; -;
DR EMBL; U07643; AAB60324.1; -;
DR EMBL; M93150; AAA36159.1; -;
DR EMBL; M83202; AAA59511.1; -;
DR EMBL; M83205; AAA58656.1; -;
DR EMBL; M18642; AAA86665.1; -;
DR EMBL; AF332168; AAC48753.1; -;
DR EMBL; BC015822; AAH15822.1; -;
DR EMBL; BC015823; AAH15823.1; -;
DR EMBL; M73700; AAA59479.1; -;
DR EMBL; X52941; CAA37116.1; -;
DR EMBL; U95626; AAB57795.1; -;
DR PIR; S11228; TPHEL.
DR PDB; 1LCP; 31-AUG-94.
DR PDB; 1LCT; 31-OCT-93.
DR PDB; 1LFG; 31-JUL-94.
DR PDB; 1LFH; 31-OCT-93.
DR PDB; 1LFI; 31-OCT-93.
DR PDB; 1LGB; 31-AUG-94.
DR PDB; 1LGC; 31-AUG-94.
DR PDB; 1BKA; 08-NOV-96.
DR PDB; 1DSN; 08-MAR-96.
DR PDB; 1HSE; 12-MAR-97.
DR PDB; 1VFD; 21-APR-97.

Query Match 92.9%; Score 65; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.00037;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNRAVR 12
 DB 39 CFQWQNRNRAVR 50

RESULT 2
 TRFL CAMDR STANDARD; PRT; 708 AA.
 AC Q2TUMG; Q2MZS5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Camelus dromedarius (Dromedary) (Arabic camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;
 RA Kappeler S.R.; Ackermann M.; Farah Z.; Puhon Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
 RL Int. Dairy J. 9:481-486(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M.; Srinivasan A.; Singh R.; Sahani M.S.; Singh T.P.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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 or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AJ131674; CAB53387.1; -;
 DR EMBL; AF165879; AAF82241.1; -;
 DR HSP: 077811; 1BLX
 DR InterPro; IPR011156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SMC00094; TR FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN 1; 2.
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.
 DR PROSITE; PS00207; TRANSFERRIN 3; 2.
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 708 LACTOTRANSFERRIN.
 FT REPEAT 20 363 1.
 FT REPEAT 364 708 2.
 FT DISULFID 28 64 BY SIMILARITY.
 FT DISULFID 38 55 BY SIMILARITY.
 FT DISULFID 134 217 BY SIMILARITY.
 FT DISULFID 176 192 BY SIMILARITY.
 FT DISULFID 189 200 BY SIMILARITY.
 FT DISULFID 250 264 BY SIMILARITY.
 FT DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.
 FT DISULFID 424 703 BY SIMILARITY.
 FT DISULFID 444 666 BY SIMILARITY.
 FT DISULFID 476 551 BY SIMILARITY.
 FT DISULFID 500 694 BY SIMILARITY.
 FT DISULFID 510 524 BY SIMILARITY.
 FT DISULFID 521 534 BY SIMILARITY.
 FT DISULFID 592 606 BY SIMILARITY.
 FT DISULFID 644 649 BY SIMILARITY.
 FT METAL 79 79 IRON 1 (BY SIMILARITY).
 FT METAL 111 111 IRON 1 (BY SIMILARITY).
 FT METAL 211 211 IRON 1 (BY SIMILARITY).
 FT METAL 272 272 IRON 1 (BY SIMILARITY).
 FT METAL 414 414 IRON 2 (BY SIMILARITY).
 FT METAL 452 452 IRON 2 (BY SIMILARITY).
 FT METAL 545 545 IRON 2 (BY SIMILARITY).
 FT METAL 614 614 IRON 2 (BY SIMILARITY).
 FT BINDING 140 140 ANION (BY SIMILARITY).
 FT BINDING 482 482 ANION (BY SIMILARITY).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 261 261 F -> S (IN REF. 2).
 FT CONFLICT 304 304 G -> A (IN REF. 2).
 FT CONFLICT 330 330 S -> P (IN REF. 2).
 FT CONFLICT 492 494 LLS -> PLP (IN REF. 2).
 FT CONFLICT 506 506 L -> F (IN REF. 2).
 FT CONFLICT 609 609 A -> P (IN REF. 2).
 FT CONFLICT 642 642 R -> Q (IN REF. 2).
 SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match 68.6%; Score 48; DB 1; Length 708;
 Best Local Similarity 66.7%; Pred. No. 0.41; Mismatches 1; Indels 0; Gaps 0;
 Matches 8; Conservative 1;

QY 1 CFQWQNRNRAVR 12
 DB 38 CAQWQRNRAVR 49

RESULT 3
 TRFL CAPHI STANDARD; PRT; 708 AA.
 ID TRFL CAPHI STANDARD; PRT; 708 AA.
 AC Q29477; Q29479;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Lee T.; Yu S.; Kim S.; Lee K.; Yu D.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=94380047; PubMed=8093048;
 RA le Provost F.; Nocart M.; Guerin G.; Martin P.;
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the
 relevant locus to bovine U12 syntenic group."
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 OF AN ANION, USUALLY BICARBONATE.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.

DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin) (Fragment).
 GN LTF.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "cDNA sequence of mare lactoferrin";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RC TISSUE=Milk;
 RX MEDLINE=92296631; PubMed=10366507;
 RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "Three-dimensional structure of mare diferric lactoferrin at 2.6-A resolution";
 RL J. Mol. Biol. 289:303-317(1999).
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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 DR EMBL; AJ010930; CRA09407.1; -.
 DR PDB; 1BX; 02-DEC-98.
 DR PDB; 1B7U; 02-FEB-99.
 DR PDB; 1B7Z; 02-FEB-99.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN 1; 2.
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.
 DR PROSITE; PS00207; TRANSFERRIN 3; 1.
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 FT Signal; 3D-structure.
 FT NON_TER 1 1
 FT SIGNAL <1 6
 FT CHAIN 7 695 LACTOTRANSFERRIN.
 FT REPEAT 7 350 1.
 FT REPEAT 351 695 2.
 FT DISULFID 15 51
 FT DISULFID 25 42
 FT DISULFID 121 204
 FT DISULFID 163 179
 FT DISULFID 166 189
 FT DISULFID 176 187
 FT DISULFID 237 251
 FT DISULFID 354 386
 FT DISULFID 364 377
 FT DISULFID 411 690
 FT DISULFID 431 653
 FT DISULFID 463 538
 FT DISULFID 487 681
 FT DISULFID 497 511
 FT DISULFID 508 521
 FT DISULFID 579 593
 FT DISULFID 631 636
 FT METAL 66 66 IRON 1 (BY SIMILARITY).

FT METAL 98 98 IRON 1 (BY SIMILARITY).
 FT METAL 198 198 IRON 1 (BY SIMILARITY).
 FT METAL 259 259 IRON 1 (BY SIMILARITY).
 FT METAL 401 401 IRON 2 (BY SIMILARITY).
 FT METAL 439 439 IRON 2 (BY SIMILARITY).
 FT METAL 532 532 IRON 2 (BY SIMILARITY).
 FT METAL 601 601 IRON 2 (BY SIMILARITY).
 FT BINDING 127 127 ANION (BY SIMILARITY).
 FT BINDING 469 469 ANION (BY SIMILARITY).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 482 482 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 695 AA; 75991 MW; 07BB84D50E1B165D CRC64;

Query Match 57.1%; Score 40; DB 1; Length 695;
 Best Local Similarity 58.3%; Pred. No. 11;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRNRAVR 12
 | : ||| : ||
 Db 25 CAKFQNRNKKVR 36

RESULT 6

TRFL MOUSE
 ID TRFL_MOUSE STANDARD; PRT; 707 AA.
 AC P08071; P70690; Q61799; Q922P2;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RX MEDLINE=87280033; PubMed=3611056;
 RA Pentecost B.T., Teng C.T.;
 RT "Lactotransferrin is the major estrogen inducible protein of mouse uterine secretions";
 RL J. Biol. Chem. 262:10134-10139(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA Morilishi K.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-14 FROM N.A.
 RX MEDLINE=92042099; PubMed=1939212;
 RA Liu Y., Teng C.T.;
 RT "Characterization of estrogen-responsive mouse lactoferrin promoter";
 RL J. Biol. Chem. 266:21880-21885(1991).
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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CC EMBL; J03298; AA40525.1; -.
DR EMBL; D88510; BAA13633.1; -.
DR EMBL; BC006904; AAB06904.1; -.
DR EMBL; M74778; AAA39427.1; -.
DR PIR; A28438; A28438.
DR HSP; P02788; 1CB6.
DR MGD; MGI:96837; Lcf.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SMC0094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 707 LACTOTRANSFERRIN.
FT REPEAT 20 357 1.
FT REPEAT 358 707 2.
FT DISULFID 27 63 BY SIMILARITY.
FT DISULFID 37 54 BY SIMILARITY.
FT DISULFID 133 216 BY SIMILARITY.
FT DISULFID 175 191 BY SIMILARITY.
FT DISULFID 188 199 BY SIMILARITY.
FT DISULFID 249 263 BY SIMILARITY.
FT DISULFID 366 398 BY SIMILARITY.
FT DISULFID 376 389 BY SIMILARITY.
FT DISULFID 423 702 BY SIMILARITY.
FT DISULFID 443 665 BY SIMILARITY.
FT DISULFID 475 550 BY SIMILARITY.
FT DISULFID 499 693 BY SIMILARITY.
FT DISULFID 509 523 BY SIMILARITY.
FT DISULFID 520 533 BY SIMILARITY.
FT DISULFID 591 605 BY SIMILARITY.
FT DISULFID 643 648 BY SIMILARITY.
FT METAL 78 78 IRON 1 (BY SIMILARITY).
FT METAL 110 110 IRON 1 (BY SIMILARITY).
FT METAL 210 210 IRON 1 (BY SIMILARITY).
FT METAL 271 271 IRON 1 (BY SIMILARITY).
FT METAL 413 413 IRON 2 (BY SIMILARITY).
FT METAL 451 451 IRON 2 (BY SIMILARITY).
FT METAL 544 544 IRON 2 (BY SIMILARITY).
FT METAL 613 613 IRON 2 (BY SIMILARITY).
FT BINDING 139 139 ANION (POTENTIAL).
FT BINDING 481 481 ANION (POTENTIAL).
FT CARBOHYD 118 118 N-LINKED (GLCNAC. ...) (POTENTIAL).
FT CARBOHYD 494 494 MR -> IQG (IN REF. 1).
FT CONFLICT 1 2 R -> Q (IN REF. 2).
FT CONFLICT 25 25 M -> L (IN REF. 2).
FT CONFLICT 82 82 S -> T (IN REF. 2).
FT CONFLICT 359 359 A -> D (IN REF. 1).
FT CONFLICT 382 382 E -> G (IN REF. 2).
FT CONFLICT 449 449 L -> V (IN REF. 1).
FT CONFLICT 629 629
SQ SEQUENCE 707 AA; 77865 MW; F26AE03404C19A8 CRC64;
Query Match 55.7%; Score 39; DB 1; length 707;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 CFWQNRWRAV 11
Db 37 CLRQWENMRKV 47
RESULT 7
CAN_SCHWA
ID CAN_SCHWA STANDARD; PRT; 758 AA.
AC P27730;
DR 01-AUG-1992 (Rel. 23, Created)

```

01-AUG-1992 (Rel. 23, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Calpain (EC 3.4.22.17) (Calcium-activated neutral proteinase) (CANP).

Schistosoma mansoni (Blood fluke)

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;

Schistosomatidae; Schistosomatidae; Schistosoma.

NCBI_TaxID=6183;

[1]

SEQUENCE FROM N.A.

MEDLINE=92131071; PubMed=1775175;

Karcz S.R., Podesta R.B., Siddiqui A.A., Dekaban G.A., Strejan G.H.,

Clarke M.W.;

"Molecular cloning and sequence analysis of a calcium-activated

neutral protease (calpain) from Schistosoma mansoni.";

Mol. Biochem. Parasitol. 49:333-336(1991).

[2]

SEQUENCE FROM N.A.

STRAIN=Puerto Rican;

MEDLINE=91332027; PubMed=1869543;

Andresen K., Tom T.D., Strand M.;

"Characterization of cDNA clones encoding a novel calcium-activated

neutral proteinase from Schistosoma mansoni.";

J. Biol. Chem. 266:15085-15090(1991).

-1- FUNCTION: CALPAINS ARE CALCIUM-ACTIVATED NON-LYSOSOMAL THIO-

PROTEASES.

-1- CATALYTIC ACTIVITY: Preferential cleavage: Tyr|-Xaa, Met|-Xaa or

Arg|-Xaa with Leu or Val as the P2 residue.

-1- ENZYME REGULATION: IS ACTIVATED BY FREE CYTOSOLIC CALCIUM.

-1- DEVELOPMENTAL STAGE: IN SPOROCYSTS AND ADULT WORMS.

-1- MISCELLANEOUS: THIS PROTEIN BINDS CALCIUM.

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.

-1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.

-1- CAUTION: POSSESSES AN ADDITIONAL EF-HAND REGION LOCATED BETWEEN

DOMAINS II AND III.

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or send an email to license@sib-sib.ch).

EMBL; M74233; AAA29857.1; -.

EMBL; M67499; AAA29858.1; -.

PIR; A39343; A39343.

HSP; Q07009; IDFO.

MEROPS; C02.UFV; -.

InterPro; IPR002048; EF-hand.

InterPro; IPR001300; Protease C2.

InterPro; IPR00169; SHprot_acsite.

Pfam; PF00036; ehand; 3.

Pfam; PF00648; Peptidase C2; 1.

Pfam; PF01067; Calpain III; 1.

PRINTS; PR00704; CALPAIN.

SMART; SMO0230; Cyspc; 1.

PROSITE; PS00018; EF HAND; FALSE NEG.

PROSITE; PS00139; THIOL PROTEASE CYS; 1.

PROSITE; PS00639; THIOL PROTEASE HIS; FALSE NEG.

PROSITE; PS00640; THIOL PROTEASE ASN; FALSE NEG.

Hydrolase; Thiol protease; Calcium-binding.

DOMAIN 74 262 THIOL PROTEASE DOMAIN I.

DOMAIN 263 412 THIOL PROTEASE DOMAIN II.

DOMAIN 413 562 DOMAIN III, C2-LIKE DOMAIN.

DOMAIN 563 582 LINKER.

DOMAIN 583 757 DOMAIN IV.

CA_BIND 641 652 EF-HAND 1 (PROBABLE).

CA_BIND 671 682 EF-HAND 2 (PROBABLE).

DOMAIN 707 718 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).

DOMAIN 737 748 ANCESTRAL CALCIUM SITE 4 (POTENTIAL).

ACT_SITE 154 154 BY SIMILARITY.

ACT_SITE 313 313 BY SIMILARITY.

ACT_SITE 337 337 BY SIMILARITY.

```

FT CONFLICT 128 128 H -> L (IN REF. 2).
FT CONFLICT 214 214 R -> L (IN REF. 2).
FT CONFLICT 385 397 VTC -> CYL (IN REF. 2).
FT CONFLICT 441 441 S -> N (IN REF. 2).
FT CONFLICT 755 755 S -> R (IN REF. 2).
FT CONFLICT 757 757 Y -> D (IN REF. 2).
SQ SEQUENCE 758 AA; 86863 MW; 9F5E0C98B62AF19 CRC64;

Query Match 52.9%; Score 37; DB 1; Length 758;
Best Local Similarity 75.0%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWQNRMEA 10
DB 421 QWQNRVNA 428

RESULT 8
IP3T_HUMAN STANDARD; PRT; 2671 AA.
AC Q14573; Q14649;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Inositol 1,4,5-trisphosphate receptor type 3 (Type 3 inositol 1,4,5-
DE trisphosphate receptor) (Type 3 InSP3 receptor) (IP3 receptor isoform
DE 3) (InSP3R3).
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94363219; PubMed=8081734;
RA Yamamoto-Hino M., Sugiyama T., Hikiti K., Mattei M.G., Hasegawa K.,
RA Sekine S., Sakurada K., Miyawaki A., Furuichi T., Hasegawa M.,
RA Mikoshiba K.;
RT "Cloning and characterization of human type 2 and type 3 inositol
RT 1,4,5-trisphosphate receptors.";
RL Recept. Channels 2:9-22(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=94117432; PubMed=8288584;
RA Maranto A.R.;
RT "Primary structure, ligand binding, and localization of the human type
RT 3 inositol 1,4,5-trisphosphate receptor expressed in intestinal
RT epithelium.";
RL J. Biol. Chem. 269:1222-1230(1994).
CC -!- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, A SECOND
CC MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY). INTERACTS WITH TRPC1,
CC TRPC3 AND TRPC4.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN INTESTINAL CRYPT AND VILLUS
CC EPITHELIAL CELLS.
CC -!- DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL
CC EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-
CC BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE-
CC PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.
CC -!- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
CC -----
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EMBL; D26351; BAA05385.1; -

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DR EMBL; U01062; AAC50064.1; -.
DR Genew; HGNC:6182; ITPR3.
DR MIN; 147267;
DR InterPro; IPR000699; Ca-rel_channel.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR000493; InSP3_receptor.
DR InterPro; IPR000636; M+channel_mlg.
DR InterPro; IPR003608; MIR.
DR Pfam; PF00520; ion_trans; 1.
DR Pfam; PF01365; RYDE_ITPR; 2.
DR Pfam; PF02835; MIR; 4.
DR PRINTS; PR00779; INSP3RECEPTR.
DR SMART; SM00472; MIR; 4.
KW Receptor; Transmembrane; Phosphorylation; Endoplasmic reticulum;
KW Ionic channel; Ion transport; Calcium channel.
FT DOMAIN 1 2202 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2203 2223 POTENTIAL.
FT DOMAIN 2224 2235 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2236 2256 POTENTIAL.
FT DOMAIN 2257 2264 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2265 2285 POTENTIAL.
FT DOMAIN 2286 2325 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2326 2346 POTENTIAL.
FT DOMAIN 2347 2368 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2369 2389 POTENTIAL.
FT DOMAIN 2390 2496 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2497 2517 POTENTIAL.
FT DOMAIN 2518 2671 CYTOPLASMIC (POTENTIAL).
FT MOD_RES 2583 2583 PHOSPHORYLATION (POTENTIAL).
FT CONFLICT 524 524 A -> V (IN REF. 2).
FT CONFLICT 562 562 H -> Y (IN REF. 2).
FT CONFLICT 989 989 H -> Y (IN REF. 2).
FT CONFLICT 1143 1143 A -> T (IN REF. 2).
FT CONFLICT 1391 1391 L -> V (IN REF. 2).
FT CONFLICT 1496 1497 TI -> PV (IN REF. 2).
FT CONFLICT 1674 1674 L -> V (IN REF. 2).
FT CONFLICT 2436 2436 V -> L (IN REF. 2).
SQ SEQUENCE 2671 AA; 304036 MW; 69F618CF7B681D7 CRC64;

Query Match 52.9%; Score 37; DB 1; Length 2671;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 QWQNRMEA 11
DB 2183 QWQNRVRS 2191

RESULT 9
REV_OMVVS STANDARD; PRT; 144 AA.
AC P16503;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE REV protein (Anti-repression transactivator protein) (ART/TRS).
GN REV.
OS Ovine lentivirus (strain SA-OMV).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11664;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90223989; PubMed=2158181;
RA Querat G., Audoly G., Sonigo P., Vigne R.;
RT "Nucleotide sequence analysis of SA-OMV, a visna-related ovine
RT lentivirus: phylogenetic history of lentiviruses.";
RL Virology 175:434-447(1990).
CC -----
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CC -----
EMBL; D26351; BAA05385.1; -

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CC EMBL: M31646; AAA66816.1; -
 DR PIR: F46335; F46335.
 DR HIV: M3419; REVSONVUSAG.
 KW Transcription regulation; Trans-acting factor; Activator;
 Nuclear protein.
 SQ SEQUENCE 144 AA; 16546 MW; 3B7B34E7F0611F2E CRC64;

Query Match 51.4%; Score 36; DB 1; Length 144;

Best Local Similarity 66.7%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWORNRA 10
 ||| | : ||
 Db 81 FQWLRLRA 89

RESULT 10

IDA DROME STANDARD; PRT; 292 AA.
 AC Q9XZL8; Q9V391;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Nebula protein.
 GN NLA OR CG6072.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McCormick A.V., Goldberg M.L.;
 RT "Gene required for elongation of meiosis I spindle in Drosophila females";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Branton D.C., Rogers Y.-H.C., Siatz G., Champagne M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Allir J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Beres P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiot E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fouts C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glisak A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
 CC -1- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.

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DR EMBL: AF147700; AAD33987.1; -
 DR EMBL: AE003712; AAP55285.1; -
 DR FlyBase; FBgn0026629; nla.
 SQ SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;

Query Match 51.4%; Score 36; DB 1; Length 292;

Best Local Similarity 54.5%; Pred. No. 23;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 FQWORNRAVR 12
 ||| | : ||
 Db 150 FQWLRSFRLR 160

RESULT 11

IDA NOV_CHICK STANDARD; PRT; 351 AA.
 AC P28686;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE NOV protein precursor (Nephroblastoma overexpressed gene protein).
 GN NOV.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brown leghorn;
 RX MEDLINE=92107157; PubMed=1309586;
 RA Joliet V., Martinierie C., Dambrine G., Plassiat G., Brisac M.,
 RA Crochet J., Perbal B.;
 RT "Proviral rearrangements and overexpression of a new cellular gene
 (nov) in myeloblastosis-associated virus type 1-induced
 nephroblastomas";
 RL Mol. Cell. Biol. 12:10-21(1992).
 CC -1- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
 GROWTH REGULATION. ITS OVEREXPRESSION IS ASSOCIATED WITH
 TUMORIGENESIS AND EXPRESSION OF A N-TERMINAL-TRUNCATED VERSION
 OF NOV GENE IN CHICKEN EMBRYONIC FIBROBLASTS (CEF) IS SUFFICIENT
 TO INDUCE THE TRANSFORMATION OF CEF IN VITRO.
 CC -1- TISSUE SPECIFICITY: BRAIN AND HEART, AND AT A LOWER LEVEL IN
 MUSCLE AND INTESTINE, IN THE EMBRYO. LUNG AND LESS SO IN BRAIN AND
 SPLEEN, IN ADULT CHICKEN.
 CC -1- DEVELOPMENTAL STAGE: MAV1-INDUCED NEPHROBLASTOMAS EXPRESS A HIGH
 LEVEL OF NOV GENE WHOSE TRANSCRIPTION IS NORMALLY ARRESTED IN
 ADULT KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
 PROTEIN FAMILY. CEF-10/CYR61/CFGF/FISP-12/NOV PROTEIN SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 VMFC DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTCK) DOMAIN.


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Db 40 QWTRHMEAVK 49

RESULT 13
SOA2_MOUSE
ID SOA2_MOUSE STANDARD; PRT; 525 AA.
AC O88908;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Sterol O-acyltransferase 2 (EC 2.3.1.26) (Cholesterol acyltransferase 2) (ACAT-2).
GN SOA2 OR ACAT2 OR ACAT-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=98434591; PubMed=9756919;
RA Cases S., Novak S., Zheng Y.-W., Myers H.M., Lear S.R., Sande E.,
RA Welch C.B., Luis A.J., Spencer T.A., Krause B.R., Erickson S.K.,
RA Parsae R.V., Jr.;
RT "ACAT-2, a second mammalian acyl-CoA:cholesterol acyltransferase. Its
RT cloning, expression, and characterization."
RL J. Biol. Chem. 273:26755-26764(1998).
CC -1- FUNCTION: PLAYS A ROLE IN LIPOPROTEIN ASSEMBLY AND DIETARY
CC CHOLESTEROL ABSORPTION. IN ADDITION TO ITS ACYLTRANSFERASE
CC ACTIVITY, IT MAY ACT AS A LIGASE. MAY PROVIDE CHOLESTERYL ESTERS
CC FOR LIPOPROTEIN SECRETION FROM HEPATOCYTES AND INTESTINAL MUCOSA.
CC -1- CATALYTIC ACTIVITY: Acyl-CoA + cholesterol = CoA + cholesterol
CC ester.
CC -1- SUBUNIT: MAY FORM HOMO- OR HETERODIMERS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum.
CC -1- SIMILARITY: BELONGS TO THE STEROL O-ACYLTRANSFERASE FAMILY.
CC
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CC
CC EMBL: AF078751; AAC64057.1; -.
CC MGD; MGI:1332226; Soat2.
CC InterPro: IPR002688; Soat2.
CC Pfam: PF01800; ACAT; 1.
CC Transferrase, Acyltransferase; Transmembrane; Endoplasmic reticulum;
CC Cholesterol metabolism.
CC TRANSMEM 123 143 POTENTIAL.
CC TRANSMEM 154 174 POTENTIAL.
CC TRANSMEM 197 217 POTENTIAL.
CC TRANSMEM 265 285 POTENTIAL.
CC TRANSMEM 307 327 POTENTIAL.
CC TRANSMEM 350 370 POTENTIAL.
CC TRANSMEM 440 460 POTENTIAL.
CC TRANSMEM 475 495 POTENTIAL.
CC SEQUENCE 525 AA; 60823 MW; 01CD5E2E06B5C397 CRC64;
Query Match 51.4%; Score 36; DB 1; Length 525;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 3 QWQRMNRAVR 12
| | | | |
Db 39 QWTRHMEAVK 48

RESULT 14
VIA_BMV
ID VIA_BMV STANDARD; PRT; 961 AA.
AC P03588;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 1A protein [includes: Helicase; Methyltransferase].
OS Brome mosaic virus (BMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Bromovirus.
OX NCBI_TaxID=12302;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=84114904; PubMed=6594215;
RA Ahlquist P., Dasgupta R., Kaesberg P.;
RT "Nucleotide sequence of the brome mosaic virus genome and its
RT implications for viral replication."
RL J. Mol. Biol. 172:369-383(1984).
CC -1- FUNCTION: MAY BE INVOLVED IN THE REPLICATION OF THE VIRUS.
CC CONTAINS AN HELICASE DOMAIN AND A METHYLTRANSFERASE DOMAIN. THE
CC METHYLTRANSFERASE DOMAIN IS PROBABLY INVOLVED IN VIRAL RNA
CC CAPPING.
CC -1- SIMILARITY: TO 1A PROTEIN FROM CCMV, CMV, PSV AND TAV.
CC
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CC
CC EMBL: X02380; CAA36228.1; -.
CC F1R; A04196; P1EVA.
CC InterPro: IPR002588; Vmethyltransf.
CC InterPro: IPR000606; Viral_helicase1.
CC Pfam: PF01443; Viral_helicase1; 1.
CC Pfam: PF01660; Vmethyltransf; 1.
CC Helicase; ATP-binding; Transferrase; Methyltransferase.
CC NP_BIND 585 692 ATP (POTENTIAL).
CC SEQUENCE 961 AA; 109209 MW; 4F315CB2E2F4FBC CRC64;
Query Match 51.4%; Score 36; DB 1; Length 961;
Best Local Similarity 46.7%; Pred. No. 80;
Matches 7; Conservative 2; Mismatches 2; Indels 4; Gaps 1;
Qy 1 CF----QWQRMNRAVR 11
| | | | |
Db 346 CFKESKWTENMKAV 360

RESULT 15
ABCR_HUMAN
ID ABCR_HUMAN STANDARD; PRT; 2273 AA.
AC P78363; O60438; O60915; O15112;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Retinal-specific ATP-binding cassette transporter (RIM ABC
DE transporter) (RIM protein) (RMP) (Stargardt disease protein).
GN ABCA4 OR ABCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. VARIANTS STGD, AND VARIANTS HIS-846 AND GLN-943.
RX MEDLINE=97207641; PubMed=9054934;
RA Allikmets R., Singh N., Sun H., Shroyer N.F., Hutchinson A.,
RA Chidambaram A., Gerrard B., Baird L., Stauffer D., Peiffer A.,
RA Rattner A., Smallwood P.M., Li Y., Anderson K.L., Lewis R.A.,
RA Nathans J., Leppert M., Dean M., Lupski J.R.;
RT "A photoreceptor cell-specific ATP-binding transporter gene (ABCR) is
RT mutated in recessive Stargardt macular dystrophy."

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RL Nat. Genet. 15:236-246(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97345663; PubMed=9202155;
 RA Aarlan S.M., Travis G.H.;
 RT "The photoreceptor rim protein is an ABC transporter encoded by the
 RT gene for recessive Stargardt's disease (ABCR).";
 RL FEBS Lett. 409:247-252(1997).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS STGD TRP-18 AND CYS-212.
 RX MEDLINE=98163759; PubMed=9503029;
 RA Garber S., Rozet J.-M., van de Pol T.J.R., Hoyng C.B., Munnich A.,
 RA Blankenagel A., Kaplan J., Cremers F.P.M.;
 RT "Complete exon-intron structure of the retina-specific ATP binding
 RT transporter gene (ABCR) allows the identification of novel mutations
 RT underlying Stargardt disease.";
 RL Genomics 48:139-142(1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS STGD.
 RX MEDLINE=98141123; PubMed=9490294;
 RA Nasonkin I., Illing M., Koehler M.R., Schmid M., Molday R.S.,
 RA Weber B.H.F.;
 RT "Mapping of the rod photoreceptor ABC transporter (ABCR) to 1p21-p22.1
 RT and identification of novel mutations in Stargardt's disease.";
 RL Hum. Genet. 102:21-26(1998).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=99175213; PubMed=10075733;
 RA Sun H., Molday R.S., Nathans J.;
 RT "Retinal stimulates ATP hydrolysis by purified and reconstituted ABCR,
 RT the photoreceptor-specific ATP-binding cassette transporter
 RT responsible for Stargardt disease.";
 RL J. Biol. Chem. 274:8269-8281(1999).
 RN [6]
 RP DISEASE.
 RX MEDLINE=98133912; PubMed=9466990;
 RA Cremers F.P.M., van de Pol D.J.R., van Hollander A.I.,
 RA van Haren F.J.J., Knoers N.V.A.M., Tijmes N., Bergen A.A.B.,
 RA Rohrschneider K., Blankenagel A., Pinckers A.J.L.G., Deutman A.F.,
 RA Hoyng C.B.;
 RT "Autosomal recessive retinitis pigmentosa and cone-rod dystrophy
 RT caused by splice site mutations in the Stargardt's disease gene
 RT ABCR.";
 RL Hum. Mol. Genet. 7:355-362(1998).
 RN [7]
 RP VARIANTS ARMD2, AND VARIANTS.
 RX MEDLINE=97442530; PubMed=9295268;
 RA Allikmets R., Shroyer N.F., Singh N., Seddon J.M., Lewis R.A.,
 RA Bernstein P.S., Peiffer A., Zabriske N.A., Li Y., Hutchinson A.,
 RA Dean M., Lupske J.R., Leppert M.;
 RT "Mutation of the Stargardt disease gene (ABCR) in age-related macular
 RT degeneration.";
 RL Science 277:1805-1807(1997).
 RN [8]
 RP VARIANTS STGD W-18; C-212; H-636; M-1019; V-1038; C-1108; W-1640;
 RP S-1977 AND H-2107, AND VARIANTS FFM P-11; P-541; V-1038; E-1091;
 RP C-1508; F-1970 AND R-1971.
 RX MEDLINE=98454319; PubMed=9781034;
 RA Rozet J.-M., Gerber S., Souied E., Perrault I., Chatelain S., Ghazi I.,
 RA Leowski C., Dufier J.-L., Munnich A., Kaplan J.;
 RT "Spectrum of ABCR gene mutations in autosomal recessive macular
 RT dystrophies";
 RL Eur. J. Hum. Genet. 6:291-295(1998).
 RN [9]
 RP VARIANTS STGD.
 RX MEDLINE=99138655; PubMed=9973280;
 RA Lewis R.A., Shroyer N.F., Singh N., Allikmets R., Hutchinson A.,
 RA Li Y., Lupske J.R., Leppert M., Dean M.;
 RT "Genotype/phenotype analysis of a photoreceptor-specific ATP-binding
 RT cassette transporter gene, ABCR, in Stargardt disease.";
 RL Am. J. Hum. Genet. 64:422-434(1999).
 RN [10]
 RP VARIANTS STGD, AND VARIANTS.
 RX MEDLINE=99192348; PubMed=10090887;
 RA Maugeri A., van Driel M.A., van de Pol D.J.R., Klevering B.J.,
 RA van Haren F.J.J., Tijmes N., Bergen A.A.B., Rohrschneider K.,
 RA Blankenagel A., Pinckers A.J.L.G., Dahl N., Brunner H.G.,
 RA Deutman A.F., Hoyng C.B., Cremers F.P.M.;
 RT "The 258GG->C mutation in the ABCR gene is a mild frequent founder
 RT mutation in the western European population and allows the
 RT classification of ABCR mutations in patients with Stargardt disease.";
 RL Am. J. Hum. Genet. 64:1024-1035(1999).
 RN [11]
 RP VARIANTS STGD TYR-54, AND VARIANT ALA-863.
 RX MEDLINE=2007755; PubMed=10612508;
 RA Zhang K., Garibaldi D.C., Kniazeva M., Albini T., Chiang M.F.,
 RA Kerrigan M., Sunness J.S., Han M., Allikmets R.;
 RT "A novel mutation in the ABCR gene in four patients with autosomal
 RT recessive Stargardt disease.";
 RL Am. J. Ophthalmol. 128:720-724(1999).
 RN [12]
 RP VARIANTS STGD V-60; R-206; N-300; P-541; A-849; P-974; V-1038; C-1108;
 RP L-1408; R-1488; D-1652; P-1729; E-1961; W-2038; W-2077; H-2107; R-2128
 RP AND Y-2150.
 RX MEDLINE=99221420; PubMed=10206579;
 RA Fishman G.A., Stone E.M., Grover S., Derlacki D.J., Kaines H.L.,
 RA Hockey R.R.;
 RT "Variation of clinical expression in patients with Stargardt dystrophy
 RT and sequence variations in the ABCR gene.";
 RL Arch. Ophthalmol. 117:504-510(1999).
 RN [13]
 RP VARIANTS GLU-1961 AND ASN-2177.
 RX MEDLINE=20349288; PubMed=10880298;
 RA Allikmets R., Tamur J., Hutchinson A., Lewis R.A., Shroyer N.F.,
 RA Dalakishvili K., Lupske J.R., Steiner K., Paulikhoff D., Holz F.G.,
 RA Weber B.H.F., Dean M., Atkinson A., Gail M.H., Bernstein P.S.,
 RA Singh N., Peiffer A., Zabriske N.A., Leppert M., Seddon J.M.,
 RA Zhang K., Sunness J.S., Udar N.S., Velchits S., Silva-Garcia R.,
 RA Small K.W., Simonelli F., Testa F., D'Urso M., Brancato R.,
 RA Rinaldi E., Ingavat J.J.M., ten Brink J.B., de Jong P.T.V.M.,
 RA Kaplan J., Maugeri A., van Driel M.A., Hoyng C.B., Cremers F.P.M.,
 RA Stanga P., Chakraborty S.S., Bird A.C.;
 RT "Further evidence for an association of ABCR alleles with age-related
 RT macular degeneration.";
 RL Am. J. Hum. Genet. 67:487-491(2000).
 RN [14]
 RP VARIANTS STGD E-60; T-60; E-65; L-68; R-72; C-212; S-230; S-247;
 RP V-328; K-471; P-541; Q-572; R-607; K-635; C-653; Y-764; R-765; A-901;
 RP I-959; K-1036; P-1038; P-1063; D-1087; C-1097; C-1108; L-1380; K-1399;
 RP P-1430; V-1440; H-1443; L-1486; Y-1488; M-1537; P-1689; L-1705;
 RP T-1733; R-1748; P-1763; K-1885; H-1898; E-1961; R-1975; S-1977; G-2077
 RP W-2077 AND V-2241, AND VARIANTS Q-152; H-212; R-423; I-552; R-914;
 RP Q-943; T-1562; I-1868; M-1921; L-1948; F-1970; A-2059; N-2177 AND
 RP V-2216.
 RX MEDLINE=20442027; PubMed=10958763;
 RA Rivera A., White K., Stoehr H., Steiner K., Hemmrich N., Grimm T.,
 RA Jurkiles B., Lorenz B., Scholl H.P.N., Apfelstedt-Sylla B.,
 RA Weber B.H.F.;
 RT "A comprehensive survey of sequence variation in the ABCA4 (ABCR) gene
 RT in Stargardt disease and age-related macular degeneration.";
 RL Am. J. Hum. Genet. 67:800-813(2000).
 RN [15]
 RP VARIANTS CORD3 GLU-65; CYS-212; PRO-541; ALA-863; GLY-863 DEL;
 RP VAL-1038; LYS-1122; TYR-1490 AND ASP-1598.
 RX MEDLINE=20442040; PubMed=10958761;
 RA Maugeri A., Klevering B.J., Rohrschneider K., Blankenagel A.,
 RA Brunner H.G., Deutman A.F., Hoyng C.B., Cremers F.P.M.;
 RT "Mutations in the ABCA4 (ABCR) gene are the major cause of autosomal
 RT recessive cone-rod dystrophy.";
 RL Am. J. Hum. Genet. 67:960-966(2000).
 RN [16]
 RP VARIANTS STGD ASP-340; GLN-572; ALA-863; SER-965; VAL-1038; ALA-1780
 RP AND HIS-1898, AND VARIANT GLN-943.
 RX MEDLINE=20208356; PubMed=10746567;

RA Shroyer N.F., Lewis R.A., Lupeki J.R.;
 RT "Complex inheritance of ABCR mutations in Stargardt disease: linkage
 RL disequilibrium, complex alleles, and pseudodominance.";
 Hum. Genet. 106:244-248(2000).
 RN [17]
 RP VARIANTS STGD.
 RX MEDLINE=20098082; PubMed=10634594;
 RA Papaicannou M., Ocaka L., Bessant D., Lois N., Bird A.C., Payne A.,
 RA Bhattacharya S.S.;
 RT "An analysis of ABCR mutations in British patients with recessive
 RT retinal dystrophies.";
 RT Invest. Ophthalmol. Vis. Sci. 41:16-19(2000).
 RN [18]
 RP VARIANTS STGD C-212; D-767; I-897; V-1038; K-1087; K-1399; Q-1640 AND
 RP E-1961, AND VARIANT HIS-212.
 RX MEDLINE=20174852; PubMed=10711710;
 RA Simonelli F., Testa F., de Crechcio G., Rinaldi E., Hutchinson A.,
 RA Atkinson A., Dean M., D'Urso M., Allikmets R.;
 RT "New ABCR mutations and clinical phenotype in Italian patients with
 RT Stargardt disease.";
 RT Invest. Ophthalmol. Vis. Sci. 41:892-897(2000).
 RN [19]
 RP CHARACTERIZATION OF VARIANTS, AND MUTAGENESIS OF GLY-966; LYS-969;
 RP GLY-1975 AND LYS-1978.
 RX MEDLINE=20472331; PubMed=11017087;
 RA Sun H., Smallwood P.M., Nathans J.;
 RT "Biochemical defects in ABCR protein variants associated with human
 RT retinopathies.";
 RL Nat. Genet. 26:242-246(2000).
 RN [20]
 RP VARIANT STGD ASN-972, AND VARIANTS GLN-943; ILE-1868 AND LEU-1948.
 RX MEDLINE=21478761; PubMed=11594993;
 RA Eksandh L., Ekstroem U., Abrahamson M., Bauer B., Andreasson S.;

Query Match 51.4%; Score 36; DB 1; Length 2273;
 Best local similarity 60.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQNNMRA 10
 Db 779 CFQWQNNMRA 788

Search completed: February 21, 2003, 07:27:52
 Job time : 5.6 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds
(without alignments)
118.873 Million cell updates/sec

Title: US-09-743-107b-77

Perfect score: 70

Sequence: 1 CFQWQNRWRAV 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	85.7	711	4 Q8TCD2	Q8tcd2 homo sapien
2	56	80.0	38	4 Q9UCY5	Q9ucy5 homo sapien
3	45	84.3	33	6 Q9TR80	Q9tr80 ovis aries
4	42	60.0	932	5 Q19153	Q19153 caenorhabdi
5	41	58.6	148	10 Q9XHP1	Q9xhp1 sesamum ind
6	41	58.6	279	16 Q8XSE2	Q8xse2 ralestonia s
7	40	57.1	306	4 Q8TAX2	Q8tax2 homo sapien
8	40	57.1	466	4 Q9NUS2	Q9nus2 homo sapien
9	40	57.1	531	10 Q9LTD4	Q9ltd4 arabidopsis
10	40	57.1	864	5 Q62582	Q62582 encephalito
11	40	57.1	864	5 Q8SRG3	Q8srg3 encephalito
12	40	57.1	864	5 Q8SQ16	Q8sq16 encephalito
13	39.5	56.4	395	12 Q92283	Q92283 molluscum c
14	39	55.7	205	8 Q98RR2	Q98rr2 guillardia
15	39	55.7	274	4 Q96M21	Q96m21 homo sapien
16	39	55.7	367	16 Q8UCR7	Q8ucr7 agrobacteri

17	39	55.7	372	10 Q81653	Q81653 hemerocalli
18	39	55.7	488	10 Q8S934	Q8s934 diospyros k
19	39	55.7	726	5 Q9BNX0	Q9bnx0 unidentified
20	39	55.7	727	5 Q9BNW0	Q9bnw0 peripatus s
21	39	55.7	728	5 Q9BNW7	Q9bnw7 scolopendra
22	39	55.7	844	5 Q9BME7	Q9bme7 aedes aegypt
23	39	55.7	844	5 Q9SP39	Q9sp39 aedes aegypt
24	39	55.7	844	5 Q8T4S0	Q8t4s0 aedes aegypt
25	39	55.7	844	5 Q8T4R9	Q8t4r9 aedes aegypt
26	38	54.3	105	10 Q9XPD5	Q9xpd5 oryza sativ
27	38	54.3	143	9 Q8ZXA7	Q8zxa7 bacterioph
28	38	54.3	341	11 Q8R2A4	Q8r2a4 mus musculu
29	38	54.3	356	16 Q9AK86	Q9ak86 streptomyce
30	38	54.3	515	10 Q22185	Q22185 arabidopsis
31	38	54.3	543	10 Q22188	Q22188 arabidopsis
32	38	54.3	544	10 Q949E1	Q949e1 oryza sativ
33	38	54.3	553	4 Q9NZL7	Q9nzl7 homo sapien
34	38	54.3	554	4 Q9NY67	Q9ny67 homo sapien
35	38	54.3	558	4 Q9UFK6	Q9ufk6 homo sapien
36	38	54.3	1130	4 Q9H1V5	Q9h1v5 homo sapien
37	38	54.3	1778	5 Q9NE65	Q9ne65 leishmania
38	38	54.3	2186	5 Q9N906	Q9n906 trypanosoma
39	37	52.9	222	16 P96876	P96876 mycobacteri
40	37	52.9	298	16 Q8YP77	Q8yp77 anabaena sp
41	37	52.9	332	10 Q8SAC4	Q8sag4 oryza sativ
42	37	52.9	357	10 Q22170	Q22170 arabidopsis
43	37	52.9	415	5 Q9U4M9	Q9u4m9 leishmania
44	37	52.9	447	10 Q948R1	Q948r1 arabidopsis
45	37	52.9	469	9 Q98115	Q98115 bacterioph

ALIGNMENTS

RESULT 1

Q8TCD2 ID Q8TCD2 PRELIMINARY; PRT; 711 AA.
AC Q8TCD2;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Lactotransferrin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022347; AAH2347.1; --
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;

Query Match 85.7%; Score 60; DB 4; Length 711;
Best Local Similarity 90.9%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRWRAV 11
DB 39 CFQWQNRWRAV 49

RESULT 2

Q9UCY5 ID Q9UCY5 PRELIMINARY; PRT; 38 AA.
AC Q9UCY5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Lactoferrin homolog (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96081613; PubMed=8551695;
RA Sato I.;
RT "Characterization of the 84-kDa protein with ABH activity in human
RL seminal plasma.";
RL Jpn. J. Legal Med. 49:281-293(1995).
DR HSSP; P02788; 1BKA.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDDB CRC64;

Query Match 80.0%; Score 56; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQWQNNRAVR 12
Db 21 FQWQNNRAVR 31

RESULT 3
Q9TR80 PRELIMINARY; PRT; 33 AA.
AC Q9TR80;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Lactoferrin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=95127729; PubMed=7827104;
RA Qian Z.Y., Jollies P., Migliore-Samour D., Fiat A.M.;
RL Biochim. Biophys. Acta 1243:25-32(1995).
DR HSSP; O77698; ICE2.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 64.3%; Score 45; DB 6; Length 33;
Best Local Similarity 66.7%; Pred. No. 0.25;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNR 9
Db 19 CYQWQNNR 27

RESULT 4
Q19153 PRELIMINARY; PRT; 932 AA.
AC Q19153;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical 105.1 kDa protein.
GN F07C3.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;

```

```

RT "Genome sequence of the nematode C. elegans: a platform for
RL investigating biology. The C. elegans Sequencing Consortium.";
RN Science 282:2012-2018(1998).
RP [2]
RX SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Pavello A., Gattung S.;
RT "The sequence of C. elegans cosmid F07C3.";
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U50308; AAG24025.1;
DR InterPro; IPR000731; HMGCR/patch_5TM.
DR PROSITE; PS0156; SSD; 1.
KW Hypothetical protein.
SQ SEQUENCE 932 AA; 105144 MW; 66680619ADACBFD5 CRC64;

Query Match 60.0%; Score 42; DB 5; Length 932;
Best Local Similarity 63.6%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNNRAVR 12
Db 579 FQWQNNRAVR 589

RESULT 5
Q9XHP1 PRELIMINARY; PRT; 148 AA.
AC Q9XHP1;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE 2S albumin.
OS Sesamum indicum (Oriental sesame) (gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
OX NCBI_TaxID=4182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TAINAN 1;
RX MEDLINE=20074970; PubMed=10606554;
RA Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;
RT "Molecular cloning of 11S globulin and 2S albumin, the two major seed
RL storage proteins in sesame.";
RL J. Agric. Food Chem. 47:4932-4938(1999).
DR EMBL; AF091841; AAD42943.1; -.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR000617; Napin.
DR InterPro; IPR001768; Try/alpha_inhbt.
DR Pfam; PF00234; try_alpha_aml; 1.
DR PRINTS; PR00496; NAPIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;

Query Match 58.6%; Score 41; DB 10; Length 148;
Best Local Similarity 66.7%; Pred. No. 6.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNNR 9
Db 54 CMQWQNNR 62

RESULT 6
Q8XSE2 PRELIMINARY; PRT; 279 AA.
ID Q8XSE2
AC Q8XSE2;

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DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Purative ICC protein homolog.
 GN ICC OR RSP0534 OR RS00414.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OG Plasmid megaplasmid.
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gapin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Sigulier F., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RL "Genome sequence of the plant pathogen Ralstonia solanacearum.";
 RL Nature 415:497-502(2002).
 DR EMBL; AL646079; CAD17685.1; -;
 DR InterPro; IPR004843; M-PP5strase.
 DR InterPro; IPR004844; S/T_phosphatase.
 DR Pfam; PF00149; Metallophos; 1.
 KW Plasmid; Complete proteome.
 SQ SEQUENCE 279 AA; 31541 MW; ABB38818004B2EDA CRC64;

Query Match 58.6%; Score 41; DB 16; Length 279;
 Best Local Similarity 41.7%; Pred. No. 13;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CFQWQRMRAVR 12
 |||||:
 Db 244 CFQWEKGRITAK 255

RESULT 7
 ID Q8TAX2 PRELIMINARY; PRT; 306 AA.
 AC Q8TAX2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Similar to hypothetical protein FLJ11175.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PANCREAS;
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025708; AAH25708.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;

Query Match 57.1%; Score 40; DB 4; Length 306;
 Best Local Similarity 50.0%; Pred. No. 21;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMRA 10
 |||||:
 Db 269 CFQWESTLRS 278

RESULT 8
 ID Q9NUS2 PRELIMINARY; PRT; 466 AA.
 AC Q9NUS2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE CDNA FLJ11175 fis. clone PLACB1007375, weakly similar to phorbol
 ester/diacylglycerol-binding protein UNC-13.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Isozaki T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi N., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Yamanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
 RA Ninomiya K., Iwavanagi T.,
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK002037; BAA92048.1; -;
 DR HSSP; P21707; 1BYN.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR000504; RNA_rec_mct.
 DR Pfam; PF00168; C2; 1.
 DR PRINTS; PRO0360; C2DOMAIN.
 DR SMART; SM00239; C2; 1.
 DR PROSITE; PS00499; C2_DOMAIN_1; UNKNOWN_1.
 DR PROSITE; PS00004; C2_DOMAIN_2; 1.
 DR PROSITE; PS00030; RNP_RNP_1; UNKNOWN_1.
 SQ SEQUENCE 466 AA; 53192 MW; E4113A5062F58D6E CRC64;

Query Match 57.1%; Score 40; DB 4; Length 466;
 Best Local Similarity 50.0%; Pred. No. 33;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMRA 10
 |||||:
 Db 269 CFQWESTLRS 278

RESULT 9
 ID Q9LTD4 PRELIMINARY; PRT; 531 AA.
 AC Q9LTD4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Similarity to unknown protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsiis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT clones.";
 RL DNA Res. 7:131-135(2000).
 DR EMBL; AB025608; BAA95727.1; -;
 SQ SEQUENCE 531 AA; 60377 MW; C229982FFFB175E CRC64;

Query Match 57.1%; Score 40; DB 10; Length 531;
 Best Local Similarity 60.0%; Pred. No. 39;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNMRA 10
 ||:|:|
 Db 518 CFQWQSCRA 527
 ||:|:|
 RESULT 10
 O62582 PRELIMINARY; PRT; 864 AA.
 AC O62582;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Amino-peptidase (EC 3.4.11.7).
 OS Encephalitozoon cuniculi.
 OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
 OX NCBI_TaxID=6035;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20468003; PubMed=11013707;
 RA Duffieux F., Peyret P., Roe B.A., Vivares C.P.;
 RT "First report on the systematic sequencing of the small genome of
 RT Encephalitozoon cuniculi (Microsporida, Protozoa) : gene organization of
 RT a 4.3 kbp region on chromosome I.";
 RL Microb. Comp. Genomics 3:1-11(1998).
 DR EMBL; AJ005644; CRA06646.1; -;
 DR InterPro; IPR000130; Ala-peptidase.
 DR Pfam; PF01433; Peptidase M1; 1.
 DR PRINTS; PR00756; ALADPTASE.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
 DR Amino-peptidase; Hydrolase.
 SQ SEQUENCE 864 AA; 97387 MW; 6617AE5B6472F703 CRC64;
 Query Match 57.1%; Score 40; DB 5; Length 864;
 Best Local Similarity 60.0%; Pred. No. 64;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 3 QWQNMRAVR 12
 ||:|:|
 Db 842 QWRMRMGIR 851
 ||:|:|
 RESULT 11
 O8SRG3 PRELIMINARY; PRT; 864 AA.
 AC O8SRG3;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Glutamyl aminopeptidase.
 GN ECU08.0070.
 OS Encephalitozoon cuniculi.
 OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
 OX NCBI_TaxID=6035;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RA Katinaka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
 RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
 RA Weissbach J., Vivares C.P.;
 RT "Genome sequence and gene compaction of the eukaryote parasite
 RT Encephalitozoon cuniculi";
 RL Nature 414:450-453(2001).
 DR EMBL; AL590448; CAD26312.1; -;
 SQ SEQUENCE 864 AA; 97387 MW; 6617AE5B6472F703 CRC64;

Query Match 57.1%; Score 40; DB 5; Length 864;
 Best Local Similarity 60.0%; Pred. No. 64;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 3 QWQNMRAVR 12
 ||:|:|
 Db 842 QWRMRMGIR 851
 ||:|:|
 RESULT 11
 O8SRG3 PRELIMINARY; PRT; 864 AA.
 AC O8SRG3;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Glutamyl aminopeptidase.
 GN ECU08.0070.
 OS Encephalitozoon cuniculi.
 OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
 OX NCBI_TaxID=6035;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RA Katinaka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
 RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
 RA Weissbach J., Vivares C.P.;
 RT "Genome sequence and gene compaction of the eukaryote parasite
 RT Encephalitozoon cuniculi";
 RL Nature 414:450-453(2001).
 DR EMBL; AL590448; CAD26312.1; -;

SQ SEQUENCE 864 AA; 97521 MW; EF6500S145C57CF5 CRC64;
 Query Match 57.1%; Score 40; DB 5; Length 864;
 Best Local Similarity 60.0%; Pred. No. 64;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 3 QWQNMRAVR 12
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 Db 842 QWRMRMGIR 851
 ||:|:|
 RESULT 12
 O8SQI6 PRELIMINARY; PRT; 864 AA.
 AC O8SQI6;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Glutamyl aminopeptidase.
 GN ECU01.0140 OR ECU01.1470.
 OS Encephalitozoon cuniculi.
 OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
 OX NCBI_TaxID=6035;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RA Katinaka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
 RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
 RA Weissbach J., Vivares C.P.;
 RT "Genome sequence and gene compaction of the eukaryote parasite
 RT Encephalitozoon cuniculi";
 RL Nature 414:450-453(2001).
 DR EMBL; AL391737; CAD24886.1; -;
 DR EMBL; AL391737; CAD25018.1; -;
 SQ SEQUENCE 864 AA; 97364 MW; 44DD93320CC5B153 CRC64;

Query Match 57.1%; Score 40; DB 5; Length 864;
 Best Local Similarity 60.0%; Pred. No. 64;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 3 QWQNMRAVR 12
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 Db 842 QWRMRMGIR 851
 ||:|:|
 RESULT 13
 O92283 PRELIMINARY; PRT; 395 AA.
 AC O92283;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE MC080R.
 OS Molluscum contagiosum virus subtype 2 (MCVII).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OX Molluscipoxvirus.
 OX NCBI_TaxID=10281;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99011469; PubMed=9792850;
 RA Senkevich T.G., Moss B.;
 RT "Domain structure, intracellular trafficking, and beta2-microglobulin
 RT binding of a major histocompatibility complex class I homolog encoded
 RT by molluscum contagiosum virus";
 RL Virology 250:397-407(1998).
 DR EMBL; AF085225; AAC72821.1; -;

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DR InterPro; IPR003597; IG ci.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR Pfam; PF00129; MHC_I; 1.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
SQ SEQUENCE 395 AA; 43312 MW; D98B574419AC0AD CRC64;

Query Match 56.4%; Score 39.5; DB 12; Length 395;
Best Local Similarity 63.6%; Pred. No. 34;
Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 CFQW-QRNMRA 10
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Db 224 CFQWLERHLRA 234

RESULT 14
Q98RR2 Q98RR2 PRELIMINARY; PRT; 205 AA.
AC Q98RR2:
DT 01-OCT-2001 (TrEMBLrel. 19, Created)
DT 01-OCT-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 26S proteasome SU B5.
GN PRS5.
OS Guillardia theta (Cryptomonas phi).
OC Nucleomorph.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55523;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21223349; PubMed=1133671;
RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,
RA Wu X., Reith M., Cavalier-Smith T., Maier U.G.;
RT "The highly reduced genome of an enslaved algal nucleus.";
RL Nature 410:1091-1096(2001).
DR EMBL; AF165818; AAK39885.1; -.
DR InterPro; IPR000243; Proteasome_B.
DR Pfam; PF00227; proteasome; 1.
DR PRINTS; PR00141; PROTEASOME.
KW Proteasome.
SQ SEQUENCE 205 AA; 22691 MW; D30F5289CBC85049 CRC64;

Query Match 55.7%; Score 39; DB 8; Length 205;
Best Local Similarity 45.5%; Pred. No. 21;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRNMRAV 11
   ||||| :||:
Db 63 CFFWERNLSSL 73

RESULT 15
Q96M21 Q96M21 PRELIMINARY; PRT; 274 AA.
AC Q96M21:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CDNA FLJ32891. fis, clone TESTI2004929.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,

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RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahori K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK057453; BAB71493.1; -.
SQ SEQUENCE 274 AA; 30083 MW; 1DD43654D4135B2F CRC64;

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Query Match 55.7%; Score 39; DB 4; Length 274;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 1 CFQWQRNMRAVR 12
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Db 66 CFQWRNGVRYLR 77

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Search completed: February 21, 2003, 07:44:31
Job time : 21.8 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds
(without alignments)
56.502 Million cell updates/sec

Title: US-09-743-107B-78
Perfect score: 71
Sequence: 1 CFQWRNMRXR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	12	21	AAV78078 Human lactoferrin
2	67	94.4	12	21	AAV78038 Human lactoferrin
3	67	94.4	12	21	AAV78046 Human lactoferrin
4	67	94.4	12	21	AAV78047 Human lactoferrin
5	67	94.4	13	21	AAV78037 Human lactoferrin
6	67	94.4	13	21	AAV78048 Human lactoferrin
7	67	94.4	13	21	AAV78049 Human lactoferrin
8	67	94.4	14	21	AAV78036 Human lactoferrin
9	67	94.4	14	21	AAV78050 Human lactoferrin
10	67	94.4	14	21	AAV78051 Human lactoferrin

11	67	94.4	15	17	AAV98554 Peptide for anti-u
12	67	94.4	15	21	AAV78035 Human lactoferrin
13	67	94.4	15	21	AAV78062 Human lactoferrin
14	67	94.4	15	21	AAV78063 Human lactoferrin
15	67	94.4	16	21	AAV78031 Human lactoferrin
16	67	94.4	16	21	AAV78064 Human lactoferrin
17	67	94.4	16	21	AAV78065 Human lactoferrin
18	67	94.4	17	21	AAV78034 Human lactoferrin
19	67	94.4	17	21	AAV78066 Human lactoferrin
20	67	94.4	17	21	AAV78067 Human lactoferrin
21	67	94.4	18	15	AAV69352 Human lactoferrin
22	67	94.4	18	17	AAV13397 Advanced glycosyla
23	67	94.4	18	21	AAV78033 Human lactoferrin
24	67	94.4	19	21	AAV68867 Amino acid sequenc
25	67	94.4	19	21	AAV78032 Human lactoferrin
26	67	94.4	20	13	AAV21810 Anti microbial pep
27	67	94.4	20	14	AAV44841 Lactoferrin-relate
28	67	94.4	20	15	AAV48530 Lactoferrin derive
29	67	94.4	20	15	AAV48531 Lactoferrin derive
30	67	94.4	20	15	AAV57461 Lactoferrin derive
31	67	94.4	20	15	AAV57462 Lactoferrin derive
32	67	94.4	20	16	AAV84698 Bovine lactoferrin
33	67	94.4	20	16	AAV84699 Bovine lactoferrin
34	67	94.4	20	16	AAV80263 Anti-parasitic lac
35	67	94.4	20	16	AAV80264 Anti-parasitic lac
36	67	94.4	20	17	AAV98553 Peptide for anti-u
37	67	94.4	20	17	AAV91852 Lactoferrin-derive
38	67	94.4	20	17	AAV03045 Lactoferrin-derive
39	67	94.4	20	17	AAV90607 Lactoferrin-derive
40	67	94.4	20	17	AAV87621 Lactoferrin-derive
41	67	94.4	20	17	AAV87622 Lactoferrin-derive
42	67	94.4	20	18	AAV26150 Lactoferrin deriva
43	67	94.4	20	18	AAV14036 Anti-parasitic pep
44	67	94.4	20	19	AAV70310 Thrombus formation
45	67	94.4	20	19	AAV53224 Lactoferrin hydrol

ALIGNMENTS

RESULT 1
AAV78078
ID AAV78078 standard; Peptide; 12 AA.
XX AAV78078;
AC AAV78078;
XX
XX
DT 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:78.
DE Human; lactoferrin; modification; infection; inflammation; tumour;
XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
XX
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-SE01230.
XX
XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
DR

XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX
PS Claim 22; Page 35; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX SQ Sequence 12 AA;
Query Match 100.0%; Score 71; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFQWQRNRKAR 12
DB 1 CFQWQRNRKAR 12
RESULT 2
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ID AAY78038 standard; Peptide; 12 AA.
XX
AC AAY78038;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:38.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
XX
PR 17-JUL-1998; 98SE-0002562.
XX
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX
PS Claim 12; Page 70; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX SQ Sequence 12 AA;
Query Match 94.4%; Score 67; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 6.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWQRNRKAR 12
DB 1 CFQWQRNRKAR 12
RESULT 3
AAY78046
ID AAY78046 standard; Peptide; 12 AA.
XX
AC AAY78046;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:46.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
XX
PR 17-JUL-1998; 98SE-0002562.
XX
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX
PS Claim 15; Page 35; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;
 Query Match 94.4%; Score 67; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 6.3e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKAR 12
 |||||
 Db 1 CFQWQRNMRKVR 12

RESULT 4
 ID AAY78047 standard; Peptide; 12 AA.
 XX AC AAY78047;
 XX DT 25-APR-2000 (first entry)
 DE Human lactoferrin derived peptide SEQ ID NO:47.
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200001730-A1.
 XX PD 13-JAN-2000.
 XX PF 06-JUL-1999; 99WO-SE01230.
 XX PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX PA (ASCI-) A+ SCI INVEST AB.
 XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 18; Page 73; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;
 Query Match 94.4%; Score 67; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 6.3e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKAR 12
 |||||
 Db 1 CFQWQRNMRKVR 12

RESULT 5
 ID AAY78037 standard; Peptide; 13 AA.
 XX AC AAY78037;
 XX DT 25-APR-2000 (first entry)
 DE Human lactoferrin derived peptide SEQ ID NO:37.
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200001730-A1.
 XX PD 13-JAN-2000.
 XX PF 06-JUL-1999; 99WO-SE01230.
 XX PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX PA (ASCI-) A+ SCI INVEST AB.
 XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 12; Page 70; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 13 AA;
 Query Match 94.4%; Score 67; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 6.8e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKAR 12
 |||||
 Db 2 CFQWQNNRKVR 13

RESULT 6

AAV78048
 ID AAY78048 standard; Peptide; 13 AA.

XX AAY78048;

AC AAY78048;
 XX 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:48.

DE Human lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 13 AA;

XX Query Match 94.4%; Score 67; DB 21; Length 13;

XX Best Local Similarity 91.7%; Pred. No. 6.8e-05;

XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKAR 12

Db 2 CFQWQNNRKVR 13

RESULT 7

AAV78049

ID AAY78049 standard; Peptide; 13 AA.

XX AAY78049;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:49.

DE Human lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 18; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 13 AA;

XX Query Match 94.4%; Score 67; DB 21; Length 13;

XX Best Local Similarity 91.7%; Pred. No. 6.8e-05;

XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKAR 12

Db 2 CFQWQNNRKVR 13

RESULT 8

AAV78036

ID AAY78036 standard; Peptide; 14 AA.

XX AAY78036;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:36.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS WO200001730-A1.
 XX
 XX 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SE01230.
 XX
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 XX (ASCI-) A+ SCI INVEST AB.
 XX
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PS Claim 12; Page 69; 102pp; English.
 XX
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 XX Sequence 14 AA;
 QY Query Match 94.4%; Score 67; DB 21; Length 14;
 Db Best Local Similarity 91.7%; Pred. No. 7.3e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQNRNKKAR 12
 Db 3 CFQWQNRNKKVR 14
 RESULT 9
 AAY78050
 ID AAY78050 standard; Peptide; 14 AA.
 XX
 XX AAY78050;
 XX
 XX 25-APR-2000 (first entry)
 XX
 XX Human lactoferrin derived peptide SEQ ID NO:50.
 XX
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 XX Homo sapiens.
 OS

OS Synthetic.
 XX
 XX WO200001730-A1.
 XX
 XX 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SE01230.
 XX
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 XX (ASCI-) A+ SCI INVEST AB.
 XX
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PS Claim 15; Page 75; 102pp; English.
 XX
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 XX Sequence 14 AA;
 QY Query Match 94.4%; Score 67; DB 21; Length 14;
 Db Best Local Similarity 91.7%; Pred. No. 7.3e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQNRNKKAR 12
 Db 3 CFQWQNRNKKVR 14
 RESULT 10
 AAY78051
 ID AAY78051 standard; Peptide; 14 AA.
 XX
 XX AAY78051;
 XX
 XX 25-APR-2000 (first entry)
 XX
 XX Human lactoferrin derived peptide SEQ ID NO:51.
 XX
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS WO200001730-A1.
 XX
 XX 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SE01230.
 PF

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XX PR 06-JUL-1998; 98SE-0002441.
XX PR 17-JUL-1998; 98SE-0002562.
XX PR 29-DEC-1998; 98SE-0004614.
XX PA (ASCI-) A+ SCI INVEST AB.
XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX DR WPI; 2000-147388/13.
XX PT New peptides used for treatment and prevention of infections,
XX PT inflammations and tumors and for use in infant formula food -
XX PS Claim 18; Page 75; 102pp; English.
XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
XX CC lactoferrin. The peptides are taken up in the intestine through
XX CC binding to specific lactoferrin receptors and are then transported
XX CC through the circulation. A medicinal product of the peptide or fragment
XX CC can be used for treating and/or prevention of infections (such as
XX CC urinary tract infections, colitis, and Candida infection on a mucosal
XX CC membrane), inflammations and/or tumors. The peptides can also be used
XX CC in food stuffs such as infant formula food. The peptides are also
XX CC fungicidal and bactericidal and may also be used as preservatives.
XX CC Even though native human lactoferrin have been shown to have desired
XX CC anti-inflammatory anti-infectious and anti-tumoural properties they
XX CC cannot be used clinically on a broad basis because of high production
XX CC costs. Therefore, provision of peptides based on lactoferrin would
XX CC enable them to be used for the same purposes as lactoferrin at lower
XX CC cost.
XX SQ Sequence 14 AA;

Query Match 94.4%; Score 67; DB 21; Length 14;
Best Local Similarity 91.7%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRNKRKAR 12
Db 3 CFQWQNRNKRKVR 14

RESULT 11
AAR98554
ID AAR98554 standard; Peptide; 15 AA.
XX AC AAR98554;
XX DT 12-NOV-1996 (first entry)
XX DE Peptide for anti-ulcer agent.
XX KW anti-ulcer agent; low toxicity; stable; heat-resistant.
XX OS Synthetic.
XX PN JP08143468-A.
XX XX
XX PD 04-JUN-1996.
XX PF 17-NOV-1994; 94JP-0283869.
XX PR 17-NOV-1994; 94JP-0283869.
XX PA (MORG) MORINAGA MILK IND CO LTD.
XX DR WPI; 1996-318857/32.
XX PT Anti-ulcer agent contg. peptide - has low toxicity, is
XX PT heat-resistant and water-soluble
XX PS Claim 1; Page 11; 11pp; Japanese.

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XX AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
XX in toxicity, is heat-resistant and stable in aqueous soln.. It can be
XX administered orally and be produced in large amounts.
XX SQ Sequence 15 AA;

Query Match 94.4%; Score 67; DB 17; Length 15;
Best Local Similarity 91.7%; Pred. No. 7.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRNKRKAR 12
Db 2 CFQWQNRNKRKVR 13

RESULT 12
AAY78035
ID AAY78035 standard; Peptide; 15 AA.
XX AC AAY78035;
XX DT 25-APR-2000 (first entry)
XX DE Human lactoferrin derived peptide SEQ ID NO:35.
XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX KW urinary tract infection; colitis; Candida infection; fungicidal;
XX KW bactericidal; preservative.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200001730-A1.
XX PD 13-JAN-2000.
XX PF 06-JUL-1999; 99WO-SE01230.
XX PR 06-JUL-1999; 98SE-0002441.
XX PR 17-JUL-1998; 98SE-0002562.
XX PR 29-DEC-1998; 98SE-0004614.
XX PA (ASCI-) A+ SCI INVEST AB.
XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX DR WPI; 2000-147388/13.
XX PT New peptides used for treatment and prevention of infections,
XX PT inflammations and tumors and for use in infant formula food -
XX PS Claim 12; Page 69; 102pp; English.
XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
XX CC lactoferrin. The peptides are taken up in the intestine through
XX CC binding to specific lactoferrin receptors and are then transported
XX CC through the circulation. A medicinal product of the peptide or fragment
XX CC can be used for treating and/or prevention of infections (such as
XX CC urinary tract infections, colitis, and Candida infection on a mucosal
XX CC membrane), inflammations and/or tumors. The peptides can also be used
XX CC in food stuffs such as infant formula food. The peptides are also
XX CC fungicidal and bactericidal and may also be used as preservatives.
XX CC Even though native human lactoferrin have been shown to have desired
XX CC anti-inflammatory anti-infectious and anti-tumoural properties they
XX CC cannot be used clinically on a broad basis because of high production
XX CC costs. Therefore, provision of peptides based on lactoferrin would
XX CC enable them to be used for the same purposes as lactoferrin at lower
XX CC cost.
XX SQ Sequence 15 AA;

```

Query Match 94.4%; Score 67; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 7.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKR 12
DB 4 CFQWQNNRKR 15

RESULT 13

AAV78062
ID AAV78062 standard; Peptide; 15 AA.

XX AC AAV78062;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:62.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX KW urinary tract infection; colitis; Candida infection; fungicidal;
XX KW bactericidal; preservative.

XX OS Homo sapiens.
XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 15; Page 81; 102pp; English.

XX CC AAV78001 to AAV78100 represent peptides having sequences based on human
XX CC lactoferrin. The peptides are taken up in the intestine through
XX CC binding to specific lactoferrin receptors and are then transported
XX CC through the circulation. A medicinal product of the peptide or fragment
XX CC can be used for treating and/or prevention of infections (such as
XX CC urinary tract infections, colitis, and Candida infection on a mucosal
XX CC membrane), inflammations and/or tumors. The peptides can also be used
XX CC in food stuffs such as infant formula food. The peptides are also
XX CC fungicidal and bactericidal and may also be used as preservatives.
XX CC Even though native human lactoferrin have been shown to have desired
XX CC anti-inflammatory anti-infectious and anti-tumoural properties they
XX CC cannot be used clinically on a broad basis because of high production
XX CC costs. Therefore, provision of peptides based on lactoferrin would
XX CC enable them to be used for the same purposes as lactoferrin at lower
XX CC cost.

XX SQ Sequence 15 AA;

Query Match 94.4%; Score 67; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 7.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKR 12
DB 4 CFQWQNNRKR 15

RESULT 14

AAV78063
ID AAV78063 standard; Peptide; 15 AA.

XX AC AAV78063;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:63.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX KW urinary tract infection; colitis; Candida infection; fungicidal;
XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 18; Page 81; 102pp; English.

XX CC AAV78001 to AAV78100 represent peptides having sequences based on human
XX CC lactoferrin. The peptides are taken up in the intestine through
XX CC binding to specific lactoferrin receptors and are then transported
XX CC through the circulation. A medicinal product of the peptide or fragment
XX CC can be used for treating and/or prevention of infections (such as
XX CC urinary tract infections, colitis, and Candida infection on a mucosal
XX CC membrane), inflammations and/or tumors. The peptides can also be used
XX CC in food stuffs such as infant formula food. The peptides are also
XX CC fungicidal and bactericidal and may also be used as preservatives.
XX CC Even though native human lactoferrin have been shown to have desired
XX CC anti-inflammatory anti-infectious and anti-tumoural properties they
XX CC cannot be used clinically on a broad basis because of high production
XX CC costs. Therefore, provision of peptides based on lactoferrin would
XX CC enable them to be used for the same purposes as lactoferrin at lower
XX CC cost.

XX SQ Sequence 15 AA;

Query Match 94.4%; Score 67; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 7.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKR 12
DB 4 CFQWQNNRKR 15

RESULT 15

AAV78031
ID AAV78031 standard; Peptide; 16 AA.

XX AC AAV78031;

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XX 25-APR-2000 (first entry)
DT
XX Human lactoferrin derived peptide SEQ ID NO:31.
DE
XX
XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX PN WC200001730-A1.
XX
XX 13-JAN-2000.
PD
XX
XX 06-JUL-1999; 99WO-SE01230.
XX
XX 06-JUL-1998; 98SE-0002441.
PR
XX 17-JUL-1998; 98SE-0002562.
PR
XX 29-DEC-1998; 98SE-0004614.
XX
XX (ASCII-) A+ SCI INVEST AB.
PA
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
PT
XX
XX Claim 11; Page 68; 102pp; English.
XX
XX AA78001 to AA78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX Sequence 16 AA;
SQ
Query Match 94.4%; Score 67; DB 21; Length 16;
Best Local Similarity 91.7%; Pred. No. 8.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWQNNRKR 12
DB 5 CFQWQNNRKR 16

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Job time : 28.35 secs

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OM protein - protein search, using sw model

Ran on: February 21, 2003, 07:25:59 ; Search time 8.65 Seconds
(without alignments)
40.818 Million cell updates/sec

Title: US-09-743-107B-78
Perfect score: 71
Sequence: 1 CFQWQNMEXAR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
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6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	94.4	18	1	US-08-204-487-3
2	67	94.4	18	2	US-08-485-948-8
3	67	94.4	18	2	US-08-628-380-8
4	67	94.4	18	2	US-08-475-055-8
5	67	94.4	20	1	US-07-755-161A-3
6	67	94.4	20	1	US-07-891-174-3
7	67	94.4	20	1	US-08-204-487-1
8	67	94.4	20	1	US-08-256-771-24
9	67	94.4	20	1	US-08-256-771-25
10	67	94.4	20	1	US-08-381-984-24
11	67	94.4	20	1	US-08-381-984-25
12	67	94.4	22	4	US-09-508-734-4
13	67	94.4	24	4	US-09-508-734-6
14	67	94.4	25	1	US-07-755-161A-10
15	67	94.4	25	1	US-07-891-174-10
16	67	94.4	25	1	US-08-204-487-7
17	67	94.4	29	4	US-09-508-734-8
18	67	94.4	36	1	US-07-755-161A-8
19	67	94.4	36	1	US-07-891-174-8
20	67	94.4	36	1	US-08-256-771-30
21	67	94.4	36	1	US-08-381-984-29
22	67	94.4	47	2	US-08-464-182A-6
23	67	94.4	47	2	US-08-406-271-6
24	67	94.4	50	2	US-08-693-274A-7
25	67	94.4	52	4	US-09-017-043A-3
26	67	94.4	53	2	US-08-464-182A-5
27	67	94.4	53	2	US-08-406-271-5

28	67	94.4	54	2	US-08-464-182A-2	Sequence 2, Appli
29	67	94.4	54	2	US-08-406-271-2	Sequence 2, Appli
30	67	94.4	694	3	US-08-724-586-2	Sequence 2, Appli
31	67	94.4	694	4	US-09-421-632-2	Sequence 2, Appli
32	67	94.4	694	4	US-09-932-190-2	Sequence 2, Appli
33	67	94.4	705	2	US-08-655-640-2	Sequence 2, Appli
34	67	94.4	708	2	US-08-655-640-4	Sequence 4, Appli
35	67	94.4	711	1	US-08-154-019-4	Sequence 4, Appli
36	67	94.4	711	1	US-08-461-333-4	Sequence 4, Appli
37	67	94.4	711	3	US-08-464-167-4	Sequence 4, Appli
38	67	94.4	711	3	US-09-158-313-4	Sequence 4, Appli
39	67	94.4	711	4	US-08-476-798-4	Sequence 2, Appli
40	64	90.1	711	1	US-08-145-681-2	Sequence 2, Appli
41	64	90.1	711	1	US-08-250-308-2	Sequence 2, Appli
42	64	90.1	711	1	US-08-453-703-2	Sequence 2, Appli
43	64	90.1	711	2	US-08-456-106-2	Sequence 2, Appli
44	64	90.1	711	3	US-08-456-108-2	Sequence 2, Appli
45	64	90.1	711	4	US-09-265-577-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOIKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: RJN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "HUMAN LACTOPERRIN PEPTIDE"

/ OTHER INFORMATION: (20-37) "
US-08-204-487-3

Query Match 94.4%; Score 67; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 1.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKAR 12
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Db 1 CFQWQRMNRKVR 12

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,948
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,217
; FILING DATE: JUNE 7, 1995
; APPLICATION NUMBER: 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-485-948-8

Query Match 94.4%; Score 67; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 1.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKAR 12
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Db 1 CFQWQRMNRKVR 12

RESULT 3

US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341
; GENERAL INFORMATION:
; APPLICANT: LI YONG MING
; APPLICANT: VLASSARA, HELEN
; APPLICANT: CERAMI, ANTHONY
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,380
; FILING DATE: April 4, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-628-380-8

Query Match 94.4%; Score 67; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 1.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKAR 12
| | | | | | | | | | | | | | | | | |
Db 1 CFQWQRMNRKVR 12

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; NUMBER OF SEQUENCES: 9


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;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Klauber & Jackson
;; STREET: 411 Hackensack Avenue
;; CITY: Hackensack
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07601
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/475.055
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/485,948
;; FILING DATE:
;; APPLICATION NUMBER: 08/488,217
;; FILING DATE: JUNE 7, 1995
;; APPLICATION NUMBER: 08/419,642
;; FILING DATE: APRIL 7, 1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 947-1-008A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; DESCRIPTION: LF-C1, 8-25
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
;;
US-08-475-055-8
Query Match 94.4%; Score 67; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 1.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFWQWRNMRKAR 12
Db 1 CFWQWRNMRKVR 12

RESULT 5
US-07-755-161A-3
; Sequence 3, Application US/07755161A
; Patent No. 5304633
;
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
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;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: DisplayWrite
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/755,161A
;; FILING DATE: 19910905
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX: 202-371-8855
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE:
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURES:
;; NAME/KEY: modified site
;; LOCATION: 2
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 19"
;; FEATURE:
;; NAME/KEY: modified site
;; LOCATION: 19
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 2"
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3
Query Match 94.4%; Score 67; DB 1; Length 20;
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Best Local Similarity 91.7%; Pred. No. 2.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRNRKAR 12
| | | | | | | | | |
Db 2 CFQWRNRKVR 13

RESULT 6
US-07-891-174-3
; Sequence 3, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLER:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site

; LOCATION: 2
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 19"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 19
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 2"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-07-891-174-3

Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRNRKAR 12
| | | | | | | | | |
Db 2 CFQWRNRKVR 13

RESULT 7
US-08-204-487-1
; Sequence 1, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIAKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESS: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/204,487
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FJN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000

```
TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..20
; OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
; OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
US-08-204-487-1

Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKAR 12
Db 2 CFQWQNRMRKVR 13

RESULT 8
US-08-256-771-24
; Sequence 24, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are linked by
; OTHER INFORMATION: disulfide bond"

Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKAR 12
Db 2 CFQWQNRMRKVR 13

RESULT 9
US-08-256-771-25
; Sequence 25, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are protected to
; OTHER INFORMATION: prevent disulfide bond"

Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKAR 12
Db 2 CFQWQNRMRKVR 13

RESULT 10
US-08-381-994-24
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US-08-256-771-24
Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKAR 12
Db 2 CFQWQNRMRKVR 13

RESULT 9
US-08-256-771-25
; Sequence 25, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are protected to
; OTHER INFORMATION: prevent disulfide bond"

Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKAR 12
Db 2 CFQWQNRMRKVR 13

RESULT 10
US-08-381-994-24
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Sequence 24, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
US-08-381-984-24
Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWQRMNRKAR 12
DB 2 CFQWQRMNRKVR 13
RESULT 11
US-08-381-984-25
Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
US-08-381-984-25
Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWQRMNRKAR 12
DB 2 CFQWQRMNRKVR 13
RESULT 12
US-09-508-734-4
Sequence 4, Application US/09508734
Patent No. 6423509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4

STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
US-08-381-984-25
Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWQRMNRKAR 12
DB 2 CFQWQRMNRKVR 13
RESULT 12
US-09-508-734-4
Sequence 4, Application US/09508734
Patent No. 6423509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4

LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
US-09-508-734-4

Query Match 94.4%; Score 67; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMVKAR 12
| | | | | | | | | | | | | | | | | | | | | |
DB 2 CFQWQRNMVKR 13

RESULT 13

US-09-508-734-6
Sequence 6, Application US/09508734
Patent No. 6423509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: KopatentIn 1.71
SEQ ID NO 6
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
US-09-508-734-6

Query Match 94.4%; Score 67; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 2.5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMVKAR 12
| | | | | | | | | | | | | | | | | | | | | |
DB 3 CFQWQRNMVKR 14

RESULT 14

US-07-755-161A-10
Sequence 10, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:

ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:

CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:

FEATURE:
NAME/KEY: modified site

LOCATION: 4

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"

FEATURE:

NAME/KEY: modified site

LOCATION: 21

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10

Query Match 94.4%; Score 67; DB 1; Length 25;

Best Local Similarity 91.7%; Pred. No. 2.6e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMVKAR 12

| | | | | | | | | | | | | | | | | | | | | |

DB 4 CFQWQRNMVKR 15

RESULT 15

US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21

IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
Query Match 94.4%; Score 67; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 2.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWQRNWRKAR 12
DB 4 CFQWQRNWRKVR 15
Search completed: February 21, 2003, 07:50:35
Job time : 9.7 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds
(without alignments)
35.508 Million cell updates/sec

Title: US-09-743-107b-78
Perfect score: 71
Sequence: 1 CFQWQRNMRKAR 12

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_FUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_FUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_FUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_FUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_FUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_FUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_FUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	94.4	15	9	US-09-798-869-2
2	67	94.4	25	9	US-09-798-869-20
3	67	94.4	694	9	US-10-023-096-2
4	59	83.1	15	9	US-09-798-869-6
5	53	74.6	15	9	US-09-798-869-3
6	53	74.6	25	9	US-09-798-869-23
7	45	63.4	15	9	US-09-798-869-7
8	41	57.7	15	9	US-09-798-869-4
9	41	57.7	15	9	US-09-798-869-29
10	41	57.7	15	9	US-09-798-869-30
11	41	57.7	25	9	US-09-798-869-22
12	38	53.5	15	9	US-09-798-869-8
13	37	52.1	21	10	US-09-864-761-47985
14	37	52.1	489	9	US-09-868-320-2
15	36	50.7	209	10	US-09-904-536-8
16	36	50.7	209	10	US-09-904-536-9
17	36	50.7	209	10	US-09-904-536-11
18	36	50.7	209	10	US-09-904-536-12
19	36	50.7	209	10	US-09-904-536-13

20	36	50.7	209	10	US-09-904-536-14	Sequence 14, Appl
21	36	50.7	209	10	US-09-904-536-15	Sequence 15, Appl
22	36	50.7	209	10	US-09-904-536-16	Sequence 16, Appl
23	36	50.7	209	10	US-09-904-536-17	Sequence 17, Appl
24	36	50.7	209	10	US-09-904-536-18	Sequence 18, Appl
25	36	50.7	212	10	US-09-904-536-10	Sequence 10, Appl
26	36	50.7	235	9	US-10-095-449-6	Sequence 6, Appl
27	36	50.7	235	10	US-09-448-378-1	Sequence 1, Appl
28	36	50.7	235	10	US-09-983-806-6	Sequence 6, Appl
29	36	50.7	235	10	US-09-904-536-1	Sequence 1, Appl
30	36	50.7	607	9	US-09-881-579-10	Sequence 10, Appl
31	36	50.7	688	9	US-09-881-579-15	Sequence 15, Appl
32	35	49.3	97	9	US-09-738-626-5597	Sequence 5597, Ap
33	35	49.3	738	9	US-10-173-123-13	Sequence 13, Appl
34	35	49.3	745	9	US-10-173-123-11	Sequence 11, Appl
35	35	49.3	846	9	US-10-051-409-4	Sequence 4, Appl
36	34	47.9	15	9	US-09-798-869-5	Sequence 5, Appl
37	34	47.9	40	10	US-09-864-761-46393	Sequence 46393, A
38	34	47.9	95	10	US-09-764-864-1031	Sequence 1031, Ap
39	34	47.9	119	10	US-09-205-658-244	Sequence 244, App
40	34	47.9	239	10	US-09-864-761-37353	Sequence 37353, A
41	34	47.9	338	9	US-09-978-295A-119	Sequence 119, App
42	34	47.9	338	9	US-09-978-697-119	Sequence 119, App
43	34	47.9	338	9	US-09-978-192A-119	Sequence 119, App
44	34	47.9	338	9	US-09-999-832A-119	Sequence 119, App
45	34	47.9	338	9	US-09-978-189-119	Sequence 119, App

ALIGNMENTS

RESULT 1

US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798, 869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB8818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2

Query Match 94.4% ; Score 67; DB 9; Length 15;
Best Local Similarity 91.7% ; Pred. No. 2.4e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0;

QY 1 CFQWQRNMRKAR 12
DB 3 CFQWQRNMRKVR 14

RESULT 2

US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON

```
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match      94.4%; Score 67; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CFQWQNNMKR 12
      |||||
Db      3 CFQWQNNMKR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; TITLE OF INVENTION: Lactoferrin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William B.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-023-096-2
```

```
Query Match      94.4%; Score 67; DB 9; Length 694;
Best Local Similarity 91.7%; Pred. No. 0.00087;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CFQWQNNMKR 12
      |||||
Db      22 CFQWQNNMKR 33

RESULT 4
US-09-798-869-6
; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-6

Query Match      83.1%; Score 59; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.00052;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CFQWQNNMKR 12
      |||||
Db      3 CFQWQNNMKR 14

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-3

Query Match      74.6%; Score 53; DB 9; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.0052;
```


Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRK 10
|:|:|:|:|:|:|
Db 3 CYQWQRMNRK 12

RESULT 6
US-09-798-869-23
; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23

Query Match 74.6%; Score 53; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.0084;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRK 10
|:|:|:|:|:|:|
Db 3 CYQWQRMNRK 12

RESULT 7
US-09-798-869-7
; Sequence 7, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-7

Query Match 63.4%; Score 45; DB 9; Length 15;
Best Local Similarity 70.0%; Pred. No. 0.11;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMNRK 10
|:|:|:|:|:|:|
Db 3 CYQWQRMNRK 12

RESULT 8
US-09-798-869-4
; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4

Query Match 57.7%; Score 41; DB 9; Length 15;
Best Local Similarity 60.0%; Pred. No. 0.53;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMNRK 10
|:|:|:|:|:|:|
Db 3 CLRWQRMNRK 12

RESULT 9
US-09-798-869-29
; Sequence 29, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29

Query Match 57.7%; Score 41; DB 9; Length 15;
Best Local Similarity 60.0%; Pred. No. 0.53;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMNRK 10
|:|:|:|:|:|:|
Db 3 CLRWQRMNRK 12

RESULT 10

```

US-09-798-869-30
; Sequence 30, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (VSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ(RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/G899/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9819938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-30

```

RESULT 11

```

US-09-798-869-22
; Sequence 22, Application US/09798869
; Publication No. US2003022821A1
;
; GENERAL INFORMATION:
;
; APPLICANT: JOHN SIGURD SVENSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVIRINJAT (RNSSON
; APPLICANT: LARS VORLAND
;
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
;
; FILE REFERENCE: A34049-PCT-USA-A
;
; CURRENT APPLICATION NUMBER: US/09/798,869
;
; CURRENT FILING DATE: 2001-03-27
;
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
;
; PRIOR FILING DATE: 1999-08-31
;
; PRIOR APPLICATION NUMBER: GB9818938.4
;
; PRIOR FILING DATE: 1998-08-28
;
; NUMBER OF SEQ ID NOS: 30
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 22
;
; LENGTH: 25
;
; TYPE: PRT
;
; ORGANISM: MURINE
;
US-09-798-869-22

```

RESULT 12.

RESOL 12
US-09-798-869-8
; Sequence 8, Application US/09798869
; Publication No. US20030022821A1
: GENERAL INFORMATION:

```

/ APPLICANT: JOHN SIGURD SVENDSEN
/
/ APPLICANT: (YSTEIN REKDAL
/ APPLICANT: BALDUR SVEINUG (RNSSON
/ APPLICANT: LARS VORLAND
/ TITLE OF INVENTION: BIOACTIVE PEPTIDES
/ FILE REFERENCE: A34049-PCT-USA-A
/ CURRENT APPLICATION NUMBER: US/09/798,869
/ CURRENT FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: PCT/GB99/02851
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: GB9818938.4
/ PRIOR FILING DATE: 1998-08-28
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine
/ - OTHER INFORMATION: sequence)
/ IS-09-798-869-8

```

RESULT 13

US-09-864-761-47985
; Sequence 47985, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47985
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL096701.14
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EST_HUMAN HIT: AW294800.1, EVALUATE 1.00e-06
US-09-864-761-47985

Query Match 52.1%; Score 37; DB 10; Length 21;
Best Local Similarity 83.3%; Pred. No. 3.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWR 6
|||:
Db 16 CFQWR 21

RESULT 14
US-09-888-320-2
; Sequence 2, Application US/09888320
; Publication No. US20030013090A1
; GENERAL INFORMATION:
; APPLICANT: Barry III, Clifton E.
; APPLICANT: DeBarber, Andrea E.
; APPLICANT: Mdull, Khisimuzi
; APPLICANT: Bekker, Linda-Gail
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
; FILE REFERENCE: 015280-41310005
; CURRENT APPLICATION NUMBER: US/09/888,320
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/214,187
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: wild-type BtaA monooxygenase (Rv3854C, EthA)
US-09-888-320-2

Query Match 52.1%; Score 37; DB 9; Length 489;
Best Local Similarity 60.0%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWRNRK 10
|||:
Db 253 CQWPRYRK 262

RESULT 15
US-09-904-536-8
; Sequence 8, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:

; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-8

Query Match 50.7%; Score 36; DB 10; Length 209;
Best Local Similarity 50.0%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWRNRK 10
|||:
Db 178 CLHWQTRRR 187

Search completed: February 21, 2003, 08:08:06
Job time : 10.55 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 / Search time 9.6 Seconds
(without alignments)
120.168 Million cell updates/sec

Title: US-09-743-107b-78

Perfect score: 71

Sequence: 1 CFQQRNRYKAR 12

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 73.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	94.4	711	1 TFHUL	lactotransferrin p
2	53	74.6	708	2 JC2323	lactoferrin - goat
3	50	70.4	33	2 S52107	lactoferrin - sheep
4	43	60.6	298	2 AD2346	hypothetical prote
5	42	59.2	4568	2 T08030	dynein beta heavy
6	41	57.7	222	2 H70978	hypothetical prote
7	41	57.7	275	2 T22597	hypothetical prote
8	41	57.7	707	1 A28438	lactoferrin precu
9	40	56.3	584	2 C84325	hypothetical prote
10	39	54.9	742	2 T25415	hypothetical prote
11	39	54.9	1693	2 AC3240	helicase, SNF2 fam
12	38	53.5	205	2 B30094	26S proteasome SU
13	38	53.5	275	1 JCL113	interleukin-2 rece
14	38	53.5	275	1 S07442	interleukin-2 rece
15	38	53.5	397	2 T35361	hypothetical prote
16	38	53.5	464	2 A12343	hypothetical prote
17	38	53.5	511	2 AB0858	probable cytochrom
18	38	53.5	515	2 T00510	cytochrome P450 ho
19	38	53.5	543	2 T00513	cell division prot
20	37.5	52.8	425	2 H44185	potassium channel p
21	37	52.1	135	2 JCS272	interleukin-2 rece
22	37	52.1	272	1 UHHU2	apolipoprotein B-1
23	37	52.1	274	2 B60950	cell cycle arrest
24	37	52.1	306	1 A39654	hypothetical prote
25	37	52.1	361	2 T29571	glutamine syntheta
26	37	52.1	367	2 G97649	anthranilate synth
27	37	52.1	487	2 A82835	probable monooxyge
28	37	52.1	489	2 C70655	hypothetical sh3-c
29	37	52.1	501	2 T39801	hypothetical sh3-c

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N/Alternate names: lactoferrin

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74

R/Cho. Y.

submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:X53961; NID:G467236; PIDN:AAB60324.1; PID:G467237

R/Rey, M.M.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; MUID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>

A/Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactofer

A/Reference number: A45401; MUID:93125571; PMID:1480183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <TEN>

A/Cross-references: GB:S52659; NID:G263311; PIDN:AAB24877.1; PID:G263312

A/Experimental source: placenta

A/Note: sequence extracted from NCBI backbone (NCBIP:122202)

R/Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; MUID:90326549; PMID:2374734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POW>

A/Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A/Reference number: S15853; MUID:91264786; PMID:2049066

A/Accession: S15853

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 20-31 <ST1>

A/Accession: S20841

A/Molecule type: Protein

A/Residues: 20-28, 'X', 30-31 <ST2>

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
 Blood 70, 989-993, 1997
 A>Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
 A:Reference number: S07160; MUID:8001031; PMID:3477300
 A:Accession: S07160
 A:Molecule type: mRNA
 A:Residues: 436-487, 'A', 489-711 <RAD>
 A:Cross-references: EMBL:M18642; NID:g186815; PIDN:AAA86665.1; PID:g386855
 R;Parella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
 Cancer Res. 51, 3037-3043, 1991
 A>Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
 A:Reference number: A61169; MUID:91235214; PMID:1674448
 A:Accession: A61169
 A:Molecule type: conceptual translation
 A>Status: not compared with conceptual translation
 A:Residues: 3-701, 'SKPKVN' <PAN>
 A:Experimental source: normal breast tissue
 R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.; Eur. J. Biochem. 145, 659-666, 1984
 A>Title: Human lactotransferrin: amino acid sequence and structural comparisons with other
 A:Reference number: A31000; MUID:85076667; PMID:6510420
 A:Accession: A31000
 A:Molecule type: protein
 A:Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4
 A>Note: this is the final paper in a series
 R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L. Eur. J. Biochem. 241, 303-308, 1996
 A>Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity
 A:Reference number: S74119; MUID:97054624; PMID:8898921
 A:Accession: S74119
 A:Molecule type: protein
 A:Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOV>
 A:Experimental source: neutrophil granulocytes
 C:Genetics:
 A:Gene: GDB:LTF
 A:Cross-references: GDB:119368; OMIM:150210
 A:Map position: 3q21-3q23
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron binding; milk
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-711/Product: lactotransferrin #status experimental <MAT>
 F:21-356/Domain: transferrin repeat homology <TRH1>
 F:360-699/Domain: transferrin repeat homology <TRH2>
 F:23-65,39-56,135-218,177-193,190-201,251-285,503-597,595-609/disulfide bonds: #status e
 F:458,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:368-400,387-391,425-706,447-669,479-554,513-527,524-537,647-652/disulfide bonds: #stat

Query Match 94.4%; Score 67; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.00058;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQNNRKR 12
 | | | | | | | | | | | | | |
 Db 39 CFQWQNNRKR 50

RESULT 2
 JC2323
 Lactoferrin - goat
 C:Species: Capra aegagrus hircus (domestic goat)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 C:Accession: JC2323
 R;Le Provost, F.; Nocard, M.; Guerin, G.; Martin, P. Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A>Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
 A:Reference number: JC2323; MUID:94380047; PMID:8093048
 A:Accession: JC2323
 A:Molecule type: mRNA
 A:Residues: 1-708 <LEP>
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:359-696/Domain: transferrin repeat homology <TRH2>
 F:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 74.6%; Score 53; DB 2; Length 708;
 Best Local Similarity 80.0%; Pred. No. 0.17;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKR 10
 | | | | | | | | | |

Db 38 CFQWQNNRKR 47
 | | | | | | | | | |

RESULT 3

S52107
 Lactoferrin - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
 C:Accession: S52107
 R;Qian, Z.Y.; Jolles, P.; Magliore-Samour, D.; Fiat, A.M. Biochim. Biophys. Acta 1243, 25-32, 1995
 A>Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet
 A:Reference number: S52107; MUID:95127729; PMID:7827104
 A:Accession: S52107
 A>Status: Preliminary
 A:Molecule type: protein
 A:Residues: 1-33 <QIA>
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication

Query Match 70.4%; Score 50; DB 2; Length 33;
 Best Local Similarity 70.0%; Pred. No. 0.028;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKR 10
 | | | | | | | | | |

Db 19 CFQWQNNRKR 28
 | | | | | | | | | |

RESULT 4

AD2346
 hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.
 A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AD2346
 R;Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
 Nakazaki, N.; Shampo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
 DNA Res. 8, 205-213, 2001
 A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AD2346
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-298 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA076022.1; PID:g17133459; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr4323

Query Match 60.6%; Score 43; DB 2; Length 298;
 Best Local Similarity 70.0%; Pred. No. 4.3;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNNRKR 11
 | | | | | | | | | |

Db 163 FQWQNNRKR 172
 | | | | | | | | | |

RESULT 5

T08030
 dynein beta heavy chain - Chlamydomonas reinhardtii
 C:Species: Chlamydomonas reinhardtii
 C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
 A:Reference number: T08030
 A:Accession: T08030
 R;Mitchell, D.R.; Brown, K.S.

J. Cell Sci. 107, 635-644, 1994
 A>Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
 A:Reference number: Z16302; MUID:94274778; PMID:8066077
 A:Accession: T08030
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-4568 <MIT>
 A:CROSS-references: EMBL:U02963; NID:9409965; PIDN:AAAL19956.1; PID:g514215
 A:Experimental source: strain 21gr
 C:Genetics:
 A:Gene: ODA4
 A:Map position: IX
 A:Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 3334/3; 3686/3; 3882/3; 4240/3
 C:Superfamily: dynein heavy chain, ciliary
 C:Keywords: nucleotide binding; p-loop
 F:1919-1926/Region: nucleotide-binding motif A (p-loop)
 F:2202-2209/Region: nucleotide-binding motif A (p-loop)
 F:2530-2537/Region: nucleotide-binding motif A (p-loop)

Query Match 59.2%; Score 42; DB 2; Length 4568;
 Best Local Similarity 66.7%; Pred. No. 96;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRK 9
 |||||:
 Db 1852 CFQWQSQLR 1860

RESULT 6
 H70978
 hypothetical protein RV3271c - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2000
 C:Accession: H70978
 C:Col: S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A:Authors: Scars, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: H70978
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-222 <COL>
 A:CROSS-references: GB:Z92771; GB:AL123456; NID:g3242259; PIDN:CAB07084.1; PID:e306655;
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: RV3271c
 C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV3271c

Query Match 57.7%; Score 41; DB 2; Length 222;
 Best Local Similarity 70.0%; Pred. No. 7.3;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWQNRK 12
 :|||:
 Db 24 EWQNRVWAR 33

RESULT 7
 T22597
 hypothetical protein F53H4.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C:Accession: T22597
 R:Dobson, R.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19587
 A:Accession: T22597
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-275 <WIL>
 A:CROSS-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
 A:Experimental source: clone F53H4
 C:Genetics:
 A:Gene: CESP.F53H4.4
 A:Map position: X
 A:Introns: 67/1; 153/1
 C:Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4

Query Match 57.7%; Score 41; DB 2; Length 275;
 Best Local Similarity 63.6%; Pred. No. 9;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNRK 12
 |||||:
 Db 262 FQWQNRK 272

RESULT 8
 A28438
 lactoferrin precursor - mouse
 N:Alternate names: lactotransferrin
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A28438; A1205
 R:Pentecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A>Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre
 A:Reference number: A92596; MUID:87280033; PMID:3611056
 A:Accession: A28438
 A:Molecule type: mRNA
 A:Residues: 3-707 <PEN>
 A:CROSS-references: EMBL:J03298
 R:Jiu, Y.; Teng, C.T.
 J. Biol. Chem. 266, 21880-21885, 1991
 A>Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
 A:Reference number: A41205; MUID:92042099; PMID:1939212
 A:Accession: A41205
 A:Molecule type: DNA
 A:Residues: 1-15 <LIU>
 A:CROSS-references: GB:M74778
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-707/Product: lactotransferrin #status predicted <MAT>
 F:358-595/Domain: transferrin repeat homology <TRH2>
 F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.7%; Score 41; DB 1; Length 707;
 Best Local Similarity 60.0%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNRK 10
 :|||:
 Db 37 CLRQWNRK 46

RESULT 9
 C84325
 hypothetical protein Vngl732c [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: C84325
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A>Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: C84325
 A>Status: preliminary
 A:Molecule type: DNA

A;Residues: 1-584 <STO>
 A;Cross-references: GB:AE004437; NID:G10581192; PIDN:AA619967.1; GSPDB:GN00138
 A;Genetics:
 A;Gene: VNG1732C

Query Match 56.3%; Score 40; DB 2; Length 584;
 Best Local Similarity 41.7%; Pred. No. 29;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWQNNRKAR 12
 |||:|:|:
 Db 445 CFTWRKMERKR 456

RESULT 10
 T25415
 hypothetical protein T28D6.5 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C;Accession: T25415
 R;Wilkinson, J.
 submitted to the EMBL Data Library, October 1996
 A;Reference number: Z20031
 A;Accession: T25415
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-742 <WIL>
 A;Cross-references: EMBL:Z81134; PIDN:CAB03450.1; GSPDB:GN00021; CESP:T28D6.5
 A;Experimental source: clone T28D6
 C;Genetics:
 A;Gene: CESP:T28D6.5
 A;Map position: 3
 A;Introns: 9/3; 36/3; 70/3; 112/3; 258/3; 319/3; 468/2; 586/1; 638/3; 671/1
 C;Superfamily: Caenorhabditis elegans hypothetical protein T28D6.5

Query Match 54.9%; Score 39; DB 2; Length 742;
 Best Local Similarity 50.8%; Pred. No. 54;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CFQWQNNRKAR 12
 |||:|:|:
 Db 193 CFRWVRKSKAK 204

RESULT 11
 AC3240
 helicase, SNF2 family [imported] - Agrobacterium tumefaciens (strain C58, Dupont) plasmid
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C;Accession: AC3240
 R;Wood, D.W.; Sebval, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; PMID:11743193
 A;Accession: AC3240
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1693 <KUP>
 A;Cross-references: GB:AE008690; PIDN:AAL46337.1; PID:G17744125; GSPDB:GN00189
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu6101
 A;Genome: plasmid

Query Match 54.9%; Score 39; DB 2; Length 1693;
 Best Local Similarity 77.8%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 WQNNRKAR 12

Db 1429 WONNERKAR 1437
 |||:|:|:

RESULT 12
 E90094
 26S proteasome SU B5 [imported] - Guillardia theta nucleomorph
 C;Species: nucleomorph Guillardia theta
 A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
 C;Accession: E90094
 R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Re;
 Nature 410, 1091-1096, 2001
 A;Title: The highly reduced genome of an enslaved algal nucleus.
 A;Reference number: A99082; MUID:11323671; PMID:11323671
 A;Accession: E90094
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-205 <DOU>
 A;Cross-references: GB:AF165818; NID:G13794510; PIDN:AAK39885.1; GSPDB:GN00150
 C;Genetics:
 A;Gene: pr8B5
 A;Map position: 1
 A;Genome: nucleomorph
 C;Keywords: nucleomorph

Query Match 53.5%; Score 38; DB 2; Length 205;
 Best Local Similarity 62.5%; Pred. No. 23;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQNNRM 8
 |||:|:|:
 Db 63 CFFWERNL 70

RESULT 13
 JC1113
 interleukin-2 receptor alpha chain precursor - sheep
 N;Alternate names: CD25
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 11-Sep-1998 #sequence_revision 11-Sep-1998 #text_change 22-Jun-1999
 C;Accession: JC1113; S18899; S18910
 R;Bujdosó, R.; Sargan, D.; Williamson, M.; McConnell, I.
 Gene 113, 283-284, 1992
 A;Title: Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa protein, CD;
 A;Reference number: JC1113; MUID:92241682; PMID:1572550
 A;Accession: JC1113
 A;Molecule type: mRNA
 A;Residues: 1-275 <BU>
 A;Cross-references: EMBL:X60149; NID:G1287; PIDN:CAA42723.1; PID:G1288
 R;Verhagen, A.A.
 submitted to the EMBL Data Library, December 1991
 A;Description: Molecular cloning, expression and characterisation of the ovine IL-2R al;
 A;Reference number: S18899
 A;Accession: S18899
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-165, 'S', 167-275 <VER>
 A;Cross-references: EMBL:Z11560; NID:G1275; PIDN:CAA77652.1; PID:G1276
 C;Complex: The high affinity receptor is a heterotrimer of alpha, beta, and gamma chain
 C;Function:
 A;Description: receptor for interleukin-2
 A;Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK
 C;Superfamily: interleukin-2 receptor alpha chain; complement factor H repeat homology
 C;Keywords: cytokine receptor; duplication; glycoprotein; T-cell proliferation; transmem
 F;1-21/Domain: signal sequence #status predicted <SIG>
 F;22-275/Product: interleukin-2 receptor alpha chain #status predicted <NAT>
 F;22-243/Domain: extracellular #status predicted <EXT>
 F;24-77/Domain: complement factor H repeat homology <PH1>
 F;123-184/Domain: complement factor H repeat homology <PH2>
 F;244-264/Domain: transmembrane #status predicted <TMW>
 F;265-275/Domain: intracellular #status predicted <INT>
 F;24-64, 51-77, 123-168, 152-184/Disulfide bonds: #status predicted

F;80/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 53.5%; Score 38; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CFQWQNRKAR 12
| | | | |
Db 261 CLTWQRWKKNR 272

RESULT 14

S07442
Interleukin-2 receptor alpha chain precursor - bovine
N:Alternate names: CD25
C:Species: Bos primigenius taurus (cattle)
C:Date: 11-Sep-1998 #sequence_revision 11-Sep-1998 #text_change 22-Jun-1999
C:Accession: S07442
R:Weinberg, A.D.; Shaw, J.; Paetkau, V.; Bleackley, R.C.; Magnuson, N.S.; Reeves, R.; Ma
Immunology 63, 603-610, 1988
A:Title: Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).
A:Reference number: S07442; MUID:88212503; PMID:2835311
A:Accession: S07442
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-275 <WEI>
A:Cross-references: EMBL:M20818; NID:G163208; PIDN:AAA51414.1; PID:G163209
C:Function: The high affinity receptor is a heterotrimer of alpha, beta, and gamma chains
A:Description: receptor for interleukin-2
A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK c
C:Superfamily: interleukin-2 receptor alpha chain; complement factor H repeat homology
C:Keywords: cytokine receptor; duplication; glycoprotein; T-cell proliferation; transmem
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-275/Product: interleukin-2 receptor alpha chain #status predicted <MAT>
F:22-243/Domain: extracellular #status predicted <EXT>
F:24-77/Domain: complement factor H repeat homology <PH1>
F:123-184/Domain: complement factor H repeat homology <PH2>
F:244-284/Domain: transmembrane #status predicted <TM>
F:265-275/Domain: intracellular #status predicted <INT>
F:24-64,51-77,123-168,152-184/Disulfide bonds: #status predicted
F:80,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 53.5%; Score 38; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CFQWQNRKAR 12
| | | | |
Db 261 CLTWQRWKKNR 272

RESULT 15

T35361
Hypothetical protein SC66T3.04 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T35361
R:Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A:Reference number: Z21576
A:Accession: T35361
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-397 <MUR>
A:Cross-references: EMBL:AL079348; PIDN:CAB45460.1; GSPDB:GN000070; SCOEDB:SC66T3.04
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC66T3.04

Query Match 53.5%; Score 38; DB 2; Length 397;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WQNNMEKA 11
| | | | |
Db 206 WRRNIRKA 213

Search completed: February 21, 2003, 07:47:50
Job time: 10.65 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 / Search time 4.6 Seconds
(without alignments)
108.199 Million cell updates/sec

Title: US-09-743-107B-78

Perfect score: 71

Sequence: 1 CFQQRNRKAR 12

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	94.4	711	1 TRFL_HUMAN	P02788 homo sapien
2	53	74.6	708	1 TRFL_CAPHI	Q29477 capra hircu
3	50	70.4	708	1 TRFL_CAMDR	Q9tun0 camelus dro
4	42	59.2	695	1 TRFL_HORSE	Q77811 equus caball
5	42	59.2	4568	1 DYHE_CHLRE	Q39565 chlamydomon
6	41	57.7	707	1 TRFL_MOUSE	P08071 mus musculu
7	38	53.5	146	1 RPOB_LIBAF	P41187 liberibacte
8	38	53.5	275	1 IL2A_BOVIN	P12342 bos taurus
9	38	53.5	275	1 IL2A_SHEEP	P26898 ovis aries
10	37.5	52.8	425	1 FTSA_HARIN	P45068 haemophilus
11	37	52.1	272	1 IL2A_HUMAN	P01589 homo sapien
12	37	52.1	222	1 NLA_DROME	Q9x218 drosophila
13	37	52.1	306	1 BUB2_YEAST	P26448 saccharomyc
14	37	52.1	455	1 YKYL_CABEL	Q19910 caenorhabdi
15	37	52.1	1293	1 XPC_DROME	Q24595 drosophila
16	36	50.7	62	1 RL32_AQUAE	Q67187 aquifex aeo
17	36	50.7	214	1 VIF_SIVS4	P12505 simian immu
18	36	50.7	235	1 FL3E_HUMAN	P49771 homo sapien
19	36	50.7	267	1 IL2A_RAT	P26897 rattus norv
20	36	50.7	268	1 IL2A_CANFA	O62802 canis fami
21	36	50.7	275	1 IL2A_FELCA	P41690 felis silve
22	36	50.7	2483	1 COA2_HUMAN	O00763 homo sapien
23	35	49.3	85	1 PMRD_SALTY	P37589 salmonella
24	35	49.3	159	1 YICN_ECOLI	P31439 escherichia
25	35	49.3	428	1 SYH_CHLMU	Q9PJ19 chlamydia m
26	35	49.3	502	1 C911_ARATH	Q9f565 arabidopsis
27	35	49.3	663	1 PD11_HUMAN	Q9ulc6 homo sapien
28	35	49.3	728	1 KDG1_ARATH	Q39017 arabidopsis
29	35	49.3	765	1 Y008_HUMAN	Q15398 homo sapien
30	35	49.3	1179	1 ATX1_ARATH	Q91t02 arabidopsis
31	35	49.3	1213	1 T2D2_DROME	Q24325 drosophila
32	35	49.3	2671	1 IF3T_HUMAN	Q14573 homo sapien
33	35	49.3	3680	1 DMD_CANFA	O97592 canis fami

RESULT 1

ID	TRFL_HUMAN	STANDARD;	PRT;	711 AA.
AC	P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96KZ4;			
AC	Q96KZ5;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin A;			
DE	Lactoferrin B; Lactoferrin C]			
GN	LTF OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RX	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper P.R.;			
RT	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RL	Nucleic Acids Res. 18:5288-5288(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cho Y.Y.;			
RL	Thesis (1994), Genetic Engineering Research Institute / Taejeon, Korea.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Connely C.M.;			
RL	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RT	"Molecular cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Rado T.A.;			
RT	"Human neutrophil lactoferrin coding and 5' flanking region DNA			
RL	sequences.";			
RN	[6]			
RP	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cheng H., Chen X., Huan L.;			
RT	"cDNA cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Straussberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN	[8]			

ALIGNMENTS

34	34	47.9	155	1	Y481_SINY3	Q55827 synechocyst
35	34	47.9	211	1	LOLB_VIBCH	P57070 vibrio chol
36	34	47.9	215	1	VIF_HV2SB	P12452 human immun
37	34	47.9	215	1	VIF_HV2ST	P20878 human immun
38	34	47.9	246	1	Y495_SINY3	Q55185 synechocyst
39	34	47.9	316	1	NQRC_CHLTR	O84281 chlamydia t
40	34	47.9	369	1	SP11_MYXVL	P12393 myxoma viru
41	34	47.9	401	1	O88A_DROME	Q9vfn2 drosophila
42	34	47.9	410	1	SECY_CYACA	P46249 cyanidium c
43	34	47.9	538	1	RO60_HUMAN	P10155 homo sapien
44	34	47.9	538	1	RO60_MOUSE	O08848 mus musculu
45	34	47.9	538	1	RO60_XENLA	P42700 xenopus lae

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE=Mammary Gland;
RX MEDLINE=90326549; PubMed=2374734;
RT Powell M.J., Ouden J.E.;
RA "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
RT Legrand D., Spik G., Montreuil J., Jolles P.;
RT "Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1984).
RN [10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RT Jolles P.;
RT "The present state of the human lactotransferrin sequence. Study and
RT alignment of the cyanogen bromide fragments and characterization of
RT N- and C-terminal domains.";
RL Biochim. Biophys. Acta 670:243-254(1981).
RN [11]
RP SEQUENCE OF 608-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J.,
RT Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
RT lactotransferrin.";
RL FEBS Lett. 142:107-110(1982).
RN [12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
RN [13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RN Nham M., Parrell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desliva U.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sagripanti J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human diferric lactoferrin refined at 2.2-A
RT resolution.";
RL Acta Crystallogr. D 51:629-646(1995).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
RA Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RT 253-->methionine mutant.";
RL Biochemistry 36:341-346(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in Aspergillus
RT awamori.";
RL Acta Crystallogr. D 55:403-407(1999).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
RT and analysis of ligand-induced conformational change.";
RL Acta Crystallogr. D 54:1319-1335(1998).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of opioid antagonist peptides derived
RT from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810(1990).
RN [20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
RA Qumsiyeh M.B., Lin P.-Y., Baati S., Reddy M.K., Kanai A., Hotta Y.,
RA Sugar J., Kumaramanickavel G., Munier P., Schorderet D.F.,
RA El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
RA Hejtmancik J.F., Teng C.T.;
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RL Mol. Vision 4:31-32(1998).
RN -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
RN -1- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
RN -1- SUBUNIT: MONOMER.
RN -1- SUBCELLULAR LOCATION: Secreted.
RN -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
RN -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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Query Match 94.4%; Score 67; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.00022;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRKVR 12
 |||||
 Db 39 CFQWQNRKVR 50

RESULT 2

TRFL CAPHI STANDARD; PRT; 708 AA.
 AC Q29477; Q29479;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactoferrin precursor (Lactoferrin).
 GN LTF.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;
 RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA MEDLINE=9438004; PubMed=8093048;
 RA le Provost F., Nocart M., Guerin G., Martin P.;
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the
 relevant locus to bovine U12 synteny group."
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 OF AN ANION, USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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 or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; U53857; AAA97958.1; --
 DR EMBL; X78902; CAA55517.1; --
 DR HSP; O77698; ICE2
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN 1; 2.
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.
 DR PROSITE; PS00207; TRANSFERRIN 3; 2.
 KM Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 708
 FT REPEAT 20 363
 FT REPEAT 364 708
 FT DISULFID 28 64
 FT DISULFID 38 55
 FT DISULFID 134 217
 FT DISULFID 176 192

FT DISULFID 189
 FT DISULFID 250
 FT DISULFID 367
 FT DISULFID 377
 FT DISULFID 424
 FT DISULFID 444
 FT DISULFID 476
 FT DISULFID 500
 FT DISULFID 510
 FT DISULFID 521
 FT DISULFID 592
 FT DISULFID 644
 FT METAL 79
 FT METAL 111
 FT METAL 211
 FT METAL 272
 FT METAL 414
 FT METAL 452
 FT METAL 545
 FT METAL 614
 FT BINDING 140
 FT BINDING 482
 FT CARBOHYD 252
 FT CARBOHYD 300
 FT CARBOHYD 387
 FT CARBOHYD 495
 FT CARBOHYD 564
 FT CONFLICT 56
 FT CONFLICT 88
 FT CONFLICT 124
 FT CONFLICT 154
 FT CONFLICT 304
 FT CONFLICT 414
 SQ SEQUENCE 708 AA; 77358 MW; P2EDA3C83539960D CRC64;

Query Match 74.6%; Score 53; DB 1; Length 708;

Best Local Similarity 80.0%; Pred. No. 0.066;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRKVR 10
 |||||
 Db 38 CFQWQNRKVR 47

RESULT 3

TRFL CAMDR STANDARD; PRT; 708 AA.
 ID TRFL CAMDR
 AC Q9TUM0; Q9MZS5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;
 RA Kapeller S.R., Ackermann M., Farah Z., Puhon Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin";
 RL Int. Dairy J. 9:481-486(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; A0131674; CAB53387.1; -;
 CC EMBL; AF165879; AAF82241.1; -;
 CC HSSP; O77811; 1B1X.
 CC InterPro; IPR001156; Transferrin.
 CC Pfam; PF00405; transferrin; 2.
 CC PRINTS; PR00422; TRANSFERRIN.
 CC SMART; SM00094; TR_FER; 2.
 CC PROSITE; PS00205; TRANSFERRIN 1; 2.
 CC PROSITE; PS00206; TRANSFERRIN 2; 2.
 CC PROSITE; PS00207; TRANSFERRIN 3; 2.
 CC Transprot; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 708 LACTOTRANSFERRIN.
 FT REPEAT 20 363 1.
 FT REPEAT 364 708 2.
 FT DISULFID 28 64 BY SIMILARITY.
 FT DISULFID 38 55 BY SIMILARITY.
 FT DISULFID 134 217 BY SIMILARITY.
 FT DISULFID 176 192 BY SIMILARITY.
 FT DISULFID 189 200 BY SIMILARITY.
 FT DISULFID 250 264 BY SIMILARITY.
 FT DISULFID 367 399 BY SIMILARITY.
 FT DISULFID 377 390 BY SIMILARITY.
 FT DISULFID 424 703 BY SIMILARITY.
 FT DISULFID 444 666 BY SIMILARITY.
 FT DISULFID 476 551 BY SIMILARITY.
 FT DISULFID 500 694 BY SIMILARITY.
 FT DISULFID 510 524 BY SIMILARITY.
 FT DISULFID 521 534 BY SIMILARITY.
 FT DISULFID 592 606 BY SIMILARITY.
 FT DISULFID 644 649 BY SIMILARITY.
 FT METAL 79 79 IRON 1 (BY SIMILARITY).
 FT METAL 111 111 IRON 1 (BY SIMILARITY).
 FT METAL 211 211 IRON 1 (BY SIMILARITY).
 FT METAL 272 272 IRON 1 (BY SIMILARITY).
 FT METAL 414 414 IRON 2 (BY SIMILARITY).
 FT METAL 452 452 IRON 2 (BY SIMILARITY).
 FT METAL 545 545 IRON 2 (BY SIMILARITY).
 FT METAL 614 614 IRON 2 (BY SIMILARITY).
 FT BINDING 140 140 ANION (BY SIMILARITY).
 FT BINDING 482 482 ANION (BY SIMILARITY).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 261 261 F -> S (IN REF. 2).
 FT CONFLICT 304 304 G -> A (IN REF. 2).
 FT CONFLICT 330 330 S -> P (IN REF. 2).
 FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).
 FT CONFLICT 506 506 L -> F (IN REF. 2).
 FT CONFLICT 609 609 A -> P (IN REF. 2).
 FT CONFLICT 642 642 R -> Q (IN REF. 2).
 CC SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;
 Query Match 70.4%; Score 50; DS 1; Length 708;
 Best Local Similarity 66.7%; Pred. No. 0.22;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWQRMKXAR 12
 DB 38 CAQWQRMKXAR 49

RESULT 4
 TRFL HORSE
 ID TRFL HORSE STANDARD; PRT; 695 AA.
 AC O77811;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin) (Fragment).
 GN LTF.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "cDNA sequence of mare lactoferrin";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RC TISSUE=Milk;
 RX MEDLINE=9296631; PubMed=10366507;
 RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "Three-dimensional structure of mare diferric lactoferrin at 2.6-A resolution.";
 RL J. Mol. Biol. 289:303-317(1999).
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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 CC -----
 CC EMBL; AJ010930; CAA09407.1; -;
 CC PDB; 1B1X; 02-DEC-98.
 CC PDB; 1B7U; 02-FEB-99.
 CC PDB; 1B7Z; 02-FEB-99.
 CC InterPro; IPR001156; Transferrin.
 CC Pfam; PF00405; transferrin; 2.
 CC PRINTS; PR00422; TRANSFERRIN.
 CC SMART; SM00094; TR_FER; 2.
 CC PROSITE; PS00205; TRANSFERRIN 1; 2.
 CC PROSITE; PS00206; TRANSFERRIN 2; 2.
 CC PROSITE; PS00207; TRANSFERRIN 3; 1.
 CC Transprot; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal; 3D-structure.
 FT SIGNAL 1 1
 FT CHAIN <1 6
 FT CHAIN 7 695 LACTOTRANSFERRIN.
 FT REPEAT 7 350 1.
 FT REPEAT 351 695 2.
 FT DISULFID 15 51
 FT DISULFID 25 42
 FT DISULFID 121 204
 FT DISULFID 163 179
 FT DISULFID 166 189
 FT DISULFID 176 187
 FT DISULFID 237 251
 FT DISULFID 354 385
 FT DISULFID 364 377
 FT DISULFID 411 690
 FT DISULFID 431 653

FT DISULFID 463 538
 FT DISULFID 487 681
 FT DISULFID 497 511
 FT DISULFID 508 521
 FT DISULFID 579 593
 FT DISULFID 631 636
 FT METAL 66 66
 FT METAL 98 98
 FT METAL 198 198
 FT METAL 259 259
 FT METAL 401 401
 FT METAL 439 439
 FT METAL 532 532
 FT METAL 601 601
 FT BINDING 127 127
 FT BINDING 469 469
 FT CARBOHYD 143 143
 FT CARBOHYD 287 287
 FT CARBOHYD 482 482
 SQ SEQUENCE 695 AA; 75991 MW; 07BB84D50E1B165D CRC64;

Query Match 59.2%; Score 42; DB 1; Length 695;
 Best Local Similarity 58.3%; Pred. No. 5.7;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRKAR 12
 : : : : :
 Db 25 CAKFQNRKVR 36

RESULT 5

DYHB_CHLRE
 ID DYHB_CHLRE STANDARD; PRT; 4568 AA.
 AC Q39565;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Dynein beta chain, flagellar outer arm.
 GN ODA4 OR ODA-4 OR SUP1.
 OS Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=21gr;
 RX MEDLINE=94274778; PubMed=8006077;
 RA Mitchell D.R.; Brown K.S.;
 RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes";
 RL J. Cell Sci. 107:635-644(1994).
 CC -!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES. DYNEIN HAS ATPASE ACTIVITY.
 CC -!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
 CC -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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 CC EMBL; U02963; AAA19956.1;
 CC InterPro; IPR004273; Dynein heavy.
 CC Pfam; PF03028; Dynein heavy; 1.
 KW Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
 KW Coiled coil.
 FT DOMAIN 277 293 COILED COIL (POTENTIAL).
 FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).

FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).
 FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
 FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
 FT DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
 FT DOMAIN 2831 2848 COILED COIL (POTENTIAL).
 FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
 FT DOMAIN 3339 3425 COILED COIL (POTENTIAL).
 FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
 FT NP_BIND 1919 1926 ATP (POTENTIAL).
 FT NP_BIND 2202 2209 ATP (POTENTIAL).
 FT NP_BIND 2530 2537 ATP (POTENTIAL).
 FT NP_BIND 2879 2886 ATP (POTENTIAL).
 SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;

Query Match 59.2%; Score 42; DB 1; Length 4568;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRMR 9
 : : : : :
 Db 1852 CFQWQQLR 1860

RESULT 6

TRFL_MOUSE
 ID TRFL_MOUSE STANDARD; PRT; 707 AA.
 AC P08071; P70690; O61799; Q922P2;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RX MEDLINE=87280033; PubMed=3611056;
 RA Pentecost B.T.; Teng C.T.;
 RT "Lactotransferrin is the major estrogen inducible protein of mouse uterine secretions";
 RL J. Biol. Chem. 262:10134-10139(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA Moriishi K.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-14 FROM N.A.
 RX MEDLINE=92042099; PubMed=1939212;
 RA Liu Y.; Teng C.T.;
 RT "Characterization of estrogen-responsive mouse lactoferrin promoter";
 RL J. Biol. Chem. 266:21880-21885(1991).
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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CC EMBL; J03298; AAA40525.1; -
CC EMBL; D88510; BAA13633.1; -
CC EMBL; BC006904; AAH08904.1; -
CC EMBL; M74778; AAA39427.1; -
CC FIR; A28438; A28438.
CC HSSP; P02788; 1CB6.
CC MGD; MGI:96837; Ltf.
CC InterPro; IPR001156; Transferrin.
CC Pfam; PF00405; transferrin; 2.
CC PRINTS; PR00422; TRANSFERRIN.
CC SMART; SM00094; TR FER; 2.
CC PROSITE; PS00205; TRANSFERRIN_1; 1.
CC PROSITE; PS00206; TRANSFERRIN_2; 2.
CC PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 707 LACTOTRANSFERRIN.
FT REPEAT 20 357 1.
FT REPEAT 358 707 2.
FT DISULFID 27 63 BY SIMILARITY.
FT DISULFID 37 54 BY SIMILARITY.
FT DISULFID 133 216 BY SIMILARITY.
FT DISULFID 175 191 BY SIMILARITY.
FT DISULFID 188 199 BY SIMILARITY.
FT DISULFID 249 263 BY SIMILARITY.
FT DISULFID 366 398 BY SIMILARITY.
FT DISULFID 376 389 BY SIMILARITY.
FT DISULFID 423 702 BY SIMILARITY.
FT DISULFID 443 665 BY SIMILARITY.
FT DISULFID 475 550 BY SIMILARITY.
FT DISULFID 499 693 BY SIMILARITY.
FT DISULFID 509 523 BY SIMILARITY.
FT DISULFID 520 533 BY SIMILARITY.
FT DISULFID 591 605 BY SIMILARITY.
FT DISULFID 643 648 BY SIMILARITY.
FT METAL 78 78 IRON 1 (BY SIMILARITY).
FT METAL 110 110 IRON 1 (BY SIMILARITY).
FT METAL 210 210 IRON 1 (BY SIMILARITY).
FT METAL 271 271 IRON 1 (BY SIMILARITY).
FT METAL 413 413 IRON 2 (BY SIMILARITY).
FT METAL 451 451 IRON 2 (BY SIMILARITY).
FT METAL 544 544 IRON 2 (BY SIMILARITY).
FT METAL 613 613 IRON 2 (BY SIMILARITY).
FT BINDING 139 139 ANION (POTENTIAL).
FT BINDING 481 481 ANION (POTENTIAL).
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 494 494 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 1 2 MR -> IQG (IN REF. 1).
FT CONFLICT 25 25 R -> Q (IN REF. 2).
FT CONFLICT 82 82 M -> L (IN REF. 2).
FT CONFLICT 359 359 S -> T (IN REF. 2).
FT CONFLICT 382 382 A -> D (IN REF. 1).
FT CONFLICT 449 449 E -> G (IN REF. 2).
FT CONFLICT 629 629 L -> V (IN REF. 1).
SQ SEQUENCE 707 AA; 77865 MW; F26AE03404C19A8 CRC64;
Query Match 57.7%; Score 41; DB 1; Length 707;
Best Local Similarity 60.0%; Pred. No. 8.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFQWQNRK 10
DB 37 CLRQWNRK 46
RESULT 7
RPOB_LIBAF STANDARD; PRT; 146 AA.
ID _RPOB_LIBAF
AC P41187;
DT 01-FEB-1995 (Rel. 31, Created)

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DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase
DE beta chain) (RNA polymerase beta subunit) (Fragment).
GN RPOB.
OS Liberibacter africanus (Liberibacter africanus).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Candidatus Liberibacter.
OX NCBI_TaxID=34020;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-Nelspruit;
RA Planet P.; Jagoueix S.; Bove J.M.; Garnier M.;
RT "Detection and characterization of the African citrus Greening
RT Liberibacter by amplification, cloning and sequencing of the rplKJL-
RT rpoBC operon.";
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
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CC or send an email to license@sib-sib.ch).
CC EMBL; U09675; AAA1957.1; -
CC InterPro; IPR001572; RNA_pol_B.
CC Pfam; PF00562; RNA_pol_B_1.
CC PROSITE; PS01166; RNA_POL_BETA; PARTIAL.
KW Transferase; Transcription; DNA-directed RNA polymerase.
FT NON TER 146 146
SQ SEQUENCE 146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
Query Match 53.5%; Score 38; DB 1; Length 146;
Best Local Similarity 60.0%; Pred. No. 5.8;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CFQWQNRK 10
DB 10 CVQWSRGARK 19
RESULT 8
ID IL2A_BOVIN STANDARD; PRT; 275 AA.
AC P12342;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
DE subunit) (P55) (TAC antigen) (CD25).
GN IL2RA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=8212503; PubMed=2835311;
RA Weinberg A.D.; Shaw J.; Paetkau V.; Bleackley R.C.; Magnuson N.S.;
RA Reeves R.; Magnuson J.A.;
RT "Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";

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Immunology 63:603-610 (1988).

SEQUENCE OF 1-21 FROM N.A.

RA Yoo J., de Leon P.A., Stone R.T., Beattie C.W.;
"Cloning and chromosomal assignment of the bovine interleukin-2
receptor alpha (IL-2R alpha) gene";
Mamm. Genome 6:751-753 (1995).

CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
WITH A GAMMA CHAIN.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.

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EMBL; M20818; AAC51414.1; -;
EMBL; U24226; AAC48487.1; -;
PIR; S07442; S07442.
HSP; P01589; IILM.
Pfam; PF00084; sushi; 2.
SMART; SM00032; CCP; 2.
Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
SIGNAL 1 21
CHAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).
TRANSMEM 244 262 POTENTIAL.
DOMAIN 263 275 CYTOPLASMIC (POTENTIAL).
DOMAIN 223 78 SUSHI 1.
DOMAIN 122 185 SUSHI 2.
DISULFID 24 64 BY SIMILARITY.
DISULFID 751 77 BY SIMILARITY.
DISULFID 123 168 BY SIMILARITY.
DISULFID 152 184 BY SIMILARITY.
CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 275 AA; 31238 MW; 4901BBFP9A4862390 CRC64;

Query Match 53.5%; Score 38; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQNRKAR 12
Db 261 CLTWQRWKKR 272

RESULT 9
IL2A-SHEEP STANDARD; PRT; 275 AA.
AC P26898;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
subunit) (P55) (TAC antigen) (CD25).
GN IL2RA.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID:9940;
RN [1]

SEQUENCE FROM N.A.

RP TISSUE-T-cell;
RA Verhagen A.A.;
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
[2]

SEQUENCE FROM N.A.

RX MEDLINE=92241682; PubMed=1572550;
RA Bujdoso R., Sargan D.R., Williams M.L., McConnell I.;
RT "Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa
protein, CD25.";
RL Genes 113:283-284 (1992).

CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
WITH A GAMMA CHAIN.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.

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EMBL; Z11560; CAA77652.1; -;
EMBL; X60149; CAA42723.1; -;
EMBL; A19167; CAA01447.1; -;
PIR; S18910; S18910.
PIR; S18899; S18899.
PIR; JC1113; JC1113.
HSP; P01589; IILM.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00084; sushi; 2.
SMART; SM00032; CCP; 2.
Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
SIGNAL 1 21
CHAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).
TRANSMEM 244 262 POTENTIAL.
DOMAIN 263 275 CYTOPLASMIC (POTENTIAL).
DOMAIN 223 78 SUSHI 1.
DOMAIN 122 185 SUSHI 2.
DISULFID 24 64 BY SIMILARITY.
DISULFID 751 77 BY SIMILARITY.
DISULFID 123 168 BY SIMILARITY.
DISULFID 152 184 BY SIMILARITY.
CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
CONFLICT 166 166 S -> T (IN REF. 2).
SEQUENCE 275 AA; 30904 MW; 1101A2DE5AC5A088 CRC64;

Query Match 53.5%; Score 38; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQNRKAR 12
Db 261 CLTWQRWKKR 272

RESULT 10
FTSA HAEIN STANDARD; PRT; 425 AA.
AC P45068;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cell division protein ftSa.
GN FTSA OR Hll42.
OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kervatage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA Scott J.D., Shirley R., Litz G., Fitchum W., Fields C.A., Gocayne J.D.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd.";
 RL Science 269:496-512(1995).
 CC -1- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN ANOMALOUS FILAMENT
 CC GROWTH (BY SIMILARITY). MAY BE A COMPONENT OF THE SEPTUM. IT
 CC MAY INTERACT WITH FTSZ (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FTSZ/MREB FAMILY.
 CC -----
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 CC -----
 CC EMBL; U32794; AAC22797.1; -;
 DR TIGR; H11142; -;
 DR InterPro; IPR003494; FtsA.
 DR Pfam; PF02491; FtsA; 2.
 DR TIGRFAMs; TIGR01174; ftsA; 1.
 DR Cell division; Cell shape; Complete proteome.
 KW SQ SEQUENCE 425 AA; 45836 MW; AF5C4B808D73CE9D CRC64;
 SQ
 Query Match 52.8%; Score 37.5; DB 1; Length 425;
 Best Local Similarity 58.3%; Pred. No. 21;
 Matches 7; Conservative 2; Mismatches 1; Gaps 1;
 QY 1 CFQ-WQRMKKA 11
 DB 163 CHQDQNNLKA 174

 RESULT 11
 IL2A_HUMAN STANDARD; PRT; 272 AA.
 AC P01589;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
 DE subunit) (P55) (TAC antigen) (CD25 antigen).
 GN IL2RA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=85012734; PubMed=6090949;
 RA Nishida T., Shimizu A., Ishida N., Sabe H., Teshigawara K., Maeda M.,
 RA Uchiyama T., Yodoi J., Honjo T.;
 RT "Molecular cloning of cDNA encoding human interleukin-2 receptor.";
 RL Nature 311:631-635 (1984).
 [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=85012733; PubMed=6090948;
 RA Leonard W.J., Depper J.M., Crabtree G.R., Rudikoff S., Pumphrey J.,
 RA Robb R.J., Kroenke M., Svetlik P.B., Peffer N.J., Waldmann T.A.,
 RA Greene W.C.;
 RT "Molecular cloning and expression of cDNAs for the human
 RT interleukin-2 receptor.";
 RL Nature 311:626-631(1984).
 [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=86067183; PubMed=2999698;
 RA Ishida N., Kanamori H., Noma T., Nishida T., Sabe H., Suzuki N.,
 RA Shimizu A., Honjo T.;
 RT "Molecular cloning and structure of the human interleukin 2 receptor
 RT gene.";
 RL Nucleic Acids Res. 13:7579-7589(1985).
 [4]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=86018868; PubMed=2996141;
 RA Leonard W.J., Depper J.M., Kanehisa M., Kroenke M., Peffer N.J.,
 RA Svetlik P.B., Sullivan M., Greene W.C.;
 RT "Structure of the human interleukin-2 receptor gene.";
 RL Science 230:633-639(1985).
 [5]
 RN SEQUENCE OF 1-21 FROM N.A.
 RX MEDLINE=87159546; PubMed=3030566;
 RA Cross S.L., Feinberg M.B., Wolf J.B., Holbrook N.J., Wong-Stall F.,
 RA Leonard W.J.;
 RT "Regulation of the human interleukin-2 receptor alpha chain promoter:
 RT activation of a nonfunctional promoter by the transactivator gene of
 RT HTLV-I.";
 RL Cell 49:47-56(1987).
 [6]
 RN 3D-STRUCTURE MODELING OF 23-83.
 RX MEDLINE=95111955; PubMed=7529123;
 RA Bamorough P., Hedgecock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 RT modelling.";
 RL Structure 2:839-851(1994).
 CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
 CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
 CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
 CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
 CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
 CC WITH A GAMMA CHAIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD25 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd25.htm".
 CC -----
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 CC -----
 CC EMBL; X01057; CAA25525.1; -;
 DR EMBL; X03131; CAA26906.1; -;
 DR EMBL; X03132; CAA26906.1; JOINED.
 DR EMBL; X03133; CAA26906.1; JOINED.
 DR EMBL; X03134; CAA26906.1; JOINED.
 DR EMBL; X03135; CAA26906.1; JOINED.
 DR EMBL; X03136; CAA26906.1; JOINED.
 DR EMBL; X03137; CAA26906.1; JOINED.
 DR EMBL; X03138; CAA26906.1; JOINED.
 DR EMBL; X03122; AAB59535.1; -;
 DR EMBL; M1066; AAA67527.1; -;
 DR EMBL; M10222; AAA67527.1; JOINED.
 DR EMBL; M1060; AAA67527.1; JOINED.
 DR EMBL; M1061; AAA67527.1; JOINED.
 DR EMBL; M1062; AAA67527.1; JOINED.
 DR EMBL; M1063; AAA67527.1; JOINED.
 DR EMBL; M1064; AAA67527.1; JOINED.

DR EMBL; M11065; AAA67527.1; JOINED.
 DR EMBL; M15864; AAA59162.1; -.
 DR PIR; A01856; UHHU2.
 DR PIR; A24113; A24113.
 DR PIR; A44186; A44186.
 DR PDB; 1ILM; 26-JAN-95.
 DR PDB; 1ILN; 28-JAN-95.
 DR Genew; HGNC:6008; IL2RA.
 DR MIM; 147730; -.
 DR MIM; 606367; -.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00084; sushi; 2.
 DR SMART; SM00032; CCP; 2.
 KW Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi;
 3D-structure.
 FT SIGNAL 1 21
 FT CHAIN 22 272
 FT DOMAIN 22 240
 FT TRANSMEM 241 259
 FT DOMAIN 260 272
 FT DOMAIN 23 81
 FT DOMAIN 124 185
 FT DISULFID 24 67
 FT DISULFID 751 80
 FT DISULFID 125 168
 FT DISULFID 152 184
 FT CARBOHYD 70 70
 FT CARBOHYD 89 89
 SQ SEQUENCE 272 AA; 30819 MW; 83D907C8B1D2C0E CRC64;
 Query Match 52.1%; Score 37; DB 1; Length 272;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 WQRNRKAR 12
 DB 261 WQRNRKAR 269
 RESULT 12
 ID NL4 DROME STANDARD; PRT; 292 AA.
 AC Q9XZL8; Q9V391;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 18-OCT-2001 (Rel. 40, Last annotation update)
 DE Nebula protein.
 GN NL4 OR CG6072.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McCormick A.V., Goldberg M.L.;
 RT "Gene required for elongation of meiosis I spindle in Drosophila females.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu P., Beeson P.V., Bhandari D., Boleslavsky E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mervulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson X.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC - FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
 CC - SIMILARITY: BELONGS TO THE DSCR1 FAMILY.
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 DR EMBL; AF147700; AAD33987.1; -.
 DR EMBL; AE003712; AAF5285.1; -.
 DR FlyBase; FBgn026629; nla
 SQ SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;
 Query Match 52.1%; Score 37; DB 1; Length 292;
 Best Local Similarity 54.5%; Pred. No. 18;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FQWRNRKAR 12
 DB 150 FQWRNRKAR 160
 RESULT 13
 ID BUB2_YEAST STANDARD; PRT; 306 AA.
 AC P28448;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 15-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitotic check point protein BUB2 (Cell cycle arrest protein BUB2).
 GN BUB2 OR YMR055C OR YMR796.08C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=91330299; PubMed=16511171;
 RA Hoyt M.A., Totis L., Roberts B.T.;
 RA "S. cerevisiae genes required for cell cycle arrest in response to
 RT loss of microtubule function.";

```

Cell 66:507-517(1991).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=8289c / AB972;
RC Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A.;
RA Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
[3]
RN CHARACTERIZATION.
RP MEDLINE=21385309; PubMed=11493673;
RA Lee S.E., Jensen S., Frenz L.M., Johnson A.L., Fesquet D.,
RA Johnston L.H.;
RT "The Bub2-dependent mitotic pathway in yeast acts every cell cycle and
RT regulates cytokinesis.";
RL J. Cell Sci. 114:2345-2354(2001).
CC -!- FUNCTION: Part of a checkpoint which monitors spindle integrity
CC and prevents premature exit from mitosis. This cell-cycle arrest
CC depends upon inhibition of the G-protein Tem1 by the BFA1/BUB2
CC complex.
CC -!- SUBUNIT: Interacts with BFA1.
CC -!- SUBCELLULAR LOCATION: Spindle poles.
CC -!- SIMILARITY: TO S.POMBE CDC16.
CC
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CC
CC EMBL; M64706; AAA16885.1; -.
CC DR EMBL; Z49703; CAA89785.1; -.
CC DR PIR; A39654; A39654.
CC DR SGD; S0004659; BUB2.
CC DR InterPro; IPR000195; RadCAP_TBC.
CC DR Pfam; PF00566; TBC; 1.
CC DR SMART; SM00164; TBC; 1.
CC KW Cell cycle; Mitosis.
CC SQ SEQUENCE 306 AA; 35027 MW; ALDDBFB549E81EA3 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 306;
Best Local Similarity 41.7%; Pred. No. 19;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQNRKAR 12
+ + + + +
Db 108 CFAWQQRQK 119
+ + + + +

RESULT 14
ID YKYL CAEEL STANDARD; PRT; 455 AA.
AC Q19910;
DT 16-OCT-2001 (Rel. 40, Created)
DT 18-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein F30B5.4 in chromosome IV.
GN F30B5.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Ploloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RA Miller N., Bradshaw H.;
RA Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
[2]
RN REVISIONS.
RA Waterston R.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE OKL38 FAMILY.
CC
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CC
CC EMBL; Z28622; CAA82262.1; -.
CC DR FlyBase; FBgn0004698; mus210.
CC DR InterPro; IPR004583; Rad4.
CC DR TIGRFAMs; TIGR00605; rad4; 1.
CC KW DNA repair; DNA-binding; Nuclear protein.
CC FT DOMAIN 33 40 POLY-ASP.
CC FT DOMAIN 632 637 POLY-SER.
CC FT DOMAIN 686 693 POLY-SER.
CC
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CC
CC EMBL; U42437; AAA83493.2; -.
CC DR WormPep; F30B5.4; CE28552.
CC KW Hypothetical protein.
CC SQ SEQUENCE 455 AA; 51148 MW; D8E6909408FD6C69 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 455;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNRK 10
+ + + + +
Db 102 CIQWELNRR 111
+ + + + +

RESULT 15
ID XPC DROME STANDARD; PRT; 1293 AA.
AC Q24595;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-repair protein complementing XP-C cells homolog (Xeroderma
DE pigmentosum group C complementing protein homolog) (XPCDM) (Mutagen-
DE sensitive 209 protein).
GN MUS210 OR XPC OR XPC.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophilla.
OX NCBI_TaxID=7227;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=DP CN BW; TISSUE=Embryo;
RC MEDLINE=94173663; PubMed=8127661;
RA Henning K.A., Peterson C., Legerski R., Friedberg E.C.;
RT "Cloning the Drosophila homolog of the Xeroderma pigmentosum
RT complementation group C gene reveals homology between the predicted
RT human and Drosophila polypeptides and that encoded by the yeast RAD4
RT gene.";
RL Nucleic Acids Res. 22:257-261(1994).
CC -!- FUNCTION: INVOLVED IN DNA EXCISION REPAIR. MAY PLAY A PART IN DNA
CC DAMAGE RECOGNITION AND/OR IN ALTERING CHROMATIN STRUCTURE TO
CC ALLOW ACCESS BY DAMAGE-PROCESSING ENZYMES (BY SIMILARITY).
CC -!- FUNCTION: INVOLVED IN NUCLEOTIDE EXCISION REPAIR OF DNA DAMAGED
CC WITH UV LIGHT, BULKY ADDUCTS, OR CROSS-LINKING AGENTS.
CC -!- SUBUNIT: HETERODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: TO YEAST RAD4 AND MAMMALIAN XPC.
CC
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CC
CC EMBL; Z28622; CAA82262.1; -.
CC DR FlyBase; FBgn0004698; mus210.
CC DR InterPro; IPR004583; Rad4.
CC DR TIGRFAMs; TIGR00605; rad4; 1.
CC KW DNA repair; DNA-binding; Nuclear protein.
CC FT DOMAIN 33 40 POLY-ASP.
CC FT DOMAIN 632 637 POLY-SER.
CC FT DOMAIN 686 693 POLY-SER.
CC

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FT DOMAIN 922 938 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 1195 1211 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 1275 1291 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 1293 AA; 144177 MW; 99DF671F9A4151C5 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 1293;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 CFOWGRNMRKAR 12

DB 1016 CASWSTTVRKAR 1027

Search completed: February 21, 2003, 07:27:53
Job time : 5.6 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds
(without alignments)
118.873 Million cell updates/sec

Title: US-09-743-107b-78

Perfect score: 71

Sequence: 1 CFQWQNNRKR 12

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	87.3	711	4 Q8TCD2	Q8tcd2 homo sapien
2	58	81.7	38	4 Q9UCV5	Q9ucv5 homo sapien
3	50	70.4	33	6 Q9TR80	Q9tr80 ovis aries
4	44	62.0	279	16 Q8XSE2	Q8xse2 ralestonia s
5	43	60.6	298	16 Q8YF77	Q8yf77 anabaena sp
6	41	57.7	148	10 Q9XHP1	Q9xhp1 sesamum ind
7	41	57.7	222	16 P96876	P96876 mycobacteri
8	41	57.7	275	5 Q93780	Q93780 caenorhabdi
9	40	56.3	108	9 Q8SC55	Q8sc55 stx2 conver
10	40	56.3	373	16 Q9RJP2	Q9rjp2 streptomyce
11	40	56.3	469	9 Q38115	Q38115 bacterioph
12	40	56.3	584	17 Q9HPA3	Q9hpa3 halobacteri
13	40	56.3	647	3 Q93843	Q93843 emericella
14	40	56.3	2348	5 Q9V346	Q9v346 drosophila
15	39	54.9	105	10 Q9XFD5	Q9xdf5 oryza sativ
16	39	54.9	121	10 Q9LTD4	Q9ltd4 arabidopsis

17	39	54.9	306	4 Q8TAX2	Q8tax2 homo sapien
18	39	54.9	372	10 Q81653	Q81653 hemerocalli
19	39	54.9	466	4 Q9NUS2	Q9nus2 homo sapien
20	39	54.9	488	10 Q8S934	Q8s934 diospyros k
21	39	54.9	531	10 Q9LTD4	Q9ltd4 arabidopsis
22	39	54.9	742	5 Q18151	Q18151 caenorhabdi
23	39	54.9	1693	2 Q9F5F7	Q9f5f7 agrobacteri
24	39	54.9	1693	2 Q9R6L2	Q9r6l2 agrobacteri
25	39	54.9	1693	16 Q8U634	Q8u634 agrobacteri
26	38	53.5	191	15 Q77857	Q77857 human immun
27	38	53.5	165	7 Q78039	Q78039 triakis scy
28	38	53.5	205	8 Q98RR2	Q98rr2 guillardia
29	38	53.5	341	11 Q8R2A4	Q8r2a4 mus musculu
30	38	53.5	343	7 Q46819	Q46819 triakis scy
31	38	53.5	343	7 Q46838	Q46838 triakis scy
32	38	53.5	343	7 Q46886	Q46886 triakis scy
33	38	53.5	397	16 Q9XAX9	Q9xax9 streptomyce
34	38	53.5	464	16 Q8Y9P5	Q8y9p5 anabaena sp
35	38	53.5	511	16 Q8Z462	Q8z462 salmonella
36	38	53.5	515	10 Q22185	Q22185 arabidopsis
37	38	53.5	543	10 Q22188	Q22188 arabidopsis
38	38	53.5	2186	5 Q9N906	Q9n906 trypanosoma
39	37	52.1	169	4 Q9BWJ9	Q9bwj9 homo sapien
40	37	52.1	273	2 Q31090	Q31090 rhizobium l
41	37	52.1	274	4 Q96M21	Q96m21 homo sapien
42	37	52.1	331	10 Q9XEU4	Q9xeu4 oryza sativ
43	37	52.1	363	5 Q8SX19	Q8sxi9 drosophila
44	37	52.1	367	16 Q8UCR7	Q8ucr7 agrobacteri
45	37	52.1	393	10 Q9ZTP0	Q9ztp0 oryza sativ

ALIGNMENTS

RESULT 1

Q8TCD2	PRELIMINARY;	PRT;	711 AA.
ID Q8TCD2	DT 01-JUN-2002 (TREMREL. 21, Created)		
AC Q8TCD2	DT 01-JUN-2002 (TREMREL. 21, Last sequence update)		
DT 01-JUN-2002 (TREMREL. 21, Last sequence update)	DE Lactotransferrin.		
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=PROSTATE;			
RA Strausberg R.;			
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
DR EMBL; BC022347; AAH22347.1; -.			
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;			

Query Match 87.3%; Score 62; DB 4; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 CFQWQNNRKR 10
Db	39 CFQWQNNRKR 48

RESULT 2

Q9UCV5	PRELIMINARY;	PRT;	38 AA.
ID Q9UCV5	DT 01-MAY-2000 (TREMREL. 13, Created)		
AC Q9UCV5	DT 01-MAY-2000 (TREMREL. 13, Last sequence update)		
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)	DE Lactoferrin homolog (Fragment).		
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96081613; PubMed=8551695;
RX Sato I.;
RT "Characterization of the 84-kDa protein with ABH activity in human
  seminal plasma.";
RL Jpn. J. Legal Med. 49:281-293(1995).
DR HSP; P02788; IBA.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDBE CRC64;

Query Match 81.7%; Score 58; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.0011; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 2 FQWQNRKAR 12
|:|:|:|:|:|:|
DB 21 FQWQNRKVR 31

RESULT 3
Q9TR80 PRELIMINARY; PRT; 33 AA.
AC Q9TR80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Lactoferrin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=95127729; PubMed=7827104;
RA Qian Z.Y., Jollis P., Migliore-Samou D., Fiat A.M.;
RL Biochim. Biophys. Acta 1243:25-32(1995).
DR HSP; O77696; ICE2.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 70.4%; Score 50; DB 6; Length 33;
Best Local Similarity 70.0%; Pred. No. 0.028; 1; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 1;

QY 1 CFQWQNRK 10
|:|:|:|:|
DB 19 CYQWQKMRK 28

RESULT 4
Q8XSE2 PRELIMINARY; PRT; 279 AA.
AC Q8XSE2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative ICC protein homolog.
GN ICC OR RSP0534 OR RS00414.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;

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RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
  Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
  Chandler M., Choisme N., Claudel-Renard C., Cumac S., Demange N.,
  Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
  Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,
  RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:457-502(2002).
DR EMBL; AL646079; CA017685.1; -.
DR InterPro; IPR004843; M-peptidase.
DR Pfam; PF00149; Metallophos; 1.
KW Plasmid; Complete proteome.
SQ SEQUENCE 279 AA; 31541 MW; ABB38818004B2EDA CRC64;

Query Match 62.0%; Score 44; DB 16; Length 279;
Best Local Similarity 50.0%; Pred. No. 3.5; 3; Indels 0; Gaps 0;
Matches 6; Conservative 3; Mismatches 3;

QY 1 CFQWQNRKAR 12
|:|:|:|:|:|
DB 244 CFQWQNRKAR 255

RESULT 5
Q8YP77 PRELIMINARY; PRT; 298 AA.
AC Q8YP77;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Alr4323.
GN Alr4323.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
  Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
  Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
  Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
  Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
  cyanobacterium Anabaena sp. strain PCC 7120.";
DL DNA Res. 8:205-213(2001).
DR EMBL; AP003596; BAB76022.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 298 AA; 34513 MW; 64036B552299A9F CRC64;

Query Match 60.6%; Score 43; DB 16; Length 298;
Best Local Similarity 70.0%; Pred. No. 5.8; 2; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 2;

QY 2 FQWQNRK 11
|:|:|:|:|:|
DB 163 FQWQNRK 172

RESULT 6
Q8XHP1 PRELIMINARY; PRT; 148 AA.
AC Q8XHP1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 2S albumin.
OS Sesamum indicum (Oriental sesame) (Gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
OX NCBI_TaxID=4182;

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RN  SEQUENCE FROM N.A.
RC  STRAIN=TAINAN 1;
RX  MEDLINE=20074970; PubMed=10606554;
RA  Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;
RT  "Molecular cloning of IIS globulin and 2S albumin, the two major seed
RT  storage proteins in sesame.";
RL  J. Agric. Food Chem. 47:4932-4938 (1999).
DR  EMBL; AF091841; AAD42943.1; -.
DR  InterPro; IPR003612; AAI.
DR  InterPro; IPR001768; Try/amy1_inhtr.
DR  Pfam; PF00234; tryp_alpha_amy1; 1.
DR  PRINTS; PR00496; NAPIIN.
DR  SMART; SM00499; AAI; 1.
SQ  SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;

Query Match 57.7%; Score 41; DB 10; Length 148;
Best Local Similarity 66.7%; Pred. No. 6.3;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 CFQWQNRMR 9
Db  54 CFQWQNRMR 62

RESULT 7
ID  P96876 PRELIMINARY; PRT; 222 AA.
AC  P96876;
DT  01-MAY-1997 (TrEMBLrel. 03, Created)
DT  01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE  Hypothetical protein RV3271c.
GN  RV3271c OR MTCY71.11C OR MT3371.
OS  Mycobacterium tuberculosis.
OC  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC  Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX  NCBI_TaxID=1773;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=H37RV;
RX  MEDLINE=98295987; PubMed=9634230;
RA  Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA  Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA  Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA  Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtrold S.,
RA  Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA  Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA  Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA  Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT  "Deciphering the biology of Mycobacterium tuberculosis from the
RT  complete genome sequence.";
RL  Nature 393:537-544 (1998).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CDC 1551 / OSHKOSH;
RA  Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA  Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA  Kolonay J.F., Nelson W.C., Unayai L.A., Ermolaeva M.D., Salzberg S.L.,
RA  Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA  Bishai W.;
RT  "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT  laboratory strains.";
RL  Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; Z92771; CAB07084.1; -.
DR  EMBL; AE007146; AAK47712.1; -.
DR  TIGR; MT3371; -.
DR  Tuberculist; Rv3271c; -.
KW  Hypothetical protein; Complete proteome.
SQ  SEQUENCE 222 AA; 23633 MW; B9714287801D44FB CRC64;

Query Match 57.7%; Score 41; DB 16; Length 222;

Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  3 QWQNRMRKAR 12
Db  24 QWQNRMRKAR 33

RESULT 8
ID  Q93780 PRELIMINARY; PRT; 275 AA.
AC  Q93780;
DT  01-FEB-1997 (TrEMBLrel. 02, Created)
DT  01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  F53H4.4 protein.
GN  F53H4.4.
OS  Caenorhabditis elegans.
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC  Rhabditidae; Peloderinae; Caenorhabditis.
OX  NCBI_TaxID=6239;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Dobson R.;
RL  Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=99069613; PubMed=9851916;
RA  none;
RT  "Genome sequence of the nematode C.elegans: A platform for
RT  investigating biology.";
RL  Science 282:2012-2018 (1998).
DR  EMBL; Z81089; CAB03137.1; -.
SQ  SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;

Query Match 57.7%; Score 41; DB 5; Length 275;
Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY  2 FQWQNRMRKAR 12
Db  262 FQWQNRMRKTR 272

RESULT 9
ID  Q8SC55 PRELIMINARY; PRT; 108 AA.
AC  Q8SC55;
DT  01-JUN-2002 (TrEMBLrel. 21, Created)
DT  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Hypothetical 12.3 kDa protein.
OS  Stx2 converting bacteriophage I.
OC  Viruses.
OX  NCBI_TaxID=180816;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=STX2 PHAGE-I;
RA  Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T.,
RA  Yamasaki S., Takeda Y.;
RT  "Genomic sequence of Shiga toxin 2-converting phage isolated from
RT  Escherichia coli O157:H7 Okayama strain and comparison with other
RT  Shiga toxin 2-converting phages.";
RL  Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF004402; BAB87947.1; -.
KW  Hypothetical protein.
SQ  SEQUENCE 108 AA; 12279 MW; 2FF2B76690C78BA7 CRC64;

Query Match 56.3%; Score 40; DB 9; Length 108;
Best Local Similarity 63.6%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY  1 CFQWQNRMRKA 11

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Db 31 CFQWISDNKA 41

RESULT 10
Q9RJ2P2 PRELIMINARY; PRT; 373 AA.
AC Q9RJ2P2
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein SCO0602.
GN SCO0602 OR SCF55.26.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 MB Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL132991; CAB61296.1; -
DR InterPro; IPR003447; Meth_resist.
DR Pfam; PF02388; FmA; 1.
DR Hypothetical protein.
SQ SEQUENCE 373 AA; 42190 MW; 313D32E99EAEAE58 CRC64;

Query Match 56.3%; Score 40; DB 16; Length 373;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CFQWISDNKA 11
Db 196 QWRNRNKA 204

RESULT 11
Q38115 PRELIMINARY; PRT; 469 AA.
AC Q38115;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

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DE ORE29.
OS Bacteriophage rit.
OC Viruses.
OX NCBI_TaxID=43685;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96332669; PubMed=8730874;
RA Nauta A., Van Sinderen D., Karsens H., Smit E., Venema G., Kok J.;
RT "Inducible gene expression mediated by a repressor-operator system
RT isolated from Lactococcus lactis bacteriophage rit.";
RL Mol. Microbiol. 19:1331-1341(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=96332669; PubMed=8730875;
RA Van Sinderen D., Karsens H., Kok J., Terpstra P., Ruiters M.H.,
RA Venema G., Nauta A.;
RT "Sequence analysis and molecular characterization of the temperate
RT lactococcal bacteriophage rit.";
RL Mol. Microbiol. 19:1343-1355(1996).
DR EMBL; U38906; AAB18704.1; -
SQ SEQUENCE 469 AA; 53160 MW; 1F8E02D4325C6BB9 CRC64;

Query Match 56.3%; Score 40; DB 9; Length 469;
Best Local Similarity 50.0%; Pred. No. 33;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQNRMRK 10
Db 39 CYPWQXNLLK 48

RESULT 12
Q9HPA3 PRELIMINARY; PRT; 584 AA.
AC Q9HPA3
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Vng1732c.
GN VNG1732C.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welter R., Goo Y.A.,
RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005078; AAG19967.1; -
DR InterPro; IPR001646; Speptide_repeat.
DR Pfam; PF00805; Pentapeptide; 2.
KW Complete proteome.
SQ SEQUENCE 584 AA; 65151 MW; 21BF5D5F0486CC6 CRC64;

Query Match 56.3%; Score 40; DB 17; Length 584;
Best Local Similarity 41.7%; Pred. No. 42;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQNRMRK 12
Db 445 CFTWRKDMERK 456

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RESULT 13
O93843 PRELIMINARY; PRT; 647 AA.
AC Q93843;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE GI/S regulator.
GN NIMO.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=5072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R153;
RA James S.W., Prasauckas K.A., Scacheri P.C., Gyax S.E., Matura R.A.,
RA Bullock K.A.;
RT "nimo" gene of Aspergillus nidulans.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF014812; AAD01519.1; -.
SQ SEQUENCE 647 AA; 72842 MW; A84A547CFB3D0EF1 CRC64;

Query Match 56.3%; Score 40; DB 3; Length 647;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QWQRMKKA 11
|||: |||
Db 134 QWQRYHKA 142

RESULT 14
Q9V346 PRELIMINARY; PRT; 2348 AA.
AC Q9V346;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CG8723 protein.
GN CG11198 OR CG8723.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scher S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baau A., Bavendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houson K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusaker D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
CC -!- COFACTOR: BIOTIN (BY SIMILARITY).
DR EMBL; AE003839; AAF59156.1; -.
DR HSSP; P24182; 1DVI.
DR Flybase; FBgn0033246; CG11198.
DR InterPro; IPR001882; Biotin attach.
DR InterPro; IPR000089; Biotin lipovl.
DR InterPro; IPR000022; Carboxyl_trans.
DR InterPro; IPR000901; CPSase.
DR Pfam; PF02785; Biotin_card_C; 1.
DR Pfam; PF00364; Biotin_lipovl; 1.
DR Pfam; PF01039; Carboxyl_trans; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Biotin.
SQ SEQUENCE 2348 AA; 263722 MW; ED7B6FB9976E1CD2 CRC64;

Query Match 56.3%; Score 40; DB 5; Length 2348;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQRMKRAK 12
|||: |||
Db 563 CFQWQRMKRAK 574

RESULT 15
Q9XFD5 PRELIMINARY; PRT; 105 AA.
AC Q9XFD5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome P450 (fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PANICLE;
RA Liu J., Yang J.;
RT "Suppression subtractive hybridization (SSH) identified candidate
genes that are differentially expressed at rice young panicle.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AF140486; AAD29699.1; -.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00866; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 105 AA; 11912 MW; BOEEFCD487E19F9 CRC64;

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Query Match 54.9%; Score 39; DB 10; Length 105;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWRNRK 10
| | | | :
Db 61 CFQWRLGKK 70

Search completed: February 21, 2003, 07:44:33
Job time : 22.8 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds
(without alignments)
56.502 Million cell updates/sec

Title: US-09-743-107B-79
Perfect score: 70
Sequence: 1 CFQWRNMRKVA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 101002.*
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2: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
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20: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Result No.	Score	Query Match	Length DB ID	Description
1	70	100.0	12 21 AAY78079	Human lactoferrin
2	66	94.3	12 21 AAY78038	Human lactoferrin
3	66	94.3	12 21 AAY78046	Human lactoferrin
4	66	94.3	12 21 AAY78047	Human lactoferrin
5	66	94.3	13 21 AAY78037	Human lactoferrin
6	66	94.3	13 21 AAY78048	Human lactoferrin
7	66	94.3	13 21 AAY78049	Human lactoferrin
8	66	94.3	14 21 AAY78036	Human lactoferrin
9	66	94.3	14 21 AAY78050	Human lactoferrin
10	66	94.3	14 21 AAY78051	Human lactoferrin

11	66	94.3	15 17 AAR98554	Peptide for anti-u
12	66	94.3	15 21 AAY78030	Human lactoferrin
13	66	94.3	15 21 AAY78035	Human lactoferrin
14	66	94.3	15 21 AAY78062	Human lactoferrin
15	66	94.3	15 21 AAY78063	Human lactoferrin
16	66	94.3	16 21 AAY78031	Human lactoferrin
17	66	94.3	16 21 AAY78064	Human lactoferrin
18	66	94.3	16 21 AAY78065	Human lactoferrin
19	66	94.3	17 21 AAY78034	Human lactoferrin
20	66	94.3	17 21 AAY78066	Human lactoferrin
21	66	94.3	17 21 AAY78067	Human lactoferrin
22	66	94.3	18 15 AAR69352	Human lactoferrin
23	66	94.3	18 17 AAW13397	Advanced glycosyla
24	66	94.3	18 21 AAY78033	Human lactoferrin
25	66	94.3	19 21 AAY68867	Amino acid sequenc
26	66	94.3	19 21 AAY54486	Peptide used to tr
27	66	94.3	19 21 AAY78032	Human lactoferrin
28	66	94.3	20 13 AAR21810	Anti microbial pep
29	66	94.3	20 14 AAR44841	Lactoferrin-relate
30	66	94.3	20 15 AAR48530	Lactoferrin-derive
31	66	94.3	20 15 AAR48531	Lactoferrin-derive
32	66	94.3	20 15 AAR57461	Lactoferrin-derive
33	66	94.3	20 15 AAR57462	Lactoferrin-derive
34	66	94.3	20 16 AAR84698	Bovine lactoferrin
35	66	94.3	20 16 AAR84699	Lactoferrin
36	66	94.3	20 16 AAR80263	Anti-parasitic lac
37	66	94.3	20 16 AAR80264	Anti-parasitic lac
38	66	94.3	20 17 AAR98553	Peptide for anti-u
39	66	94.3	20 17 AAR91852	Lactoferrin-derive
40	66	94.3	20 17 AAW03045	Lactoferrin-derive
41	66	94.3	20 17 AAR90607	Lactoferrin-derive
42	66	94.3	20 17 AAR87621	Lactoferrin-derive
43	66	94.3	20 17 AAR87622	Lactoferrin-derive
44	66	94.3	20 18 AAR26150	Lactoferrin-derive
45	66	94.3	20 18 AAW14036	Anti-parasitic pep

ALIGNMENTS

RESULT 1
AAY78079
ID AAY78079 standard; Peptide; 12 AA.
XX AC
XX AAY78079;
-- XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:79.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
XX
PN 13-JAN-2000.
XX
PD 06-JUL-1999; 99WO-SE01230.
XX
PF 06-JUL-1998; 98SE-0002441.
XX
PR 06-JUL-1998; 98SE-0002562.
PR 17-JUL-1998; 98SE-0004614.
PR 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
PA
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 PS Claim 22; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infections and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 12 AA;

Query Match 100.0%; Score 70; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKVA 12
 DB 1 CFQWQRMNRKVA 12

RESULT 2

AAAY78038
 ID AAY78038 standard; Peptide; 12 AA.

AC AAY78038;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:38.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

OS Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX

XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infections and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 12 AA;

Query Match 94.3%; Score 66; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.4e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKV 11
 DB 1 CFQWQRMNRKV 11

RESULT 3

AAAY78046

ID AAY78046 standard; Peptide; 12 AA.

XX AAY78046;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:46.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

OS Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

PR 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX

XX Claim 15; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 94.3%; Score 66; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.4e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKV 11
 |||||
 DB 1 CFQWQRNMRKV 11

RESULT 4

AAV78047
 ID AAY78047 standard; Peptide; 12 AA.

XX AC AAY78047;

DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:47.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX OS Homo sapiens.
 OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SB01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX PS Claim 18; Page 73; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations, colitis, and Candida infection on a mucosal
 CC in food stuffs such as infant formula food. The peptides can also be used
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 94.3%; Score 66; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.4e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKV 11
 |||||
 DB 1 CFQWQRNMRKV 11

RESULT 5

AAV78037
 ID AAY78037 standard; Peptide; 13 AA.

XX AC AAY78037;

DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:37.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX OS Homo sapiens.
 OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SB01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX PS Claim 12; Page 70; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations, colitis, and Candida infection on a mucosal
 CC in food stuffs such as infant formula food. The peptides can also be used
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 13 AA;

Query Match 94.3%; Score 66; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFOWQNRKRV 11
 DB 2 CFOWQNRKRV 12

RESULT 6

AAAY78048
 ID AAY78048 standard; Peptide; 13 AA.

XX AAY78048;

AC 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:48.

DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food

PS Claim 15; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

SQ Sequence 13 AA;

Query Match 94.3%; Score 66; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFOWQNRKRV 11

DB 2 CFOWQNRKRV 12

RESULT 7

AAAY78049

ID AAY78049 standard; Peptide; 13 AA.

XX AAY78049;

AC 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:49.

DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food

PS Claim 18; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

SQ Sequence 13 AA;

Query Match 94.3%; Score 66; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFOWQNRKRV 11

DB 2 CFOWQNRKRV 12

RESULT 8

AAAY78036

ID AAY78036 standard; Peptide; 14 AA.

XX AAY78036;

AC 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:36.

XX

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 FN 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 XX inflammations and tumors and for use in infant formula food -
 XX Claim 12; Page 69; 102pp; English.
 PS AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 14 AA;
 SQ Query Match 94.3%; Score 66; DB 21; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.5e-05; Mismatches 0; Gaps 0;
 Matches 11; Conservative 0; Indels 0; Gaps 0;
 QY 1 CFQWQRNMRKV 11
 Db 3 CFQWQRNMRKV 13
 RESULT 9
 ID AAY78050 standard; Peptide; 14 AA.
 AC AAY78050;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:50.
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS

OS Synthetic.
 XX WO200001730-A1.
 PN 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 XX inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 75; 102pp; English.
 PS AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Sequence 14 AA;
 SQ Query Match 94.3%; Score 66; DB 21; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.5e-05; Mismatches 0; Gaps 0;
 Matches 11; Conservative 0; Indels 0; Gaps 0;
 QY 1 CFQWQRNMRKV 11
 Db 3 CFQWQRNMRKV 13
 RESULT 10
 ID AAY78051 standard; Peptide; 14 AA.
 AC AAY78051;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:51.
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 FN 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 PF

XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX PA (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 18; Page 75; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX SQ Sequence 14 AA;
 Query Match 94.3%; Score 66; DB 21; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.5e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CFQWQNRKRV 11
 DB 3 CFQWQNRKRV 13
 RESULT 11
 AAR98554
 ID AAR98554 standard; Peptide; 15 AA.
 XX AC AAR98554;
 XX 12-NOV-1996 (first entry)
 XX Peptide for anti-ulcer agent.
 XX anti-ulcer agent; low toxicity; stable; heat-resistant.
 XX Synthetic.
 XX JP08143468-A.
 XX 04-JUN-1996.
 XX 17-NOV-1994; 94JP-0283869.
 XX 17-NOV-1994; 94JP-0283869.
 XX (MORG) MORINAGA MILK IND CO LTD.
 XX WPI; 1996-318857/32.
 XX Anti-ulcer agent contg. peptide - has low toxicity, is
 PT heat-resistant and water-soluble
 XX Claim 1; Page 11; 11pp; Japanese.
 PS

XX AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
 CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be
 CC administered orally and be produced in large amounts.
 XX SQ Sequence 15 AA;
 Query Match 94.3%; Score 66; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CFQWQNRKRV 11
 DB 2 CFQWQNRKRV 12
 RESULT 12
 AAY78030
 ID AAY78030 standard; Peptide; 15 AA.
 XX AC AAY78030;
 XX 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:30.
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX OS Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 11; Page 67; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX SQ Sequence 15 AA;

Query Match 94.3%; Score 66; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFQWQNRKRV 11
 DB 5 CFQWQNRKRV 15

RESULT 13

AAV78035
 ID AAV78035 standard; Peptide; 15 AA.

XX AAV78035;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:35.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

OS Homo sapiens.

OS Synthetic.

FN WO200001730-A1.

XX 13-JAN-2000.

PF 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCII-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food

PS Claim 12; Page 69; 102pp; English.

XX AAV78001 to AAV78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations, colitis, and Candida infection on a mucosal
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 15 AA;

Query Match 94.3%; Score 66; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFQWQNRKRV 11
 DB 4 CFQWQNRKRV 14

RESULT 14

AAV78062
 ID AAV78062 standard; Peptide; 15 AA.

XX AAV78062;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:62.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

OS Homo sapiens.

OS Synthetic.

PN WO200001730-A1.

XX 13-JAN-2000.

PF 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCII-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food

PS Claim 15; Page 81; 102pp; English.

XX AAV78001 to AAV78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations, colitis, and Candida infection on a mucosal
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 15 AA;

Query Match 94.3%; Score 66; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFQWQNRKRV 11
 DB 4 CFQWQNRKRV 14

RESULT 15

AAV78063
 ID AAV78063 standard; Peptide; 15 AA.

XX AAV78063;

AC AAV78063;

XX 25-APR-2000 (first entry)
DT Human lactoferrin derived peptide SEQ ID NO:63.
DE
XX Human, lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCII-) A+ SCI INVEST AB.
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
PS Claim 18; Page 81; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX Sequence 15 AA;
SQ

Query Match 94.3%; Score 66; DB 21; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFQWQNNRKV 11
| | | | |
Db 4 CFQWQNNRKV 14

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